

(19) World Intellectual Property  
Organization  
International Bureau



(43) International Publication Date  
27 May 2004 (27.05.2004)

PCT

(10) International Publication Number  
**WO 2004/044839 A2**

(51) International Patent Classification<sup>7</sup>: **G06N 3/12**

(21) International Application Number:  
PCT/US2002/038216

(22) International Filing Date:  
12 November 2002 (12.11.2002)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:  
60/424,715 8 November 2002 (08.11.2002) US

(71) Applicant: **DUKE UNIVERSITY** [US/US]; University  
Office of Science and Technology, Davidson Building,  
Room 454, DUMC 3664, Durham, NC 27710 (US).

(72) Inventors: **WEST, Mike**; Beaver Pl., Durham, NC 27705  
(US). **NEVIUS, Joseph**; 100 York Place, Chapel Hill, NC  
27514 (US).

(74) Agent: **SITLANI, Sanjay**; Ropes & Gray, 1900 K Street,  
NM, Suite 750, Washington, DC 20006 (US).

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU,  
AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU,  
CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,  
GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC,  
LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW,  
MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE,  
SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ,  
VC, VN, YU, ZA, ZM, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM,  
KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW),  
Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM),  
European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE,  
ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK,  
TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ,  
GW, ML, MR, NE, SN, TD, TG).

**Published:**

— with declaration under Article 17(2)(a); without abstract;  
title not checked by the International Searching Authority

*For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.*

(54) Title: PREDICTION OF ESTROGEN RECEPTOR STATUS OF BREST TUMORS USING BINARY PREDICTION TREE MODELING

(57) Abstract:



**WO 2004/044839 A2**

## PREDICTION OF ESTROGEN RECEPTOR STATUS OF BREST TUMORS USING BINARY PREDICTION TREE MODELING

### FIELD OF THE INVENTION

- 5 The field of this invention is the application of classification tree models incorporating Bayesian analysis to the statistical prediction of binary outcomes where the binary outcome is estrogen receptor status.

### BACKGROUND OF THE INVENTION

- 10 Bayesian analysis is an approach to statistical analysis that is based on the Bayes's law, which states that the posterior probability of a parameter  $p$  is proportional to the prior probability of parameter  $p$  multiplied by the likelihood of  $p$  derived from the data collected. This increasingly popular methodology represents an alternative to the traditional (or frequentist probability) approach:
- 15 whereas the latter attempts to establish confidence intervals around parameters, and/or falsify a-priori null-hypotheses, the Bayesian approach attempts to keep track of how a-priori expectations about some phenomenon of interest can be refined, and how observed data can be integrated with such a-priori beliefs, to arrive at updated posterior expectations about the phenomenon.
- 20 Bayesian analysis have been applied to numerous statistical models to predict outcomes of events based on available data. These include standard regression models, e.g. binary regression models, as well as to more complex models that are applicable to multi-variate and essentially non-linear data. Another such model is commonly known as the tree model which is essentially based on a
- 25 decision tree. Decision trees can be used in clarification, prediction and regression. A decision tree model is built starting with a root mode, and training data partitioned to what are essentially the "children" modes using a splitting rule. For instance, for clarification, training data contains sample vectors that have one or more measurement variables and one variable that determines that class of the
- 30 sample. Various splitting rules have been used; however, the success of the

predictive ability varies considerably as data sets become larger. Furthermore, past attempts at determining the best splitting for each node is often based on a "purity" function calculated from the data, where the data is considered pure when it contains data samples only from one class. Most frequently, used purity functions are entropy, gini-index, and towsing rule. The success of each of these tree models varies considerably and their applicability to complex biological and molecular data is often prone to difficulties. Thus, there is a need for a statistical model that can consistently deliver accurate results with high predictive capabilities. The present invention describes a statistical predictive tree model to which Bayesian analysis is applied incorporating several key innovations described herewith.

#### SUMMARY OF THE INVENTION

This invention discusses the generation and exploration of classification tree models, with particular interest in problems involving many predictors. Problems involving multiple predictors arise in situations where the prediction of an outcome is dependent on the interaction of numerous factors (predictors), such as the prediction of clinical or physiological states using various forms of molecular data. One motivating application is molecular phenotyping using gene expression and other forms of molecular data as predictors of a clinical or physiological state.

The invention addresses the specific context of a binary response  $Z$  and many predictors  $x_i$ ; in which the data arises via case-control design, *i.e.*, the numbers of 0/1 values in the response data are fixed by design. This allows for the successful relation of large-scale gene expression data (the predictors) to binary outcomes, such as a risk group or disease state. The invention elaborates on a Bayesian analysis of this particular binary context, with several key innovations.

The analysis of this invention addresses and incorporates case-control design issues in the assessment of association between predictors and outcome with nodes of a tree. With categorical or continuous covariates, this is based on an

underlying non-parametric model for the conditional distribution of predictor values given outcomes, consistent with the case-control design. This uses sequences of Bayes' factor based tests of association to rank and select predictors that define significant "splits" of nodes, and that provides an approach to forward  
5 generation of trees that is generally conservative in generating trees that are effectively self-pruning. An innovative element of the invention is the implementation of a tree-spawning method to generate multiple trees with the aim of finding classes of trees with high marginal likelihoods, and where the prediction is based on model averaging, *i.e.*, weighting predictions of trees by  
10 their implied posterior probabilities. The advantage of the Bayesian approach is that rather than identifying a single "best" tree, a score is attached to all possible trees and those trees which are very unlikely are excluded. Posterior and predictive distributions are evaluated at each node and at the leaves of each tree, and feed into both the evaluation and interpretation tree by tree, and the averaging  
15 of predictions across trees for future cases to be predicted.

To demonstrate the utility and advantages of this tree classification model, an embodiment is provided that concerns gene expression profiling using DNA microarray data as predictors of a clinical states in breast cancer. The clinical state is estrogen receptor ("ER") prediction. The example of ER status prediction  
20 demonstrates not only predictive value but also the utility of the tree modeling framework in aiding exploratory analysis that identify multiple, related aspects of gene expression patterns related to a binary outcome, with some interesting interpretation and insights. This embodiment also illustrates the use of metagene factors – multiple, aggregate measures of complex gene expression patterns – in a  
25 predictive modeling context. In the case of large numbers of candidate predictors, in particular, model sensitivity to changes in selected subsets of predictors are ameliorated through the generation of multiple trees, and relevant, data-weighted averaging over multiple trees in prediction. The development of formal, simulation-based analyses of such models provides ways of dealing with



the issues of high collinearity among multiple subsets of predictors, and challenging computational issues.

#### BRIEF DESCRIPTION OF THE FIGURES

5 Figure 1: Three ER related metagenes in 49 primary breast tumors. Samples are denoted by blue (ER negative) and red (ER positive), with training data represented by filled circles and validation data by open circles.

Figure 2: Three ER related metagenes in 49 primary breast tumors. All samples are represented by index number in 1-78. Training data are denoted by blue (ER  
10 negative) and red (ER positive), and validation data by cyan (ER negative) and magenta (ER positive).

Figure 2: Honest predictions of ER status of breast tumors. Predictive probabilities are indicated, for each tumor, by the index number on the vertical probability scale, together with an approximate 90% uncertainty interval about  
15 the estimated probability. All probabilities are referenced to a notional initial probability (incidence rate) of 0.5 for comparison. Training data are denoted by blue (ER negative) and red (ER positive), and validation data by cyan (ER negative) and magenta (ER positive).

Figure 4: Table of 491 ER metagenes in initial (random) order.

20 Figure 5: Table of 491 ER metagenes ordered in terms of nonlinear association with ER status.

#### DETAILED DESCRIPTION OF THE INVENTION

Development of the Tree Clarification Model: Model Context and Methodology

25 Data  $\{Z_i, \mathbf{x}_i\}$  ( $i = 1, \dots, n$ ) are available on a binary response variable  $Z$  and a  $p$  – dimensional covariate vector  $\mathbf{x}$ : The 0/1 response totals are fixed by design. Each predictor variable  $x_j$  could be binary, discrete or continuous.

1. Bayes' factor measures of association

At the heart of a classification tree is the assessment of association between each predictor and the response in subsamples, and we first consider this at a general level in the full sample. For any chosen single predictor  $x$ ; a specified threshold  $\tau$  on the levels of  $x$  organizes the data into the 2 x 2 table.

	$Z = 0$	$Z = 1$	
$x \leq \tau$	$n_{00}$	$n_{01}$	$N_0$
$x > \tau$	$n_{10}$	$n_{11}$	$N_1$
	$M_0$	$M_1$	

5

With column totals fixed by design, the categorized data is properly viewed as two Bernoulli sequences within the two columns, hence sampling densitie

$$p(n_{0z}, n_{1z} | M_z, \theta_{z,\tau}) = \theta_{z,\tau}^{n_{0z}} (1 - \theta_{z,\tau})^{n_{1z}}$$

for each column  $z = 0, 1$ . Here, of course,  $\theta_{0,\tau} = Pr(x \leq \tau | Z = 0)$  and  $\theta_{1,\tau} = Pr(x \leq \tau | Z = 1)$ . A test of association of the thresholded predictor with the response will now be based on assessing the difference between these Bernoulli probabilities.

The natural Bayesian approach is via the Bayes' factor  $B_\tau$  comparing the null hypothesis  $\theta_{0,\tau} = \theta_{1,\tau}$  to the full alternative  $\theta_{0,\tau} \neq \theta_{1,\tau}$ . We adopt the standard conjugate beta prior model and require that the null hypothesis be nested within the alternative. Thus, assuming  $\theta_{0,\tau} \neq \theta_{1,\tau}$ , we take  $\theta_{0,\tau}$  and  $\theta_{1,\tau}$  to be independent with common prior  $Be(a_\tau, b_\tau)$  with mean  $m_\tau = a_\tau / (a_\tau + b_\tau)$ . On the null hypothesis  $\theta_{0,\tau} = \theta_{1,\tau}$ , the common value has the same beta prior. The resulting Bayes' factor in favour of the alternative over the null hypothesis is then simply

10

$$B_\tau = \frac{\beta(n_{00} + a_\tau, n_{10} + b_\tau) \beta(n_{01} + a_\tau, n_{11} + b_\tau)}{\beta(N_0 + a_\tau, N_1 + b_\tau) \beta(a_\tau, b_\tau)}.$$

15

As a Bayes' factor, this is calibrated to a likelihood ratio scale. In contrast to more traditional significance tests and also likelihood ratio approaches, the Bayes' factor will tend to provide more conservative assessments of significance, consistent with the general conservative properties of proper Bayesian tests of null hypotheses (See Sellke, T., Bayarri, M.J. and Berger, J.O., Calibration of  $p$ -values for testing precise null hypotheses, *The American Statistician*, **55**, 62-71, (2001) and references therein).

20

In the context of comparing predictors, the Bayes' factor  $B_\tau$  may be evaluated for all predictors and, for each predictor, for any specified range of thresholds. As the threshold varies for a given predictor taking a range of (discrete or continuous)

values, the Bayes' factor maps out a function of  $\tau$  and high values identify ranges of interest for thresholding that predictor. For a binary predictor, of course, the only relevant threshold to consider is  $\tau = 0$ .

## 5 2. Model consistency with respect to varying thresholds

A key question arises as to the consistency of this analysis as we vary the thresholds. By construction, each probability  $\theta_{Z\tau}$  is a non-decreasing function of  $\tau$ , a constraint that must be formally represented in the model. The key point is that the beta prior specification must formally reflect this. To see how this is  
 10 achieved, note first that  $\theta_{Z\tau}$  is in fact the cumulative distribution function of the predictor values  $\chi_z$  conditional on  $Z = z$ ; ( $z = 0, 1$ ); evaluated at the point  $\chi = \tau$ . Hence the *sequence* of beta priors,  $Be(a_\tau, b_\tau)$  as  $\tau$  varies, represents a set of marginal prior distributions for the corresponding set of values of the cdfs. It is immediate that the natural embedding is in a non-parametric Dirichlet process  
 15 model for the complete cdf. Thus the threshold-specific beta priors are consistent, and the resulting sets of Bayes' factors comparable as  $\tau$  varies, under a Dirichlet process prior with the betas as margins. The required constraint is that the prior mean values  $m_\tau$  are themselves values of a cumulative distribution function on the range of  $\chi$ , one that defines the prior mean of each  $\theta_\tau$  as a function. Thus, we  
 20 simply rewrite the beta parameters  $(\alpha_\tau, b_\tau)$  as  $\alpha_\tau = \alpha m_\tau$  and  $b_\tau = \alpha(1 - m_\tau)$  for a specified prior mean cdf  $m_\tau$ , and where  $\alpha$  is the prior precision (or "total mass") of the underlying Dirichlet process model. Note that this specialises to a Dirichlet distribution when  $\chi$  is discrete on a finite set of values, including special cases of ordered categories (such as arise if  $\chi$  is truncated to a predefined set of bins), and  
 25 also the extreme case of binary  $\chi$  when the Dirichlet is a simple beta distribution.

## 3. Generating a tree

The above development leads to a formal Bayes' factor measure of association that may be used in the generation of trees in a forward-selection process as  
 30 implemented in traditional classification tree approaches. Consider a single tree

and the data in a node that is a candidate for a binary split. Given the data in this node, construct a binary split based on a chosen (predictor, threshold) pair  $(\chi, \tau)$  by (a) finding the (predictor, threshold) combination that maximizes the Bayes' factor for a split, and (b) splitting if the resulting Bayes' factor is sufficiently large. By reference to a posterior probability scale with respect to a notional 50:50 prior, Bayes' factors of 2.2, 2.9, 3.7 and 5.3 correspond, approximately, to probabilities of .9, .95, .99 and .995, respectively. This guides the choice of threshold, which may be specified as a single value for each level of the tree. We have utilised Bayes' factor thresholds of around 3 in a range of analyses, as exemplified below. Higher thresholds limit the growth of trees by ensuring a more stringent test for splits.

The Bayes' factor measure will always generate less extreme values than corresponding generalized likelihood ratio tests (for example), and this can be especially marked when the sample sizes  $M_0$  and  $M_1$  are low. Thus the propensity to split nodes is always generally lower than with traditional testing methods, especially with lower samples sizes, and hence the approach tends to be more conservative in extending existing trees. Post-generation pruning is therefore generally much less of an issue, and can in fact generally be ignored. Index the root node of any tree by zero, and consider the full data set of  $n$  observations, representing  $M_z$  outcomes with  $Z = z$  in 0, 1. Label successive nodes sequentially: splitting the root node, the left branch terminates at node 1, the right branch at node 2; splitting node 1, the consequent left branch terminates at node 3, the right branch at node 4; splitting node 2, the consequent left branch terminates at node 5, and the right branch at node 6, and so forth. Any node in the tree is labelled numerically according to its "parent" node; that is, a node  $j$  splits into two children, namely the (left, right) children  $(2j + 1; 2j + 2)$ : At level  $m$  of the tree ( $m = 0; 1; \dots$ ) the candidate nodes are, from left to right, as  $2^m - 1; 2^m; \dots; 2^{m+1} - 2$ .

Having generated a "current" tree, we run through each of the existing terminal nodes one at a time, and assess whether or not to create a further split at that

node, stopping based on the above Bayes' factor criterion. Unless samples are very large (thousands) typical trees will rarely extend to more than three or four levels.

5      4.      Inference and prediction with a single tree

Suppose we have generated a tree with  $m$  levels; the tree has some number of terminal nodes up to the maximum possible of  $L = 2^{m+1} - 2$ . Inference and prediction involves computations for *branch probabilities* and the predictive probabilities for new cases that these underlie. We detail this for a specific path  
10      down the tree, i.e., a sequence of nodes from the root node to a specified terminal node.

First, consider a node  $j$  that is split based on a (predictor, threshold) pair labeled  $(\chi_j, \tau_j)$ , (note that we use the node index to label the chosen predictor, for clarity). Extend the notation of Section 2.1 to include the subscript  $j$  indexing this  
15      node. Then the data at this node involves  $M_{0j}$  cases with  $Z = 0$  and  $M_{1j}$  cases with  $Z = 1$ . Based on the chosen (predictor, threshold) pair  $(\chi_j, \tau_j)$  these samples split into cases  $n_{00j}, n_{01j}, n_{10j}, n_{11j}$  as in the table of Section 2.1, but now indexed by the node label  $j$ . The implied conditional probabilities  $\theta_{z,\tau,j} = Pr(\chi_j \leq \tau_j | Z = z)$ , for  $z = 0, 1$  are the *branch probabilities* defined by such a split (note that these are also  
20      conditional on the tree and data subsample in this node, though the notation does not explicitly reflect this for clarity). These are uncertain parameters and, following the development of Section 2.1, have specified beta priors, now also indexed by parent node  $j$ , i.e.,  $Be(a_{\tau,j}, b_{\tau,j})$ . Assuming the node is split, the two sample Bernoulli setup implies conditional posterior distributions for these  
25      branch probability parameters: they are independent with posterior beta distributions

$$\theta_{0,\tau,j} \sim Be(a_{\tau,j} + n_{00j}, b_{\tau,j} + n_{10j}) \text{ and } \theta_{1,\tau,j} \sim Be(a_{\tau,j} + n_{01j}, b_{\tau,j} + n_{11j}).$$

These distributions allow inference on branch probabilities, and feed into the predictive inference computations as follows.

Consider predicting the response  $Z^*$  of a new case based on the observed set of predictor values  $\mathbf{x}^*$ . The specified tree defines a unique path from the root to the terminal node for this new case. To predict requires that we compute the posterior predictive probability for  $Z^* = 1/0$ . We do this by following  $\mathbf{x}^*$  down the tree to the implied terminal node, and sequentially building up the relevant likelihood ratio defined by successive (predictor, threshold) pairs.

For example and specificity, suppose that the predictor profile of this new case is such that the implied path traverses nodes 0, 1, 4, 9, terminating at node 9. This path is based on a (predictor, threshold) pair  $(\chi_0, \tau_0)$  that defines the split of the root node,  $(\chi_1, \tau_1)$  that defines the split of node 1, and  $(\chi_4, \tau_4)$  that defines the split of node 4. The new case follows this path as a result of its predictor values, in sequence:

$(x_0^* \leq \tau_0)$ ,  $(x_1^* > \tau_1)$  and  $(x_4^* \leq \tau_4)$ . The implied likelihood ratio for  $Z^* = 1$  relative to  $Z^* = 0$  is then the product of the ratio of branch probabilities to this terminal node, namely

$$\lambda^* = \frac{\theta_{1,\tau_0,0}}{\theta_{0,\tau_0,0}} \times \frac{(1 - \theta_{1,\tau_1,1})}{(1 - \theta_{0,\tau_1,1})} \times \frac{\theta_{1,\tau_4,9}}{\theta_{0,\tau_4,9}}.$$

Hence, for any specified prior probability  $Pr(Z^* = 1)$ , this single tree model implies that, as a function of the branch probabilities, the updated probability  $\pi^*$  is, on the odds scale, given by

$$\frac{\pi^*}{(1 - \pi^*)} = \lambda^* \frac{Pr(Z^* = 1)}{Pr(Z^* = 0)}.$$

Hence, for any specified prior probability  $\pi Pr(Z^* = 1)$ , this single tree model implies that, as a function the branch probabilities, the updated probability  $\pi^*$  is, on the odds scale, given by

$$\frac{\pi^*}{(1 - \pi^*)} = \lambda^* \frac{Pr(Z^* = 1)}{Pr(Z^* = 0)}$$

The case-control design provides no information about  $Pr(Z^* = 1)$  so it is up to the user to specify this or examine a range of values; one useful summary is obtained by simply taking a 50:50 prior odds as benchmark, whereupon the posterior probability is

$$5 \quad \pi^* = \lambda^* / (1 + \lambda^*).$$

Prediction follows by estimating  $\pi^*$  based on the sequence of conditionally independent posterior distributions for the branch probabilities that define it. For example, simply “plugging-in” the conditional posterior means of each  $\theta$ . will  
 10 lead to a plug-in estimate of  $\lambda^*$  and hence  $\pi^*$ . The full posterior for  $\pi^*$  is defined implicitly as it is a function of the  $\theta$ .. Since the branch probabilities follow beta posteriors, it is trivial to draw Monte Carlo samples of the  $\theta$ . and then simply compute the corresponding values of  $\lambda^*$  and hence  $\pi^*$  to generate a posterior sample for summarization. This way, we can evaluate simulation-based posterior  
 15 means and uncertainty intervals for  $\pi^*$  that represent predictions of the binary outcome for the new case.

#### 5. Generating and weighting multiple trees

In considering potential (predictor, threshold) candidates at any node, there may  
 20 be a number with high Bayes’ factors, so that multiple possible trees with difference splits at this node are suggested. With continuous predictor variables, small variations in an “interesting” threshold will generally lead to small changes in the Bayes’ factor – moving the threshold so that a single observation moves from one side of the threshold to the other, for example. This relates naturally to  
 25 the need to consider thresholds as parameters to be inferred; for a given predictor  $\chi$ , multiple candidate splits with various different threshold values  $\tau$  reflects the inherent uncertainty about  $\tau$ , and indicates the need to generate multiple trees to adequately represent that uncertainty. Hence, in such a situation, the tree generation can spawn multiple copies of the “current” tree, and then each will  
 30 split the current node based on a different threshold for this predictor. Similarly,

multiple trees may be spawned this way with the modification that they may involve different predictors.

In problems with many predictors, this naturally leads to the generation of many trees, often with small changes from one to the next, and the consequent need for careful development of tree-managing software to represent the multiple trees. In addition, there is then a need to develop inference and prediction in the context of multiple trees generated this way. The use of “forests of trees” has recently been urged by Breiman, L., *Statistical Modeling: The two cultures (with discussion)*, *Statistical Science*, **16** 199-225 (2001), and our perspective endorses this. The rationale here is quite simple: node splits are based on specific choices of what we regard as parameters of the overall predictive tree model, the (predictor, threshold) pairs. Inference based on any single tree chooses specific values for these parameters, whereas statistical learning about relevant trees requires that we explore aspects of the posterior distribution for the parameters (together with the resulting branch probabilities).

Within the current framework, the forward generation process allows easily for the computation of the resulting relative likelihood values for trees, and hence to relevant weighting of trees in prediction. For a given tree, identify the subset of nodes that are split to create branches. The overall marginal likelihood function for the tree is then the product of component marginal likelihoods, one component from each of these split nodes. Continue with the notation of Section 2.1 but now, again, indexed by any chosen node  $j$ : Conditional on splitting the node at the defined (predictor, threshold) pair  $(\chi_j, \tau_j)$ , the marginal likelihood component is

$$m_j = \int_0^1 \int_0^1 \prod_{z=0,1} p(n_{0zj}, n_{1zj} | M_{zj}, \theta_{z,\tau_j,j}) p(\theta_{z,\tau_j,j}) d\theta_{z,\tau_j,j}$$

where  $p(\theta_{z,\tau_j,j})$  is the  $B\psi(a_{\tau,j}, b_{\tau,j})$  prior for each  $z = 0, 1$ . This clearly reduces to

$$m_j = \prod_{z=0,1} \frac{\beta(n_{0zj} + a_{\tau,j}, n_{1zj} + b_{\tau,j})}{\beta(a_{\tau,j}, b_{\tau,j})}.$$

25



The overall marginal likelihood value is the product of these terms over all nodes  $j$  that define branches in the tree. This provides the relative likelihood values for all trees within the set of trees generated. As a first reference analysis, we may simply normalise these values to provide relative posterior probabilities over  
5 trees based on an assumed uniform prior. This provides a reference weighting that can be used to both assess trees and as posterior probabilities with which to weight and average predictions for future cases.

#### DESCRIPTION OF THE SPECIFIC EMBODIMENTS

10

Before the subject invention is described further, it is to be understood that the invention is not limited to the particular embodiments of the invention described below, as variations of the particular embodiments may be made and still fall within the scope of the appended claims. It is also to be understood that the  
15 terminology employed is for the purpose of describing particular embodiments, and is not intended to be limiting. Instead, the scope of the present invention will be established by the appended claims.

In this specification and the appended claims, the singular forms “a,” “an” and “the” include plural reference unless the context clearly dictates otherwise.

20 Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this invention belongs.

Where a range of values is provided, it is understood that each intervening value, to the tenth of the unit of the lower limit unless the context clearly dictates  
25 otherwise, between the upper and lower limit of that range, and any other stated or intervening value in that stated range, is encompassed within the invention.

The upper and lower limits of these smaller ranges may independently be included in the smaller ranges, and are also encompassed within the invention, subject to any specifically excluded limit in the stated range. Where the stated

range includes one or both of the limits, ranges excluding either or both of those included limits are also included in the invention.

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this invention belongs. Although any methods, devices and materials similar or equivalent to those described herein can be used in the practice or testing of the invention, the preferred methods, devices and materials are now described.

All publications mentioned herein are incorporated herein by reference for the purpose of describing and disclosing the subject components of the invention that are described in the publications, which components might be used in connection with the presently described invention.

#### Example 1: Metagene Expression Profiling to Predict Estrogen Receptor Status of Breast Cancer Tumors

This example illustrates not only predictive utility but also exploratory use of the tree analysis framework in exploring data structure. Here, the tree analysis is used to predict estrogen receptor ("ER") status of breast tumors using gene expression data. Prior analyses of such data involved binary regression models which utilized Bayesian generalized shrinkage approaches to factor regression. Specifically, prior statistical models involved the use of probit linear regression linking principal components of selected subsets of genes to the binary (ER positive/negative) outcomes. See West, M., Blanchette, C., Dressman, H., Ishida, S., Spang, R., Zuzan, H., Marks, J.R. and Nevins, J.R. Utilization of gene expression profiles to predict the clinical status of human breast cancer. *Proc. Natl. Acad. Sci.*, **98**, 11462-11467 (2001). However, the tree model presents some distinct advantages over Bayesian linear regression models in the analysis of large non-linear data sets such as these.

Primary breast tumors from the Duke Breast Cancer SPORE frozen tissue bank were selected for this study on the basis of several criteria. Tumors were either positive for both the estrogen and progesterone receptors or negative for both receptors. Each tumor was diagnosed as invasive ductal carcinoma and was  
5 between 1.5 and 5 cm in maximal dimension. In each case, a diagnostic axillary lymph node dissection was performed. Each potential tumor was examined by hematoxylin/eosin staining and only those that were > 60% tumor (on a per-cell basis), with few infiltrating lymphocytes or necrotic tissue, were carried on for RNA extraction. The final collection of tumors consisted of 13 estrogen receptor  
10 (ER)+ lymph node (LN)+ tumors, 12 ER LN+ tumors, 12 ER+ LN tumors, and 12 ER LN tumors

The RNA was derived from the tumors as follows: Approximately 30 mg of frozen breast tumor tissue was added to a chilled BioPulverizer H tube (Bio101) (Q-Biogene, La Jolla, CA). Lysis buffer from the Qiagen (Chatsworth, CA)  
15 RNeasy Mini kit was added, and the tissue was homogenized for 20 sec in a MiniBeadbeater (Biospec Products, Bartlesville, OK). Tubes were spun briefly to pellet the garnet mixture and reduce foam. The lysate was transferred to a new 1.5-ml tube by using a syringe and 21-gauge needle, followed by passage through the needle 10 times to shear genomic DNA. Total RNA was extracted by using  
20 the Qiagen RNeasy Mini kit. Two extractions were performed for each tumor, and total RNA was pooled at the end of the RNeasy protocol, followed by a precipitation step to reduce volume. Quality of the RNA was checked by visualization of the 28S:18S ribosomal RNA ratio on a 1% agarose gel. After the RNA preparation, the samples were subject to Affymetrix GENECHIP analysis.  
25 Affymetrix GENECHIP Analysis: The targets for Affymetrix DNA microarray analysis were prepared according to the manufacturer's instructions. All assays used the human HuGeneFL GENECHIP microarray. Arrays were hybridized with the targets at 45°C for 16 h and then washed and stained by using the GENECHIP Fluidics. DNA chips were scanned with the GENECHIP scanner,

and signals obtained by the scanning were processed by GENECHIP Expression Analysis algorithm (version 3.2) (Affymetrix, Santa Clara, CA).

The same set of  $n = 49$  samples used in the binary regression analysis described in West et al (2001) is analyzed in this study, using predictors based on *metagene*

5 summaries of the expression levels of many genes. Metagenes are useful aggregate, summary measures of gene expression profiles. The evaluation and summarization of large-scale gene expression data in terms of lower dimensional factors of some form is utilized for two main purposes: first, to reduce dimension from typically several thousand, or tens of thousands of genes to a more practical  
10 dimension; second, to identify multiple underlying “patterns” of variation across samples that small subsets of genes share, and that characterize the diversity of patterns evidenced in the full sample. Although, the analysis is conducive to the use of various factor model approaches known to those skilled in the art, a cluster-factor approach is used here to define empirical metagenes. This defines  
15 the predictor variables  $x$  utilized in the tree model.

Metagenes can be obtained by combining clustering with empirical factor methods. The metagene summaries used in the ER example in this disclosure, are based on the following steps.

Assume a sample of  $n$  profiles of  $p$  genes;

20 Screen genes to reduce the number by eliminating genes that show limited variation across samples or that are evidently expressed at low levels that are not detectable at the resolution of the gene expression technology used to measure levels. This removes noise and reduces the dimension of the predictor variable;  
Cluster the genes using  $k\_means$ , correlated-based clustering. Any standard  
25 statistical package may be used. This analysis uses the xcluster software created by Gavin Sherlock (<http://genomewww.stanford.edu/sherlock/cluster.html>). A large number of clusters are targeted so as to capture multiple, correlated patterns of variation across samples, and generally small numbers of genes within clusters;

Extract the dominant singular factor (principal component) from each of the resulting clusters. Again, any standard statistical or numerical software package may be used for this; this analysis uses the efficient, reduced singular value decomposition function ("SVD") in the Matlab software environment

5 (<http://www.mathworks.com/products/matlab>).

In the analysis of the ER data in this disclosure, the original data was developed using Affymetrix arrays with 7129 sequences, of which 7070 were used (following removal of Affymetrix controls from the data.). The expression estimates used were log2 values of the signal intensity measures computed using  
10 the dChip software for post-processing Affymetrix output data (See Li, C. and Wong, W.H. Model-based analysis of oligonucleotide arrays: Expression index computation and outlier detection. *Proc. Natl. Acad. Sci.*, **98**, 31-36 (2001), and the software site <http://www.biostat.harvard.edu/complab/dchip/>). With a target of 500 clusters, the xcluster software implementing the correlation-based  
15 k\_means clustering produced  $p = 491$  clusters. The corresponding  $p$  metagenes were then evaluated as the dominant singular factors of each of these cluster, as referenced above. See Figures 4-5 that provide tables detailing the 491 metagenes.

The data comprised 40 training samples and 9 validation cases. Among the latter,  
20 3 were initial training samples that presented conflicting laboratory tests of the ER protein levels, so casting into question their actual ER status; these were therefore placed in the validation sample to be predicted, along with an initial 6 validation cases selected at random. These three cases are numbers 14, 31 and 33. The color coding in the graphs is based on the first laboratory test  
25 (immunohistochemistry). Additional samples of interest are cases 7, 8 and 11, cases for which the DNA microarray hybridizations were of poor quality, with the resulting data exhibiting major patterns of differences relative to the rest. The metagene predictor has dimension  $p = 491$ : the analysis generated trees based on a Bayes' factor threshold of 3 on the log scale, allowing up to 10 splits  
30 of the root node and then up to 4 at each of nodes 1 and 2. Some pertinent

summaries appear in the following figures. Figures 1 and 2 display 3-D and pairwise 2-D scatterplots of three of the key metagenes, all clearly strongly related to the ER status and also correlated. However, there are in fact five or six metagenes that quite strongly associate with ER status and it is evident that they reflect multiple aspects of this major biological pathway in breast tumors. In the study reported in West *et al* (2001), Bayesian probit regression models were utilized with singular factor predictors which identified a single major factor predictive of ER. That analysis identified ER negative tumors 16, 40 and 43 as difficult to predict based on the gene expression factor model; the predictive probabilities of ER positive versus negative for these cases were near or above 0.5, with very high uncertainties reflecting real ambiguity.

In contrast to the more more traditional regression models, the current tree model identifies several metagene patterns that together combine to define an ER profile of tumors, and that when displayed as in Figures 1 and 2 isolate these three cases as quite clearly consistent with their designated ER negative status in some aspects, yet conflicting and much more in agreement with the ER positive patterns on others. Metagene 347 is the dominant ER signature; the genes involved in defining this metagene include two representations of the ER gene, and several other genes that are coregulated with, or regulated by, the ER gene.

Many of these genes appeared in the dominant factor in the regression prediction. This metagene strongly discriminates the ER 11 negatives from positives, with several samples in the mid-range. Thus, it is no surprise that this metagene shows up as defining root node splits in many high-likelihood trees. This metagene also clearly defines these three cases – 16, 40 and 43 – as appropriately ER negative. However, a second ER associated metagene, number 352, also defines a significant discrimination. In this dimension, however, it is clear that the three cases in question are very evidently much more consistent with ER positives; a number of genes, including the ER regulated PS2 protein and androgen receptors, play roles in this metagene, as they did in the factor regression; it is this second genomic pattern that, when combined together with

the first as is implicit in the factor regression model, breeds the conflicting information that fed through to ambivalent predictions with high uncertainty. The tree model analysis here identifies multiple interacting patterns and allows easy access to displays such as those shown in Figures 1 to 3 that provide insights into the interactions, and hence to interpretation of individual cases. In the full tree analysis, predictions based on averaging multiple trees are in fact dominated by the root level splits on metagene 347, with all trees generated extending to two levels where additional metagenes define subsidiary branches. Due to the dominance of metagene 347, the three interesting cases noted above are perfectly in accord with ER negative status, and so are well predicted, even though they exhibit additional, subsidiary patterns of ER associated behaviour identified in the figures. Figure 6 displays summary predictions. The 9 validation cases are predicted based on the analysis of the full set of 40 training cases. Predictions are represented in terms of point predictions of ER positive status with accompanying, approximate 90% intervals from the average of multiple tree models. The training cases are each predicted in an honest, cross-validation sense: each tumor is removed from the data set, the tree model is then refitted completely to the remaining 39 training cases only, and the hold-out case is predicted, *i.e.*, treated as a validation sample. Excellent predictive performance is observed for both these one-at-a-time honest predictions of training samples and for the out of sample predictions of the 9 validation cases. One ER negative, sample 31, is firmly predicted as having metagene expression patterns completely consistent with ER positive status. This is in fact one of the three cases for which the two laboratory tests conflicted. The other two such cases, however agree with the initial ER negative test result - number 33, for which the predictions firmly agree with the initial ER negative test result, and number 14, for which the predictions agree with the initial ER positive result though not quite so forcefully. The lack of conformity of expression patterns in some cases (Case 8, 11 and 7) are due to major distortions in the data on the DNA microarray due to hybridization problems.

## CLAIMS

What is claimed is:

1. A classification tree model incorporating Bayesian analysis for the statistical prediction of binary outcomes.
2. The tree model of claim 1, wherein the prediction of a binary outcome is dependent on the interaction of data comprising at least two predictor variables.
3. The tree model of claim 2, wherein the data arises by case control design such that the number of 0/1 values in the response data is fixed by design.
4. The tree model of claim 3, such that the case control design assesses association between predictors and binary outcome with nodes of a tree.
5. The tree model of claim 4, such that the Bayesian analysis comprises using sequences of Bayes factor based tests of association to rank and select predictors that define a node split.
6. The tree model of claim 5, further comprising the forward generation of at least one class of trees with high marginal likelihood, wherein the prediction of said class of trees is conducted using principles of model averaging.
7. The tree model of claim 6, wherein the principle of model averaging comprises the steps of:
  - weighted prediction of a tree by determining its implied posterior probability by a score;
  - evaluation of the score to exclude unlikely trees;
  - evaluation of the posterior and predictive distribution at each node and leaf of a tree; and
  - application of said posterior and predictive distribution to the evaluation of each tree and the averaging of predictions across trees for future predictive cases.
8. The tree model of claim 1 or 2, wherein the binary outcome is a clinical state.



9. The tree model of claim 1 or 2, wherein the binary outcome is a physiological state.
10. The tree model of claim 1 or 2, wherein the binary outcome is a physical state.
- 5 11. The tree model of claim 1 or 2, wherein the binary outcome is a disease state.
12. The tree model of claim 1 or 2, wherein the binary outcome is a risk group.
13. The tree model of claim 1 or 2, wherein the data is biological data.
- 10 14. The tree model of claim 1 or 2, wherein the data is statistical data.
15. The tree model of claim 1 or 2, wherein the binary outcome is estrogen receptor status.
16. Metagenes obtained using the tree model of claim 1 or 2, such that the metagenes characterize multiple patterns of genes predictive of estrogen receptor status.
- 15 17. Genes predictive of estrogen receptor status obtained using the tree model of claims 1 or 2.

Figure 1

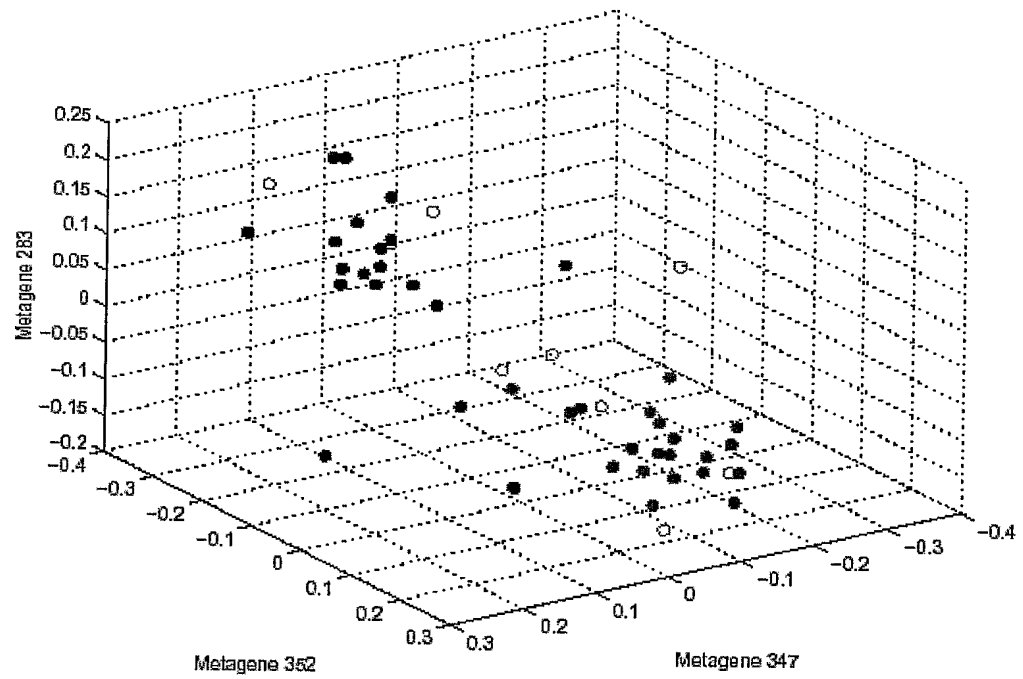


Figure 2

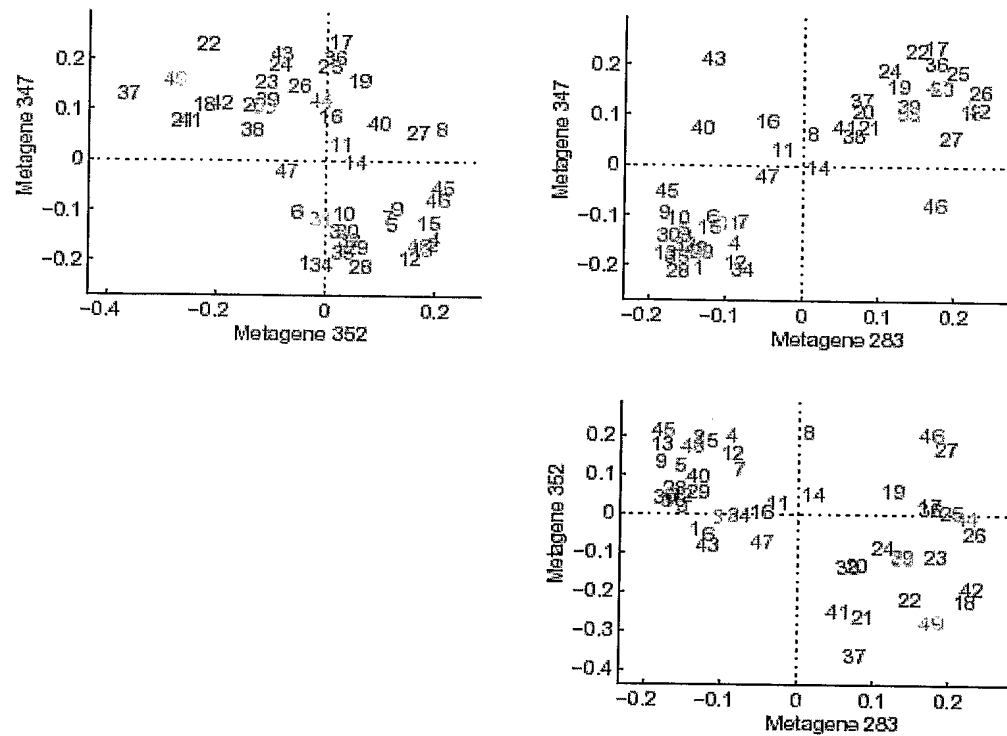
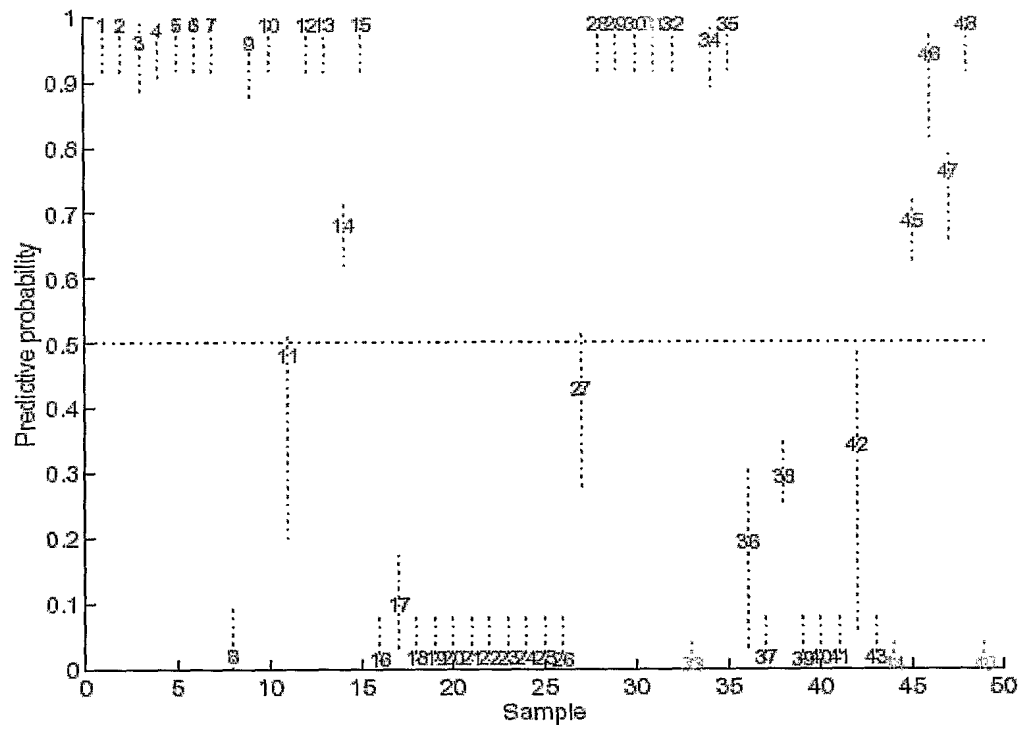


Figure 3



491 metagenes constructed (as described) in analysis of Duke breast cancer data with respect to ER status. This file lists the metagenes in order of nonlinear (tree model) association with ER status (top down).

#### Metagene 347

d50840\_1048-1474,mrna\_for\_ceramide\_glucosyltransferase,\_complete\_cds\_  
hg3125-ht3301\_s\_at\_hg3125-ht3301\_estrogen\_receptor\_  
l40401mrna\_572-992,(clone\_zap128)\_mrna,\_3'\_end\_of\_cds\_  
m14745\_5435-5981,bcl-2\_mrna  
s68805\_1972-2305,\_l-  
arginine:glycine\_amidinotransferase\_[human,\_kidney\_carcinoma\_cells,\_mrna,\_2330\_  
n  
u21931mrna\_965-1373,fructose-1,6-biphosphatase\_(fbp1)\_gene\_  
u22376exon#20\_757-1256,\_c-myb\_gene\_extracted\_from(c-  
myb)\_gene,\_complete\_primary\_cds,\_and\_five\_comple  
u41060\_2936-3416,breast\_cancer,\_estrogen\_regulated\_liv-1\_protein\_(liv-  
1)\_mrna,\_partial\_cds\_  
u67963\_590-1148,lysophospholipase\_homolog\_(hu-k5)\_mrna,\_complete\_cds\_  
u72661\_650-1196,ninjurin1\_mrna,\_complete\_cds.  
u79293\_1221-1749,clone\_23948\_mrna\_sequence\_  
u82987\_1140-1614,bcl-2\_binding\_component(bbc3)\_mrna,\_partial\_cds  
u96113\_1463-2003,nedd-4-like\_ubiquitin-  
protein\_ligase\_wwp1\_mrna,\_partial\_cds/gb=u96113/\_ntype=rna\_  
all\_x03635\_5885-6402,mrna\_for\_oestrogen\_receptor\_  
x55037mrna\_863-1448,gata-3\_mrna  
x58072mrna\_1793-2309,hgata3\_mrna\_for\_trans-acting\_t-  
cell\_specific\_transcription\_factor\_  
all\_x83425\_1831-2390,lu\_gene\_for\_lutheran\_blood\_group\_glycoprotein\_

#### Metagene 283

d26070mrna\_8922-9492,mrna\_for\_typeinositol\_1,4,5-  
trisphosphate\_receptor,\_complete\_cds\_  
l08044\_8-358,intestinal\_trefoil\_factor\_mrna,\_complete\_cds  
l38608\_1950-2478,cd6\_ligand\_(alcam)\_mrna,\_complete\_cds  
m12174\_28-493,ras-related\_rho\_mrna\_(clone\_6),\_partial\_cds  
m23263\_3498-3648,androgen\_receptor\_mrna,\_complete\_cds  
m31627\_1191-1725,x\_box\_binding\_protein-1\_(xbp-1)\_mrna,\_complete\_cds  
s37730cds\_625-916:in\_reversesequence,\_496-635,\_insulin-  
like\_growth\_factor\_binding\_protein-2\_[human,\_  
u09770\_61-391,cysteine-rich\_heart\_protein\_(hcrhp)\_mrna,\_complete\_cds\_  
u39840\_2313-2823,hepatocyte\_nuclear\_factor-3\_alpha\_(hnf-  
3\_alpha)\_mrna,\_complete\_cds  
u52522\_1047-1581,arfaptin\_2,\_putative\_target\_protein\_of\_adp-  
ribosylation\_factor,\_mrna,\_complete\_cds  
u94831\_1555-  
1933,multispanning\_membrane\_protein\_mrna,\_complete\_cds/gb=u94831/\_ntype=rna  
all\_x06614\_2300-2889,mrna\_for\_receptor\_of\_retinoic\_acid  
x12876mrna\_144-670,mrna\_fragment\_for\_cytokeratin\_18  
x52003cds\_63-213:in\_reversesequence,\_289-445,ps2\_protein\_gene

x53002cds\_2049-2356:in\_reversesequence,\_2724-2849,mrna\_for\_integrin\_beta-5\_subunit  
 all\_x76180\_2760-3115,mrna\_for\_lung\_amiloride\_sensitive\_na+\_channel\_protein\_  
 all\_z11793\_1553-2001,mrna\_for\_selenoprotein\_p

Metagene 402

d12686\_4468-4909,mrna\_for\_eukaryotic\_initiation\_factorgamma\_(eif-4\_gamma)\_  
 d13636\_3011-3539,mrna\_for\_kiaa0011\_gene,\_complete\_cds  
 d29958\_446-962,mrna\_for\_kiaa0116\_gene,\_partial\_cds  
 d42054\_2354-2828,mrna\_for\_kiaa0092\_gene,\_complete\_cds  
 d82345\_86-578,mrna\_for\_nb\_thymosin\_beta,\_complete\_cds  
 d83783\_6249-6579,mrna\_for\_kiaa0192\_gene,\_partial\_cds\_  
 hg1078-ht1078\_at\_hg1078-ht1078\_lamin-like\_protein  
 hg1614-ht1614\_at\_hg1614-ht1614\_protein\_phosphatase\_1,\_alpha\_catalytic\_subunit  
 hg1733-ht1748\_at\_hg1733-ht1748\_moloney\_murine\_sarcoma\_viral\_oncogene\_homolog\_  
 hg3432-ht3621\_at\_hg3432-ht3621\_fibroblast\_growth\_factor\_receptor\_k-  
 sam,\_altsplice\_4,\_k-sam\_iv  
 hg4073-ht4343\_at\_hg4073-ht4343\_cytosolic\_acetoacetyl-coenzyme\_a\_thiolase\_  
 hg4155-ht4425\_s\_at\_hg4155-ht4425\_zinc\_finger\_protein\_hzf8  
 hg4542-ht4947\_at\_hg4542-ht4947\_ribosomal\_protein\_l10\_  
 j05272\_2311-2809,imp\_dehydrogenase\_typemrna\_complete\_cds  
 k02574mrna\_817-1363,purine\_nucleoside\_phosphorylase\_(pnp)\_mrna,\_complete\_cds\_  
 l07592\_2760-3228,peroxisome\_proliferator\_activated\_receptor\_mrna,\_complete\_cds\_  
 l11285\_957-1509,\_homosapiens\_erk\_activator\_kinase\_(mek2)\_mrna\_  
 l26339\_4094-4580,autoantigen\_mrna,\_complete\_cds  
 l35854mrna\_3-75,dystrophin\_(dp140)\_mrna,\_5'\_end/gb=135854\_/ntype=rna\_  
 l38487mrna\_1623-2115,estrogen\_receptor-  
 related\_protein\_(herral)\_mrna,\_3'\_end,\_partial\_cds  
 m13955mrna\_904-1450,mesothelial\_keratin\_k7\_(type\_ii)\_mrna,\_3'\_end  
 m30938mrna#2\_2781-3261,ku\_(p70/p80)\_subunit\_mrna,\_complete\_cds\_  
 m33518exon\_5570-5900:in\_reversesequence,\_6168-6198,hla-b-  
 associated\_transcript(bat2)\_gene,\_5'\_flank  
 m33764cds\_1158-1350:in\_reversesequence,\_7989-  
 8235,ornithine\_decarboxylase\_gene,\_complete\_cds  
 m35198\_2073-2589,integrin\_b-6\_mrna,\_complete\_cds\_  
 m80244\_3401-3869,e16\_mrna,\_complete\_cds  
 m83651\_1947-2451,beta-1,4\_n-acetylgalactosaminyltransferase\_mrna,\_complete\_cds\_  
 u09578\_2012-2456,mapkap\_kinase\_(3pk)\_mrna,\_complete\_cds  
 u23143cds\_1258-1426:in\_reversesequence,\_3604-  
 3844,mitochondrial\_serine\_hydroxymethyltransferase\_gene  
 u33818\_1889-2351,inducible\_poly(a)-binding\_protein\_mrna,\_complete\_cds  
 u50939\_1224-1662,amyloid\_precursor\_protein-binding\_proteinmrna,\_complete\_cds  
 u68105mrna\_2540-2765,poly(a)-binding\_protein\_(pabp)\_gene,\_promoter\_region\_and  
 u78525\_2480-  
 2942,eukaryotic\_translation\_initiation\_factor\_(eif3)\_mrna,\_complete\_cds  
 u79254\_693-1113,clone\_23693\_mrna\_sequence  
 u82613\_163-685,dna-binding\_protein\_abp/zf\_mrna,\_complete\_cds\_  
 all\_x15414\_844-1349,mrna\_for\_aldose\_reductase\_(ec\_1.1.1.2)\_  
 x52882cds\_1171-1639:in\_reversesequence,\_1672-1732,t-complex\_polypeptidegene  
 x60489mrna\_381-915,mrna\_for\_elongation\_factor-1-beta\_  
 all\_x67698\_228-709,tissue\_specific\_mrna  
 all\_x74570\_1140-1711,mrna\_for\_gal-beta(1-3/1-4)glcnac\_alpha-2.3-  
 sialyltransferase  
 z25749mrna\_98-608,gene\_for\_ribosomal\_protein\_s7\_

z34918cds\_1559-2051,mrna\_for\_translation\_initiation\_factor\_eif-4gamma\_(partial)

Metagene 301

l13698\_2227-2791,gasl\_gene,\_complete\_cds\_  
 l24203\_2423-2891,ataxia-telangiectasia\_group\_d-  
 associated\_protein\_mrna,\_complete\_cds  
 m18533mrna\_13566-13926,dystrophin\_(dmd)\_mrna,\_complete\_cds  
 m24485cds\_109-604:in\_reversesequence,\_3966,(clone\_phgst-pi)\_glutathione\_s-  
 transferase\_pi\_(gstp1)\_gen  
 all\_m98539\_46-209:not\_in\_gb\_record,prostaglandin\_d2\_synthase\_gene\_  
 u03057\_2172-2724,actin\_bundling\_protein\_(hsn)\_mrna,\_complete\_cds\_  
 u33849\_2850-3366,lymphoma\_proprotein\_convertase\_(lpc)\_mrna,\_complete\_cds\_  
 u45955\_834-1362,neuronal\_membrane\_glycoprotein\_m6b\_mrna,\_partial\_cds\_  
 all\_x66534\_2622-2953,soluble\_guanylate\_cyclase\_large\_subunit\_mrna  
 all\_x87212\_1273-1772,mrna\_for\_cathepsin\_c  
 x96381mrna\_3518-4028,erm\_gene,\_exon\_2,3,4,5\_(and\_joined\_cds)

Metagene 54

l27213cds\_2481-2749:in\_reversesequence,\_2815-  
 3030,anion\_exchange\_protein\_mrna,\_complete\_cds  
 m29874\_2457-2977,cytochrome\_p450-iib\_(hiib1)\_mrna,\_complete\_cds  
 z36714mrna\_3697-4135,mrna\_for\_cyclin\_f\_

Metagene 362

s74445\_152-662,\_cellular\_retinoic\_acid-  
 binding\_protein\_[human,\_skin,\_mrna,\_735\_nt]  
 u84487\_2776-  
 3238,cx3c\_chemokine\_precursor,\_mrna,\_alternatively\_spliced,\_complete\_cds\_  
 x82554mrna\_103-571,sphar\_gene\_for\_cyclin-related\_protein

Metagene 111

d14694\_2143-2455,mrna\_for\_kiaa0024\_gene,\_complete\_cds  
 d21261\_957-1305,mrna\_for\_kiaa0120\_gene,\_complete\_cds\_  
 d25328\_2086-2536,mrna\_for\_platelet-type\_phosphofructokinase,\_complete\_cds  
 d26599\_167-707,mrna\_for\_proteasome\_subunit\_hsc7-i,\_complete\_cds  
 d26600\_354-822,mrna\_for\_proteasome\_subunit\_hsn3,\_complete\_cds  
 d31890\_1375-1909,mrna\_for\_kiaa0070\_gene,\_partial\_cds\_  
 d38521\_5541-5997,mrna\_for\_kiaa0077\_gene,\_partial\_cds\_  
 d38550\_3195-3735,mrna\_for\_kiaa0075\_gene,\_partial\_cds\_  
 d38583\_109-475,mrna\_for\_calgizzarin,\_complete\_cds  
 d43642mrna\_759-1215,yl-1\_mrna\_for\_yl-1\_protein\_(nuclear\_protein\_with\_dna-  
 binding\_ability),\_complete\_  
 d49489\_1267-1759,mrna\_for\_protein\_disulfide\_isomerase-  
 related\_protein\_p5,\_complete\_cds\_  
 d50916\_5465-5999,mrna\_for\_kiaa0126\_gene,\_complete\_cds

d80009\_3652-4048,mrna\_for\_kiaa0187\_gene,\_complete\_cds  
 d80012\_2697-3237,mrna\_for\_kiaa0190\_gene,\_partial\_cds\_  
 d86978\_5648-6086,mrna\_for\_kiaa0225\_gene,\_partial\_cds\_  
 d87953\_2449-2935,mrna\_for\_rtp,\_complete\_cds  
 hg2259-ht2348\_s\_at\_hg2259-ht2348\_tubulin,\_alpha\_1,\_isoform\_44  
 hg3494-ht3688\_at\_hg3494-ht3688\_nuclear\_factor\_nf-il6\_  
 hg4541-ht4946\_s\_at\_hg4541-ht4946\_transformation-related\_protein  
 j03827\_970-1438,\_y\_box\_binding\_protein-1\_(yb-1)\_mrna  
 l08246\_3333-3819,myeloid\_cell\_differentiation\_protein\_(mcl1)\_mrna  
 l17131mrna#1\_1646-2198,high\_mobility\_group\_protein\_(hmg-i(y))\_gene\_exons\_1-  
 8,\_complete\_cds  
 l19871\_1361-1793,activating\_transcription\_factor(atf3)\_mrna,\_complete\_cds\_  
 l20298\_2250-2790,transcription\_factor\_(cbfb)\_mrna,\_3'\_end\_  
 l39059mrna\_3327-3831,transcription\_factor\_sll\_mrna,\_complete\_cds  
 l77886\_5390-5696,protein\_tyrosine\_phosphatase\_mrna,\_complete\_cds\_  
 ml4328mrna\_1144-1704,alpha\_enolase\_mrna,\_complete\_cds  
 m23254\_2672-3164,ca2-  
 activated\_neutral\_protease\_large\_subunit\_(canp)\_mrna,\_complete\_cds  
 m31303mrna\_933-1407,oncoprotein(op18)\_gene,\_complete\_cds  
 m37721\_3297-3705,peptidylglycine\_alpha-  
 amidating\_monooxygenase\_mrna,\_complete\_cds  
 m69066\_3272-3824,moesin\_mrna,\_complete\_cds\_  
 m83088\_1722-2271,phosphoglucomutase\_(pgm1)\_mrna,\_complete\_cds  
 u24105\_4121-4355,coatomer\_protein\_(hepcop)\_mrna,\_complete\_cds  
 u26173\_1295-1775,bzip\_protein\_nf-il3a\_(il3bp1)\_mrna,\_complete\_cds  
 u28368\_841-1249,id-related\_helix-loop-helix\_protein\_id4\_mrna,\_complete\_cds\_  
 u46692mrna\_84-480,cystatin\_b\_gene,\_complete\_cds\_  
 u51711\_at\_u51711\_u51711,not\_in\_gb\_record,desmocollin-2\_mrna,\_3'\_utr\_  
 u58334\_3933-  
 4485,bcl2,\_p53\_binding\_protein\_bbp/53bp2\_(bbp/53bp2)\_mrna,\_complete\_cds  
 u90651\_1122-  
 1576,embryonic\_ectoderm\_development\_protein\_homolog\_(eed)\_mrna,\_partial\_cds  
 all\_v00572\_1364-1731,mrna\_encoding\_phosphoglycerate\_kinase\_  
 all\_x07834\_515-1026,mrna\_for\_manganese\_superoxide\_dismutase\_(ec\_1.15.1.1)  
 x53416cds\_7595-7889:in\_reversesequence,\_8097-8319,mrna\_for\_actin-  
 binding\_protein\_(filamin)\_(abp-280)  
 all\_x54941\_194-687,ckshs1\_mrna\_for\_cks1\_protein\_homologue  
 all\_x54942\_31-572,ckshs2\_mrna\_for\_cks1\_protein\_homologue\_  
 all\_x76534\_2145-2614,nmb\_mrna  
 x86018cds\_1630-1822:in\_reversesequence,\_1834-2062,mrna\_for\_muf1\_protein

Metagene 431

y08374mrna#1\_1414-1882,\_gp-  
 39\_cartilage\_protein\_gene\_extracted\_fromgene\_encoding\_cartilage\_gp-39\_pro

Metagene 157

af008445\_895-  
 1387,phospholipid\_scamblase\_mrna,\_complete\_cds/gb=af008445/\_ntype=rna\_  
 d29640\_5767-6325,mrna\_for\_kiaa0051\_gene,\_complete\_cds  
 j04088\_4377-4587,dna\_topoisomerase\_ii\_(top2)\_mrna,\_complete\_cds  
 l11239exon\_358-802,homeobox\_protein\_(hox)\_gene,\_3'\_end



l32179mrna\_1028-1556,arylacetamide\_deacetylase\_mrna,\_complete\_cds  
 m21551mrna\_158-590,neuromedin\_b\_mrna,\_complete\_cds  
 m24069mrna\_1401-1543,dna-binding\_protein\_a\_(dbpa)\_gene,\_3'\_end\_  
 m26311\_27-504,cystic\_fibrosis\_antigen\_mrna,\_complete\_cds.  
 all\_m36200\_67-428:in\_m36200cds\_194-339,synaptobrevin(syb1)\_gene  
 m36634\_1340-1450,vasoactive\_intestinal\_peptide\_(vip)\_mrna,\_complete\_cds  
 all\_x04741\_413-924,mrna\_for\_protein\_gene\_product\_(pgp)\_9.5\_  
 y09267\_1148-1664,mrna\_for\_flavin-containing\_monooxygenase/gb=y09267\_/ntype=rna

Metagene 352

ac000115cds#1\_546-684:in\_reversesequence,\_35138-  
 35366,\_wugsc:h\_gs188p18.1a\_gene\_extracted\_frombac\_cl  
 d31887\_4050-4512,mrna\_for\_kiaa0062\_gene,\_partial\_cds\_  
 d79992\_6597-6897,mrna\_for\_kiaa0170\_gene,\_complete\_cds  
 d79994\_4227-4749,mrna\_for\_kiaa0172\_gene,\_partial\_cds\_  
 l06419\_2544-3066,lysyl\_hydroxylase\_(plod)\_mrna,\_complete\_cds  
 l13391exon#5\_265-808,helix-loop-  
 helix\_basic\_phosphoprotein\_(g0s8)\_gene,\_complete\_cds\_  
 l19493exon\_1931-2064,fmr1\_gene,\_3'\_end\_  
 m11313mrna\_3966-4522,alpha-2-macroglobulin\_mrna,\_complete\_cds  
 m86699\_3355-3787,kinase\_(ttk)\_mrna,\_complete\_cds\_  
 s56151\_672-1186,\_hmfg=milk\_fat\_globule\_protein\_[human,\_mrna\_partial,\_1270\_ntl]  
 s69231\_1444-1981,\_tyrp2=tyrosinase-related-protein-  
 2\_[human,\_melanocytic\_cell\_line\_sk-mel-19,\_mrna,\_  
 u07919\_2973-3399,aldehyde\_dehydrogenasemrna,\_complete\_cds\_  
 u20391mrna#1\_720-1080,folate\_receptor\_(folr1)\_gene,\_complete\_cds  
 u26727\_512-938,p16ink4/mts1\_mrna,\_complete\_cds\_  
 u38847\_4574-5000,tar\_rna\_loop\_binding\_protein\_(trp-185)\_mrna,\_complete\_cds\_  
 u58516\_1860-1893,breast\_epithelial\_antigen\_ba46\_mrna,\_complete\_cds\_  
 u66075\_2349-2793,transcription\_factor\_hgata-6\_mrna,\_complete\_cds.  
 u72621\_2581-3145,lot1\_mrna,\_complete\_cds\_  
 u78313\_963-1515,myogenic\_repressor\_i-mf\_(mdfi)\_mrna,\_complete\_cds  
 u85193\_1817-2399,nuclear\_factor\_i-b2\_(nfib2)\_mrna,\_complete\_cds  
 all\_x16354\_2895-  
 3400,mrna\_for\_transmembrane\_carcinoembryonic\_antigen\_bgpa\_(formerly\_tm1-cea)\_  
 all\_x81420\_1150-1601,mrna\_for\_hhkb1\_protein  
 all\_x87241\_14353-14738,mrna\_for\_hfat\_protein\_  
 all\_y07909\_2383-2774,mrna\_for\_progression\_associated\_protein\_  
 z75190cds\_1747-2070:in\_reversesequence,\_2087-  
 2276,mrna\_for\_apolipoprotein\_e\_receptor\_2

Metagene 131

l12723\_1781-2360,heat\_shock\_protein\_70\_(hsp70)\_mrna,\_complete\_cds  
 l14922\_4053-4395,dna-binding\_protein\_(po-ga)\_mrna,\_complete\_cds\_  
 l38932mrna\_1076-1466,gt197\_partial\_orf\_mrna,\_3'\_end\_of\_cds  
 m27891exon\_13-58:in\_reversesequence,\_145-  
 370:not\_in\_gb\_record,cystatin\_c\_(cst3)\_gene\_  
 m81057\_749-1223,procarboxypeptidase\_b\_mrna,\_complete\_cds\_  
 s69272\_853-  
 1403,\_cytoplasmic\_antiproteinase=38\_kda\_intracellular\_serine\_proteinase\_inhibit  
 or\_[human,

u14603\_937-1483,protein-tyrosine\_phosphatase\_(hu-pp-1)\_mrna,\_partial\_sequence  
 u46689\_3317-3863,microsomal\_aldehyde\_dehydrogenase\_(ald10)\_mrna,\_complete\_cds  
 u84388\_905-1055,death\_domain\_containing\_protein\_cradd\_mrna,\_complete\_cds\_  
 all\_x65724\_1307-1746,dna\_for\_orf1\_and\_orf2\_from\_chromosome\_x\_  
 x84002cds\_210-456:in\_reversesequence,\_706-  
 862,tafi20\_mrna\_for\_transcription\_factor\_tfiid\_  
 z19585cds\_2522-2858:in\_reversesequence,\_2909-2939,mrna\_for\_thrombospondin-4\_  
 z49878cds\_367-565:in\_reversesequence,\_734-968,mrna\_for\_guanidinoacetate\_n-  
 methyltransferase\_  
 z84718mrna#1\_424-982,dna\_sequence\_from\_bac\_322b1\_on\_chromosome\_22q11.2-  
 qter\_contains\_gstt1,\_gstt2\_gl

Metagene 368

d87447\_5712-6258,mrna\_for\_kiaa0258\_gene,\_complete\_cds  
 all\_j03589\_2962-3443,ubiquitin-like\_protein\_(gdx)\_gene,\_complete\_cds\_  
 l18960\_679-1177,protein\_synthesis\_factor\_(eif-4c)\_mrna,\_complete\_cds\_  
 m60784mrna\_595-950:in\_reversesequence,\_701-886,u1\_snrnp-  
 specific\_protein\_a\_gene\_  
 m68864\_598-1078,orf\_mrna,\_complete\_cds\_  
 m74002\_2243-2681,arginine-rich\_nuclear\_protein\_mrna,\_complete\_cds\_  
 u09510\_1878-2425,glycyl-trna\_synthetase\_mrna,\_complete\_cds\_  
 u12387\_1468-1722,thiopurine\_methyltransferase\_(tpmt)\_mrna,\_complete\_cds\_  
 u33821\_1229-1661,tax1-binding\_protein\_txbp151\_mrna,\_complete\_cds\_  
 u41163exon#9\_36-266:in\_reversesequence,\_2625-  
 2862:not\_in\_gb\_record,creatine\_transporter\_(slc6a10)\_ge  
 u52111mrna#4\_1182-  
 1671,xq28\_genomic\_dna\_in\_the\_region\_of\_the\_ald\_locus\_containing\_the\_genes\_for\_c  
 rea  
 u59309\_1200-  
 1710,fumarase\_precursor\_(fh)\_mrna,\_nuclear\_gene\_encoding\_mitochondrial\_protein,  
 \_complete  
 u90716\_1825-2299,cell\_surface\_protein\_hcar\_mrna,\_complete\_cds  
 all\_x51521\_2653-3026,mrna\_for\_ezrin  
 x87237cds\_2133-2487:in\_reversesequence,\_2661-2787,mrna\_for\_processing\_a-  
 glucosidase\_i\_  
 all\_x98296\_7705-8096,mrna\_for\_ubiquitin\_hydrolase  
 z49099mrna\_1011-1521,mrna\_for\_spermine\_synthase

Metagene 198

d37965\_913-1393,mrna\_for\_pdgf\_receptor\_beta-  
 like\_tumor\_suppressor\_(prlts),\_complete\_cds  
 d42047\_3472-3970,mrna\_for\_kiaa0089\_gene,\_partial\_cds\_  
 d78134\_727-1261,mrna\_for\_glycine-rich\_rna\_binding\_protein\_cirp,\_complete\_cds\_  
 d87434\_4737-5295,mrna\_for\_kiaa0247\_gene,\_complete\_cds  
 hg2238-ht2321\_s\_at\_hg2238-  
 ht2321\_nuclear\_mitotic\_apparatus\_protein\_1,\_altsplice\_form\_2\_  
 hg2815-ht2931\_at\_hg2815-ht2931\_myosin,\_light\_chain,\_alkali,\_smooth\_muscle,\_non-  
 muscle,\_altsplice\_2\_  
 hg2815-ht4023\_s\_at\_hg2815-  
 ht4023\_myosin,\_light\_chain,\_alkali,\_smooth\_muscle,\_smooth\_muscle,\_altsplic  
 hg4679-ht5104\_at\_hg4679-ht5104\_oncogene\_ret/ptc,\_fusion\_activated

hg651-ht4201\_at\_hg651-ht4201\_adducin\_alpha\_subunit\_altsplice\_2  
 l27560mrna\_986-1262,insulin-like\_growth\_factor\_binding\_protein(igfbp5)\_mrna\_  
 l78132\_3279-3789,prostate\_carcinoma\_tumor\_antigen\_(pcta-1)\_mrna,\_complete\_cds  
 m14648\_5128-  
 5692,cell\_adhesion\_protein\_(vitronectin)\_receptor\_alpha\_subunit\_mrna,\_complete\_  
 cds\_  
 m16447\_997-1489,dihydropteridine\_reductase\_(hdhpr)\_mrna,\_complete\_cds  
 m60483mrna\_1636-2107,\_protein\_phosphatase-2a\_catalytic\_subunit-  
 alpha\_gene\_extracted\_fromprotein\_phos  
 u12778\_2243-2621,acyl-coa\_dehydrogenase\_mrna,\_complete\_cds\_  
 u20362\_2270-2792,tg737\_mrna,\_complete\_cds  
 u37690\_31-355,rna\_polymerase\_ii\_subunit\_(hsrpb10)\_mrna,\_complete\_cds\_  
 u40282\_1205-1706,integrin-linked\_kinase\_(ilkb)\_mrna,\_complete\_cds\_  
 x59834mrna\_2120-2690,rearranged\_mrna\_for\_glutamine\_synthase  
 x62654mrna\_314-788,\_me491\_gene\_extracted\_fromgene\_for\_me491/cd63\_antigen  
 x69908mrna\_151-  
 721,\_p2\_gene\_for\_c\_subunit\_of\_mitochondrial\_atp\_synthase\_gene\_extracted\_fromgen  
 e\_for\_  
 all\_x75861\_1977-2566,tegt\_gene\_  
 y00097cds\_1757-1982:in\_reversesequence,\_2114-2324,mrna\_for\_protein\_p68  
 all\_z47087\_1065-1438,mrna\_for\_rna\_polymerase\_ii\_elongation\_factor-like\_protein\_

Metagene 409

d50683\_5296-5680,mrna\_for\_tgf-beta1ir\_alpha,\_complete\_cds  
 d59253\_306-618,mrna\_for\_ncbp\_interacting\_protein\_1,\_complete\_cds\_  
 d79990\_5065-5383,mrna\_for\_kiaa0168\_gene,\_complete\_cds  
 d86961\_3678-4188,mrna\_for\_kiaa0206\_gene,\_partial\_cds\_  
 d87465\_4793-5243,mrna\_for\_kiaa0275\_gene,\_complete\_cds  
 j04162mrna\_1406-1940,leukocyte\_igg\_receptor\_(fc-gamma-r)\_mrna,\_complete\_cds  
 m14636\_2317-2665,liver\_glycogen\_phosphorylase\_mrna,\_complete\_cds\_  
 m31153exon\_34-232:in\_reversesequence,\_280-484:not\_in\_gb\_record,steroid\_17-  
 alpha-hydroxylase\_gene\_  
 m59465\_3867-  
 4341,tumor\_necrosis\_factor\_alpha\_inducible\_protein\_a20\_mrna,\_complete\_cds  
 m59964\_816-1380,stem\_cell\_factor\_mrna,\_complete\_cds  
 m59979\_2109-2511,prostaglandin\_endoperoxide\_synthase\_mrna,\_complete\_cds  
 m77016\_2106-2622,tropomodulin\_mrna,\_complete\_cds\_  
 s50223\_197-773,\_hkr-t1=kruppel-like\_zinc\_finger\_protein\_[human,\_moltt-  
 cells,\_mrna,\_798\_nt]\_  
 s72869\_2415-  
 2955,\_h4(d10s170)=putative\_cytoskeletal\_protein\_[human,\_thyroid,\_mrna,\_3011\_nt]  
 \_  
 u09284\_693-1173,pinch\_protein\_mrna,\_complete\_cds\_  
 u11732\_997-1531,ets-like\_gene\_(tel)\_mrna,\_complete\_cds\_  
 u17760mrna\_3684-4158,laminin\_s\_b3\_chain\_(lamb3)\_gene  
 u28014\_1086-1233,cysteine\_protease\_(icerel-ii)\_mrna,\_complete\_cds  
 u32849\_867-1383,hou\_mrna,\_complete\_cds\_  
 u37359\_1964-2414,mrel1\_homolog\_hmrel1\_mrna,\_complete\_cds\_  
 u60800\_3638-4010,semaphorin\_(cd100)\_mrna,\_complete\_cds\_  
 u63824\_1129-1645,transcription\_factor\_rtef-1\_(rtef1)\_mrna,\_complete\_cds  
 u68135\_7-204,scc-  
 slc\_mrna\_expressed\_in\_metastatic\_and\_relatively\_radioresistant\_squamous\_cell\_ca  
 rcin

u76638\_1947-2505,brca1-  
 associated\_ring\_domain\_protein\_(bard1)\_mrna,\_complete\_cds\_  
 all\_x07109\_2732-3303,mrna\_for\_protein\_kinase\_c\_(pkc)\_type\_beta\_ii  
 x54870mrna\_1162-1702,mrna\_for\_nkg2-d\_gene  
 x65965exon#1-2\_32-94,sod-  
 2\_gene\_for\_manganese\_superoxide\_dismutase/gb=x65965\_/ntype=dna\_/annot=exon  
 all\_x66079\_925-1400,spi-b\_mrna\_  
 all\_x66533\_1884-2365,soluble\_guanylate\_cyclase\_small\_subunit\_mrna  
 x69819cds\_1122-1620:in\_reversesequence,\_1640-1700,icam-3\_mrna\_  
 x99050mrna\_3041-3461,\_orf\_gene\_extracted\_frommrna\_for\_63\_kda\_protein  
 z25521cds\_526-884:in\_reversesequence,\_1068-  
 1179,integrin\_associated\_protein\_mrna,\_complete\_cds,.

## Metagene 353

d14520\_718-1258,mrna\_for\_gc-box\_binding\_protein\_bteb2,\_complete\_cds  
 d90097cds\_983-1499,amy2b\_gene\_for\_alpha-amylase  
 l33798\_5571-6129,dihydropyridine-sensitive\_l-type\_calcium\_channel\_alpha-  
 1\_subunit\_(cacn11a3)\_mrna,\_c  
 m12959\_1035-1486,t-cell\_receptor\_active\_alpha-  
 chain\_mrna\_from\_jm\_cell\_line,\_complete\_cds\_  
 m16750\_1699-2210,pim-1\_oncogene\_mrna,\_complete\_cds\_  
 m32334cds\_461-737:in\_reversesequence,\_186-  
 348,intercellular\_adhesion\_molecule(icam-2)\_gene\_  
 m37766\_475-955,mem-102\_glycoprotein\_mrna,\_complete\_cds\_  
 m81695\_4051-4597,leukocyte\_adhesion\_glycoprotein\_p150,95\_mrna,\_complete\_cds  
 u48959\_5397-5793,myosin\_light\_chain\_kinase\_(mlck)\_mrna,\_complete\_cds\_  
 u82979\_785-1371,immunoglobulin-like\_transcript-3\_mrna,\_complete\_cds  
 u91903\_1323-1815,fritz\_mrna,\_complete\_cds  
 all\_x00437\_966-1143,mrna\_for\_t-cell\_specific\_protein\_  
 x02910exon#4\_604-1132,gene\_for\_tumor\_necrosis\_factor\_(tnf-alpha)\_  
 all\_x63629\_2582-3126,mrna\_for\_p\_cadherin\_  
 all\_x74039\_805-1058,mrna\_for\_urokinase\_plasminogen\_activator\_receptor  
 all\_x76383\_376-821,mrna\_for\_he3(alpha)\_  
 z35278mrna\_3328-3760,pebp2ac1\_acute\_myeloid\_leukaemia\_mrna\_

## Metagene 379

d85425\_758-1328,mrna\_for\_transactivator\_hsm-1,\_complete\_cds  
 d86977\_3721-4141,mrna\_for\_kiaa0224\_gene,\_complete\_cds  
 all\_d88422\_230-483:in\_d88422cds\_13-188,dna\_for\_cystatin\_a\_  
 hg2743-ht2845\_at\_hg2743-ht2845\_caldesmon\_1,\_altsplice\_3,\_non-muscle  
 hg2743-ht2846\_s\_at\_hg2743-ht2846\_caldesmon\_1,\_altsplice\_4,\_non-muscle  
 hg4068-ht4338\_at\_hg4068-ht4338\_phosphoprotein\_tal2\_  
 l22524cds\_462-734:in\_reversesequence,\_46-197,matrilysin\_gene  
 all\_m13792\_34370-  
 35897:in\_m13792cds\_995:not\_in\_gb\_record,adenosine\_deaminase\_(ada)\_gene,\_complet  
 e\_cd  
 m16038\_1817-2255,lyn\_mrna\_encoding\_a\_tyrosine\_kinase\_  
 m36284mrna\_315-852,glycophorin\_c\_mrna,\_complete\_cds  
 all\_m37485\_1008-1230,\_igh@\_gene\_(ig\_dxp\_heavy-  
 chain\_gene)\_extracted\_fromig\_germline\_h-chain\_d-region

m77349\_2102-2642,transforming\_growth\_factor-  
 beta\_induced\_gene\_product\_(bigh3)\_mrna,\_complete\_cds\_  
 all\_m83216\_3388-3584,aorta\_caldesmon\_mrna,\_complete\_cds  
 u03688\_4501-5047,dioxin-inducible\_cytochrome\_p450\_(cyp1b1)\_mrna,\_complete\_cds  
 u04313\_1983-2523,maspin\_mrna,\_complete\_cds\_  
 u17077\_1716-2190,bene\_mrna,\_partial\_cds  
 u20240\_448-898,c/ebp\_gamma\_mrna,\_complete\_cds  
 u27185\_263-791,rar-responsive\_(tig1)\_mrna,\_complete\_cds  
 u31201mrna\_4592-  
 5106,laminin\_gamma2\_chain\_gene\_(lamc2),laminin\_gamma2\_chain\_gene\_(lamc2)\_  
 u75968\_3641-  
 4139,clone\_c3\_chl1\_protein\_(chlrl)\_mrna,\_alternatively\_spliced,\_complete\_cds\_  
 u90905\_452-992,clone\_23574\_mrna\_sequence\_  
 u90908\_1268-1784,clones\_23549\_and\_23762\_mrna,\_complete\_cds\_  
 all\_x04011\_3678-4255,mrna\_of\_x-  
 cgd\_gene\_involved\_in\_chronic\_granulomatous\_disease\_located\_on\_chromos  
 x04470cds\_24-374:in\_reversesequence,\_408-  
 495,mrna\_for\_antileukoprotease\_(alp)\_from\_cervix\_uterus  
 all\_x16662\_1399-1916,mrna\_for\_vascular\_anticoagulant-beta\_(vac-beta)\_  
 all\_x56692\_1122-1585,mrna\_for\_c-reactive\_protein\_  
 x95325mrna\_783-1250,mrna\_for\_dna\_binding\_protein\_a\_variant\_

## Metagene 303

d43682\_1584-2115,mrna\_for\_very-long-chain\_acyl-  
 coa\_dehydrogenase\_(vlcad),\_complete\_cds\_  
 j05633\_2714-3008,integrin\_beta-5\_subunit\_mrna,\_complete\_cds  
 l07615mrna\_2289-2727,neuropeptide\_y\_receptor\_y1\_(npyy1)\_mrna,\_exon\_3-  
 feb\_and\_complete\_cds/gb=l07615\_  
 l07807\_2600-3147,dynamin\_mrna,\_alternative\_exons\_and\_complete\_cds  
 l27841\_6012-6498,autoantigen\_pericentriol\_material(pcm-1)\_mrna,\_complete\_cds  
 m15182mrna\_1686-2106,beta-glucuronidase\_mrna,\_complete\_cds\_  
 m19309mrna\_382-939,slow\_skeletal\_muscle\_troponin\_t\_mrna,\_clone\_h22h  
 m29877mrna\_1434-1932,alpha-l-fucosidase,\_complete\_cds  
 m36205cds\_73-319:in\_reversesequence,\_26-  
 56:not\_in\_gb\_record,synaptobrevin(syb2)\_gene  
 m62403\_1343-1924,insulin-  
 like\_growth\_factor\_binding\_protein(igfbp4)\_mrna,\_complete\_cds  
 m74715\_1574-2080,alpha-l-iduronidas\_(idua)\_mrna,\_complete\_cds  
 m97815exon#3\_21-405,retinoic\_acid-binding\_protein\_ii\_(crabp-ii)\_gene\_  
 s80437\_1601-  
 2185,\_fatty\_acid\_synthase\_{3'\_region}\_[human,\_breast\_and\_hepg2\_cells,\_mrna\_part  
 ial,\_2237  
 s81914\_760-1180,\_lex-1=radiation-inducible\_immediate-  
 early\_gene\_[human,\_placenta,\_mrna\_partial,\_1223  
 u26726\_1548-1842,11-beta-hydroxysteroid\_dehydrogenase\_typemrna,\_complete\_cds  
 u28369\_2474-2894,semaphorin\_v\_mrna,\_complete\_cds\_  
 u49278\_2752-3262,putative\_dna-binding\_protein\_mrna,\_partial\_cds  
 u53225\_1409-1949,sorting\_nexin(snx1)\_mrna,\_complete\_cds\_  
 all\_u57316\_1593-1996,gcn5\_(hgcn5)\_gene,\_complete\_cds\_  
 u72066\_2672-3212,ctbp\_interacting\_protein\_ctip\_(ctip)\_mrna,\_complete\_cds\_  
 x13238cds\_19-199:in\_reversesequence,\_272-  
 386,mrna\_for\_cytochrome\_c\_oxidase\_subunit\_vic  
 x54232mrna\_3259-3643,mrna\_for\_heparan\_sulfate\_proteoglycan\_(glypican)  
 x57129cds\_373-583:in\_reversesequence,\_1216-1366,h1.2\_gene\_for\_histone\_h1

all\_x82456\_3287-3834,mln50\_mrna  
 y00503cds\_799-1165:in\_reversesequence,\_1221-1227,mrna\_for\_keratin\_19  
 all\_z68228\_2878-3328,mrna\_for\_plakoglobin

Metagene 176

j04027\_4061-4343,plasma\_membrane\_ca2+\_pumping\_atpase\_mrna,\_complete\_cds  
 m11119mrna\_722-1011,endogenous\_retrovirus\_envelope\_region\_mrna\_(p11)\_  
 u29656\_247-751,dr-nm23\_mrna,\_complete\_cds  
 u48251\_2308-2651:not\_in\_gb\_record,protein\_kinase\_c-  
 binding\_protein\_rack7\_mrna,\_partial\_cds  
 u68019\_1774-2218,rad\_protein\_homolog\_(hmad-3)\_mrna,\_complete\_cds  
 u77604\_13-493,microsomal\_glutathione\_s-transferase\_(gst-ii)\_mrna,\_complete\_cds  
 u96922\_2336-2822,inositol\_polyphosphate\_4-phosphatase\_type\_ii-  
 alpha\_mrna,\_complete\_cds/gb=u96922\_/nt  
 x70940cds\_1130-1298:in\_reversesequence,\_1591-  
 1722,mrna\_for\_elongation\_factoralpha-2\_  
 x71973cds\_200-530:in\_reversesequence,\_658-808,gpx-  
 4\_mrna\_for\_phospholipid\_hydroperoxide\_glutathione\_  
 y07827cds\_785-972,mrna\_for\_putb7,3\_molecule\_of\_cd80-cd60\_protein\_family

Metagene 212

d43968\_6790-  
 7222,aml1\_mrna\_for\_aml1b\_protein\_(alternatively\_spliced\_product),\_complete\_cds\_  
 d50477\_1507-2066,mrna\_for\_membrane-  
 type\_matrix\_metalloproteinase\_3,\_complete\_cds\_  
 l13286\_2671-3205,mitochondrial\_1,25-dihydroxyvitamin\_d3\_24-  
 hydroxylase\_mrna,\_complete\_cds  
 m68516mrna\_1662-  
 2172,\_pci\_gene\_(plasminogen\_activator\_inhibitor\_3)\_extracted\_fromprotein\_c\_inhi  
 bitor  
 u72649\_2206-2584,btg2\_(btg2)\_mrna,\_complete\_cds  
 x17059cds\_522-840:in\_reversesequence,\_1331-1418,nat1\_gene\_for\_arylamine\_n-  
 acetyltransferase\_  
 x81889cds\_3255-3561:in\_reversesequence,\_3774-3786,mrna\_for\_p0071\_protein

Metagene 221

hg1763-ht1780\_s\_at\_hg1763-ht1780\_prolactin-induced\_protein\_  
 l19778\_1871-2207,histone\_(h2a.1b)\_mrna,\_complete\_cds  
 m35851cds\_2287-2708:in\_reversesequence,\_200-266,androgen\_receptor\_gene

Metagene 86

d12485\_2904-3444,mrna\_for\_nucleotide\_pyrophosphatase,\_complete\_cds\_  
 d42123\_655-1135,mrna\_for\_esp1/crp2,\_complete\_cds\_  
 d63479\_5529-6079,mrna\_for\_kiaa0145\_gene,\_complete\_cds  
 m16938\_1154-1659,homeo\_box\_c8\_protein,\_mrna,\_complete\_cds

m59815mrna\_5022-5424, complement\_component\_c4a\_gene\_  
 m63167\_2039-2429, rac\_protein\_kinase\_alpha\_mrna, \_complete\_cds\_  
 u24266\_2533-3103, pyrroline-5-  
 carboxylate\_dehydrogenase\_(p5cdh)\_mrna, \_long\_form, \_complete\_cds\_  
 u33147\_43-463, mammaglobin\_mrna, \_complete\_cds\_  
 u68142\_1372-1900, ralgds-like(rgl2)\_mrna, \_partial\_cds  
 u83411\_1505-2039, carboxypeptidase\_z\_precursor, \_mrna, \_complete\_cds.  
 u94592\_1287-1809, uncoupling\_protein\_homolog\_(ucph)\_mrna, \_complete\_cds  
 all\_x78706\_1878-2443, mrna\_for\_carnitine\_acetyltransferase

Metagene 488

reverse\_ac002076\_127531-127606, \_wugsc:gs345d13.2\_gene\_(g-protein\_gamma-  
 1\_subunit)\_extracted\_frombac\_  
 d13637\_2062-2566, mrna\_for\_kiaa0012\_gene, \_complete\_cds  
 d28915cds\_1002-1272:in\_reversesequence, \_114-186, gene\_for\_hepatitis\_c-  
 associated\_microtubular\_aggrega  
 hg2705-ht2801\_s\_at\_hg2705-ht2801\_serine/threonine\_kinase\_  
 k02765\_4466-  
 4916, complement\_component\_c3\_mrna, \_alpha\_and\_beta\_subunits, \_complete\_cds\_  
 l06175\_1924-2482, p5-1\_mrna, \_complete\_cds  
 l12535\_1641-2151, rsu-1/rsp-1\_mrna, \_complete\_cds  
 m11147mrna\_251-689, ferritin\_l\_chain\_mrna, \_complete\_cds\_  
 m13699mrna\_2810-3278, ceruloplasmin\_(ferroxidase)\_mrna, \_complete\_cds  
 m30818mrna\_2384-2888, interferon-  
 induced\_cellular\_resistance\_mediator\_protein\_(mxb)\_mrna, \_complete\_cd  
 m33195\_13-457, fc-epsilon-receptor\_gamma-chain\_mrna, \_complete\_cds\_  
 m37435\_3368-3914, macrophage-specific\_colony-stimulating\_factor\_(csf-  
 1)\_mrna, \_complete\_cds  
 m55542mrna\_2310-2802, guanylate\_binding\_protein\_isoform\_i\_(gbp-  
 2)\_mrna, \_complete\_cds  
 m68874\_2293-2779, phosphatidylcholine\_2-acylhydrolase\_(cpla2)\_mrna, \_complete\_cds  
 m81750mrna\_1132-  
 1645, myeloid\_cell\_nuclear\_differentiation\_antigen\_mrna, \_complete\_cds\_  
 u52101\_61-451, ymp\_mrna, \_complete\_cds\_  
 all\_x02530\_571-1118, mrna\_for\_gamma-  
 interferon\_inducible\_early\_response\_gene\_(with\_homology\_to\_platel  
 all\_x99886\_601-2202:in\_x99886cds\_96-127, mcp-2\_gene  
 all\_z83735\_344-817, hh3/k\_gene

Metagene 144

ab006782\_1392-1672, mrna\_for\_galectin-  
 9\_isoform, \_complete\_cds/gb=ab006782\_/ntype=rna\_  
 d32129\_920-1425, mrna\_for\_hla-i\_(hla-a26)\_heavy\_chain, \_complete\_cds\_(clone\_cmiy-  
 1)  
 all\_d49824\_945-978, hla-b\_null\_allele\_mrna, hla-b\_null\_allele\_mrna  
 hg2915-ht3059\_f\_at\_hg2915-ht3059\_major\_histocompatibility\_complex, \_i, \_e  
 hg2917-ht3061\_f\_at\_hg2917-ht3061\_major\_histocompatibility\_complex, \_i, \_e  
 hg3597-ht3800\_f\_at\_hg3597-ht3800\_major\_histocompatibility\_complex, \_i\_  
 hg658-ht658\_f\_at\_hg658-ht658\_major\_histocompatibility\_complex, \_i, \_c  
 j00105\_24-520, beta-2\_microglobulin\_gene\_mrna, \_3'\_end\_  
 j04080mrna\_2136-2604, complement\_component\_clr\_mrna, \_complete\_cds\_

m13690mrna\_1190-1739,plasma\_protease\_(c1)\_inhibitor\_mrna,\_complete\_cds\_  
 m14058\_1982-2438,complement\_clr\_mrna,\_complete\_cds\_  
 m58286\_1533-2054,tumor\_necrosis\_factor\_receptor\_mrna,\_complete\_cds  
 m63838\_2097-2643,interferon-gamma\_induced\_protein\_(ifi\_16)\_gene,\_complete\_cds  
 m64099\_1873-2371,gamma-glutmyl\_transpeptidase-related\_protein\_(ggt-rel)\_mrna,\_complete\_cds\_  
 m92357\_3609-4131,b94\_protein\_mrna,\_complete\_cds\_  
 m94880\_f\_at\_m94880\_m94880,\_4040\_in\_m94880\_515-1055,mhc\_i\_(hla-a\*8001)\_mrna  
 m97935\_3412-3886,transcription\_factor\_isgf-3\_mrna\_sequence\_  
 u49020mrna#1\_4711-5228,\_mef2a\_gene\_(myocyte-specific\_enhancer\_factor\_2a,\_c9\_form)\_extracted\_frommyoc  
 u70451\_2097-  
 2607,myleoid\_differentiation\_primary\_response\_protein\_myd88\_mrna,\_complete\_cds.  
 all\_x07696\_1300-1685,mrna\_for\_cytokeratin\_15\_  
 x12451mrna\_974-1496,mrna\_for\_pro-cathepsin\_l\_(major\_excreted\_protein\_mep)\_  
 x53587mrna\_5160-5688,mrna\_for\_integrin\_beta\_4  
 all\_x82200\_2236-2801,staf50\_mrna\_  
 x83416exon\_1688-2160,prp\_gene,\_exon\_2  
 all\_z19554\_1243-1734,vimentin\_gene\_

Metagene 288

l07919\_1386-1779,homeodomain\_protein\_dlx-2\_mrna,\_3'\_end  
 u17032\_4391-4961,p190-b\_(p190-b)\_mrna,\_complete\_cds

Metagene 454

all\_102326\_2-320,(clone\_hu\_lambda-17)\_lambda-like\_gene,\_complete\_cds  
 all\_m34516\_426-  
 469,omega\_light\_chain\_protein\_14.1\_(ig\_lambda\_chain\_related)\_gene,omega\_light\_c  
 hain\_p  
 all\_m34516\_426-  
 469,omega\_light\_chain\_protein\_14.1\_(ig\_lambda\_chain\_related)\_gene,omega\_light\_c  
 hain\_p  
 m63438\_794-1195,ig\_rearranged\_gamma\_chain\_mrna,\_v-j-c\_region\_and\_complete\_cds  
 m87789\_1021-1512,(hybridoma\_h210)\_anti-  
 hepatitis\_a\_igg\_variable\_region,\_constant\_region,\_complementa  
 v00563mrna\_19-127,gene\_for\_immunoglobulin\_mu,\_part\_of\_exon\_8.  
 x53961cds\_1772-2060:in\_reversesequence,\_2450-2564,mrna\_for\_lactoferrin  
 x57809mrna\_309-  
 449,rearranged\_immunoglobulin\_lambda\_light\_chain\_mrna,rearranged\_immunoglobulin  
 \_lambd

Metagene 68

d63875\_3762-4200,mrna\_for\_kiaa0155\_gene,\_complete\_cds  
 d87002cds#2\_4-201:not\_in\_gb\_record,\_pom121-  
 likegene\_extracted\_from(lambda)\_dna\_for\_immunoglobulin\_ligh  
 all\_j00277\_3607-3724,(genomic\_clones\_lambda-[sk2-t2,\_hs578t];\_cdna\_clones\_rs-  
 [3,4,\_6])\_c-ha-ras1\_pro  
 j04810\_2923-3414,msh3\_gene,\_complete\_cds\_



m13232mrna\_1850-  
 2405, factor\_vii\_serine\_protease\_precursor\_mrna, \_complete\_cds, \_clone\_lambda-  
 hvii2463  
 m34376mrna\_2-238, (clone\_lambda\_msp131)\_beta-microseminoprotein\_(msp)\_gene\_  
 all\_m76732\_736-1273, hox7\_gene  
 s67325\_1328-  
 1712, \_propionyl\_coa\_carboxylase\_beta\_subunit\_[human, \_liver, \_placenta, \_hl1008, \_m  
 rna, \_1791  
 u09196mrna\_725-1169, 1.1\_kb\_mrna\_upregulated\_in\_retinoic\_acid\_treated\_hl-  
 60\_neutrophilic\_cells  
 u21858\_704-1064, transcriptional\_activation\_factor\_tafii32\_mrna, \_complete\_cds\_  
 u26266\_490-1046, deoxyhypusine\_synthase\_mrna, \_complete\_cds/gb=u26266/\_ntype=rna\_  
 u31176\_1677-2217, hcrv1\_mrna, \_complete\_cds  
 u37221\_1537-1981, cyclophilin-like\_protein\_mrna, \_partial\_cds  
 u43408\_2308-2668, tyrosine\_kinase\_(tnk1)\_mrna, \_complete\_cds\_  
 u50383\_2015-2441, retinoic\_acid-responsive\_protein\_(nn8-4ag)\_mrna, \_complete\_cds\_  
 u61981\_3743-  
 3819, putative\_mismatch\_repair/binding\_protein\_hmsh3\_(hmsh3)\_mrna, \_complete\_cds\_  
 u66702\_4190-4616, phogrin\_mrna, \_complete\_cds  
 u83239\_323-877, cc\_chemokine\_stcp-1\_mrna, \_complete\_cds  
 all\_x52426\_1139-1665, mrna\_for\_cytokeratin\_13\_  
 all\_x64643\_1944-2407, c6.1a\_mrna  
 x68733mrna\_1056-1488, gene\_for\_alpha1-antichymotrypsin, \_exon\_1\_  
 all\_x81836\_812-1414, mrna\_for\_dents\_disease\_candidate\_gene  
 x89984cds\_465-573:in\_reversesequence, \_1646-1820, mrna\_for\_bcl7a\_protein  
 all\_x91648\_1082-1611, mrna\_for\_pur\_alpha\_extended\_3'\_untranslated\_region  
 all\_x92106\_1361-1932, mrna\_for\_bleomycin\_hydrolase  
 x93036cds\_88-163:in\_reversesequence, \_34-37, mrna\_for\_mat8\_protein  
 all\_x96484\_497-1056, mrna\_for\_dgcr6\_protein  
 x97444cds\_2-405, mrna\_for\_transmembrane\_protein\_tmp21-iiex/gb=x97444/\_ntype=rna\_  
 x98834mrna\_4116-  
 4620, \_zinc\_finger\_protein\_hsa12\_gene\_extracted\_frommrna\_for\_zinc\_finger\_protein  
 , \_hsa  
 z78289\_35-153, mrna\_(clone\_1d2).

Metagene 47

m30496\_321-759, ubiquitin\_carboxyl-terminal\_hydrolase\_(pgp\_9.5, \_uch-  
 l3)\_isozyme\_l3\_mrna, \_complete\_cds  
 s62539\_5366-5756, \_insulin\_receptor\_substrate-  
 1\_[human, \_skeletal\_muscle, \_mrna, \_5828\_nt]  
 s77393\_43-  
 205, \_transcript\_ch138\_[human, \_rf1, rf48\_stomach\_cancer\_cell\_lines, \_mrna, \_235\_nt]  
 /gb=s77393\_  
 u17886mrna\_507-981, succinate\_dehydrogenase\_iron-protein\_subunit\_(sdhb)\_gene  
 x82068cds\_2293-2647:in\_reversesequence, \_3019-  
 3103, mrna\_for\_glutamate\_receptor\_subunit\_glurc\_  
 all\_x86163\_2233-2564, mrna\_for\_b2-bradykinin\_receptor, \_3'\_  
 x93511cds\_2-312, mrna\_for\_telomeric\_dna\_binding\_protein\_(orf1)

Metagene 474

d83243\_5401-5857, npat\_mrna, \_complete\_cds\_

hg4297-ht4567\_at\_hg4297-ht4567\_transcriptional\_coactivator\_pc4\_  
 122075\_795-1377,guanine\_nucleotide\_regulatory\_protein\_(g13)\_mrna,\_complete\_cds\_  
 140157\_4445-4907,endosome-associated\_protein\_(eea1)\_mrna,\_complete\_cds\_  
 140400mrna\_2014-2542,(clone\_zap113)\_mrna,\_3'\_end\_of\_cds\_  
 176571cds\_440-734:in\_reversesequence,\_1070-  
 1310,nuclear\_hormone\_receptor\_(shp)\_gene,\_3'\_end\_of\_cds  
 s62028\_496-1041,\_recoverin\_[human,\_retina,\_mrna,\_1108\_nt]\_  
 u31248\_1663-2209,zinc\_finger\_protein\_(znf174)\_mrna,\_complete\_cds\_  
 u49516\_4157-4691,serotonin\_5-ht2c\_receptor\_mrna,\_complete\_cds  
 x53595cds\_525-1007:in\_reversesequence,\_1054-1104,mrna\_for\_beta-2-  
 glycoprotein\_i\_(apolipoprotein\_h)  
 x90858cds#2\_396-888:in\_reversesequence,\_1270-  
 1306,mrna\_for\_uridine\_phosphorylase

Metagene 455

l12060mrna\_1032-1411,retinoic\_acid\_receptor\_(gamma-7)\_mrna  
 l32832\_11295-11853,zinc\_finger\_homeodomain\_protein\_(atbf1-  
 a)\_mrna,\_complete\_cds.  
 l33842mrna\_1213-1639,(clone\_ffe-  
 7)\_type\_ii\_inosine\_monophosphate\_dehydrogenase\_(impdh2)\_gene,\_exons\_  
 l36644mrna\_3085-3137,receptor\_protein-tyrosine\_kinase\_(hek7)\_mrna,\_3'\_end\_  
 l49219exon\_2-42:in\_reversesequence,\_70-  
 79,retinoblastoma\_susceptibility\_protein\_(rb1)\_l486wbp\_deleti  
 u21943\_2246-  
 2678,organic\_anion\_transporting\_polypeptide\_(oatp)\_mrna,\_complete\_cds  
 u41767\_2113-2688,metargidin\_precursor\_mrna,\_complete\_cds\_  
 u46461\_1591-2152,dishevelled\_homolog\_(dvl)\_mrna,\_complete\_cds  
 u50062\_1713-2181,rip\_protein\_kinase\_gene,\_complete\_cds\_  
 x52213cds\_810-1371,ltk\_mrna  
 x57025mrna\_6635-7151,igf-i\_mrna\_for\_insulin-like\_growth\_factor\_i\_  
 x66142cds\_2216-2539:in\_reversesequence,\_2600-  
 2643,mrna\_for\_rod\_cgmp\_phosphodiesterase\_  
 x99897cds\_6561-6760:in\_reversesequence,\_7057-7274,mrna\_for\_p/q-  
 type\_calcium\_channel\_alpha1\_subunit\_

Metagene 325

d86096\_cds1\_s\_at\_d86096\_d86096,not\_in\_gb\_record,\_ep3-  
 iv\_gene\_extracted\_fromdna\_for\_prostaglandin\_e\_r  
 d86096\_cds3\_at\_d86096\_d86096,not\_in\_gb\_record,\_ep3-  
 iv\_gene\_extracted\_fromdna\_for\_prostaglandin\_e\_rec  
 s74720\_1889-1995,\_dax-1=dss-  
 ahc\_critical\_region\_on\_x\_chromosome,\_gene[human,\_adrenal\_hypoplasia\_cong  
 all\_x17098\_1278-1357,psgl0\_mrna\_for\_pregnancy\_specific\_glycoprotein\_10\_

Metagene 135

l40396mrna\_1542-2028,(clone\_s22i71)\_mrna\_fragment\_  
 m21186\_122-650,neutrophil\_cytochrome\_b\_light\_chain\_p22\_phagocyte\_b-  
 cytochrome\_mrna,\_complete\_cds\_

m98833\_2383-2899,ergb\_transcription\_factor\_(fli-1\_homolog)\_mrna,\_complete\_cds\_  
u27655\_2169-2577,rgp3\_mrna,\_complete\_cds\_

## Metagene 74

l21715\_127-631,troponin\_i\_fast-twitch\_isoform\_mrna,\_complete\_cds\_  
l76687mrna\_1823-2291,grb14\_mrna,\_complete\_cds\_  
y07596cds\_1035-1149:in\_reversesequence,\_1173-1509,mrna\_for\_gpi8\_protein\_  
z19574mrna\_1039-1479,gene\_for\_cytokeratin\_17

## Metagene 372

ac002486cds\_812-1358,bac\_clone\_rg367o17\_from\_7p15-  
p21,\_complete\_sequence/gb=ac002486\_/ntype=dna\_/ann  
af002700\_931-1471,tgf-  
beta\_related\_neurotrophic\_factor\_receptor(trnr2)\_mrna,\_complete\_cds\_  
d13168exon\_2254-2800,gene\_for\_endothelin-b\_receptor\_(het-br)\_  
j00148cds#1\_103-613:in\_reversesequence,\_1796-  
1841,growth\_hormone\_(somatotropin,\_gh1)\_gene,\_complete\_  
j04093\_1842-2342,phenol\_udp-glucuronosyltransferase\_(udpgt)\_mrna,\_complete\_cds\_  
m22995\_1008-1542,ras-related\_protein\_(krev-1)\_mrna,\_complete\_cds\_  
u90336\_2606-3074,peg3\_mrna,\_partial\_cds\_  
all\_x69886\_1163-1504,mrna\_for\_glycerol\_kinase  
x92814cds\_194-458:in\_reversesequence,\_907-937,mrna\_for\_rat\_hrev107-  
like\_protein\_  
z20656mrna\_5438-5751,of\_cardiac\_alpha-myosin\_heavy\_chain\_gene

## Metagene 304

d13639\_5889-6345,mrna\_for\_kiak0002\_gene,\_complete\_cds\_  
d89077\_2160-2592,mrna\_for\_src-like\_adapter\_protein,\_complete\_cds\_  
hg1872-ht1907\_at\_hg1872-ht1907\_major\_histocompatibility\_complex,\_dg  
hg3576-ht3779\_f\_at\_hg3576-ht3779\_major\_histocompatibility\_complex,\_ii\_beta\_w52\_  
all\_j00123\_539-1020,enkephalin\_gene  
j03909\_461-995,gamma-interferon-inducible\_protein\_(ip-30)\_mrna,\_complete\_cds\_  
j04130mrna\_87-634,activation\_(act-2)\_mrna,\_complete\_cds\_  
all\_k02405\_5550-7761:in\_k02405cds\_778,mhc\_ii\_hla-dc-3-beta\_gene\_(dr3,3)\_  
m12529mrna\_562-1132,apolipoprotein\_e\_mrna,\_complete\_cds\_  
m12886\_950-1091,t-cell\_receptor\_active\_beta-chain\_mrna,\_complete\_cds\_  
m13560exon\_3-562:in\_gb\_record,ia-associated\_invariant\_gamma-chain\_gene  
m20902cds\_2-200:in\_reversesequence,\_517-5083,apolipoprotein\_c-  
i\_(vldl)\_gene,\_complete\_cds\_  
m21119\_137-591,lysozyme\_mrna,\_complete\_cds\_  
m26062\_3505-3871,interleukinreceptor\_beta\_chain\_(p70-75)\_mrna,\_complete\_cds\_  
m34996\_448-699,mhc\_cell\_surface\_glycoprotein\_(hla-dqa)\_mrna,\_3'\_end  
m57466mrna\_514-1036,mhc\_ii\_hla-dp\_light\_chain\_mrna,\_complete\_cds\_  
m59807mrna\_369-933,nk4\_mrna,\_complete\_cds\_  
m63835mrna\_896-1388,igg\_fc\_receptor\_i\_gene\_  
u15085\_821-1289,hla-dmb\_mrna,\_complete\_cds\_  
u19713\_18-374,allograft-inflammatory\_factor-1\_mrna,\_complete\_cds\_  
u20158\_1551-1911,76\_kda\_tyrosine\_phosphoprotein\_slp-76\_mrna,\_complete\_cds\_

u51240\_1679-2171,lysosomal-  
 associated\_multitransmembrane\_protein\_(laptm5)\_mrna,\_complete\_cds\_  
 u89922\_267-  
 773,lymphotoxin\_beta\_isoform\_variant,\_alternatively\_spliced\_mrna,\_complete\_cds  
 x00274exon#5\_1-337:not\_in\_gb\_record,gene\_for\_hla-  
 dr\_alpha\_heavy\_chain\_a\_ii\_antigen\_(immune\_response\_  
 x03068\_f\_at\_x03068\_x03068,\_40\_in\_x03068cds\_600-750:\_29\_in\_reversesequence,\_867-  
 1167,mrna\_for\_hla-d\_i  
 x03100mrna\_908-1124:in\_reversesequence,\_10629-10851,\_hla-  
 sb\_alpha\_gene\_(class\_ii\_antigen)\_extracted\_  
 all\_x07743\_2156-2679,mrna\_for\_pleckstrin\_(p47)\_  
 all\_x16663\_1397-1872,hs1\_gene\_for\_heamatopoietic\_lineage\_cell\_specific\_protein\_  
 all\_x59892\_2163-2542,mrna\_for\_ifn\_inducible\_gamma2\_protein\_  
 x62744cds\_469-745:in\_reversesequence,\_814-  
 1018,ring6\_mrna\_for\_hla\_ii\_alpha\_chain-like\_product\_  
 x66401cds#1\_327-615:in\_fullsequence,\_45931-  
 47208:not\_in\_gb\_record,\_lmp2\_gene\_extracted\_fromgenes\_tap  
 x68090cds\_5-61,fc-gamma-  
 riia\_gene\_for\_igg\_fc\_receptor\_ii\_a\_(5'\_flank)/gb=x68090/\_ntype=dna/\_annot=cds  
 all\_x72755\_2106-2479,humig\_mrna  
 x89109cds\_860-1326:in\_reversesequence,\_1457-1488,mrna\_for\_coronin\_  
 z36531cds\_934-1294:in\_reversesequence,\_1345-1453,mrna\_for\_fibrinogen-  
 like\_protein\_(pt49\_protein)

Metagene 10

d78333\_1188-1734,mrna\_for\_testis-specific\_tcp20,\_complete\_cds  
 m86707\_1190-1580,myristoyl\_coa:protein\_n-myristoyltransferase\_mrna  
 s77410\_1805-2225,\_typeangiotensin\_ii\_receptor\_[human,\_liver,\_mrna,\_2268\_nt]  
 u25997\_3311-3824,stanniocalcin\_precursor\_(stc)\_mrna,\_complete\_cds  
 u40490\_3673-  
 4177,nicotinamide\_nucleotide\_transhydrogenase\_mrna,\_nuclear\_gene\_encoding\_mitoc  
 hondrial\_  
 u50078\_14603-15101,guanine\_nucleotide\_exchange\_factor\_p532\_mrna,\_complete\_cds  
 u65932\_1244-1634,extracellular\_matrix\_protein(ecm1)\_mrna,\_complete\_cds  
 all\_x84373\_6655-7208,mrna\_for\_nuclear\_factor\_rip140

Metagene 273

d13666\_2630-3072,mrna\_for\_osteoblast\_specific\_factor(osf-2os)  
 d21255\_3362-3812,mrna\_for\_ob-cadherin-2,\_complete\_cds  
 hg1140-ht4817\_s\_at\_hg1140-ht4817\_collagen,\_type\_vi,\_alpha\_2,\_altsplice\_2\_  
 hg3044-ht3742\_s\_at\_hg3044-ht3742\_fibronectin,\_altsplice\_1  
 hg3431-ht3616\_s\_at\_hg3431-ht3616\_decorin,\_altsplice\_1  
 j04177\_5773-6133,alpha-1\_type\_xi\_collagen\_(col11a1)\_mrna,\_complete\_cds\_  
 all\_116895\_1511-2016,lysyl\_oxidase\_(lox)\_gene,\_exon\_7  
 m24486mrna\_2110-2684,prolyl\_4-  
 hydroxylase\_alpha\_subunit\_mrna,\_complete\_cds,\_clone\_pa-11  
 m65292\_667-1202,factor\_h\_homologue\_mrna,\_complete\_cds  
 u21128\_1254-1632,lumican\_mrna,\_complete\_cds  
 u37283\_370-868,microfibril-associated\_glycoprotein-2\_magp-2\_mrna,\_complete\_cds\_  
 all\_x02761\_7082-7646,mrna\_for\_fibronectin\_(fn\_precursor)\_  
 all\_x06700\_1946-2466,mrna\_3'\_region\_for\_pro-alpha1(iii)\_collagen\_

all\_x14787\_5124-5701,mrna\_for\_thrombospondin\_  
 x52022\_9941-10349,rna\_for\_type\_vi\_collagen\_alpha3\_chain  
 x57766mrna\_1658-2168,stromelysin-3\_mrna  
 all\_x82153\_1128-1615,mrna\_for\_cathepsin\_o  
 all\_z74615\_5320-5852,mrna\_for\_prepro-alpha1(i)\_collagen  
 all\_z74616\_4470-4992,mrna\_for\_prepro-alpha2(i)\_collagen

Metagene 330

d10040\_3243-3489,mrna\_for\_long-chain\_acyl-coa\_synthetase\_  
 d55654\_786-1224,mrna\_for\_cytosolic\_malate\_dehydrogenase,\_complete\_cds  
 d63874\_865-1153,mrna\_for\_hmg-1,\_complete\_cds\_  
 d63878\_2850-3408,mrna\_for\_kiaa0158\_gene,\_complete\_cds  
 d63880\_4952-5504,mrna\_for\_kiaa0159\_gene,\_complete\_cds  
 d79205\_5-319:in\_reversesequence,\_323-  
 325,mrna\_for\_ribosomal\_protein\_139,\_complete\_cds\_  
 d79996\_1759-2305,mrna\_for\_kiaa0174\_gene,\_complete\_cds  
 d90209\_1420-1972,mrna\_for\_dna\_binding\_protein\_taxreb67\_  
 hg1116-ht1116\_at\_hg1116-ht1116\_proliferating-cell\_nucleolar\_antigen,\_120\_kda\_  
 hg4312-ht4582\_s\_at\_hg4312-ht4582\_transcription\_factor\_iiia\_  
 hg4334-ht4604\_s\_at\_hg4334-ht4604\_glycogenin  
 j05032\_1721-2153,aspartyl-trna\_synthetase\_alpha-2\_subunit\_mrna,\_complete\_cds\_  
 l08069\_909-1347,heat\_shock\_protein,\_ecoli\_dnaj\_homologue\_mrna,\_complete\_cds  
 l13761mrna\_3838-4270,dihydrolipoamide\_dehydrogenase\_gene,\_exon\_14\_  
 l20941\_615-1143,ferritin\_heavy\_chain\_mrna,\_complete\_cds  
 l25931\_3127-3607,lamin\_b\_receptor\_(lbr)\_mrna,\_complete\_cds\_  
 l33881\_1822-2206,protein\_kinase\_c\_iota\_isoform,\_complete\_cds\_  
 l76200\_268-796,guanylate\_kinase\_(guk1)\_mrna,\_complete\_cds  
 m15990\_3916-4390,c-yes-1\_mrna  
 all\_m19283\_2724-3319,cytoskeletal\_gamma-actin\_gene,\_complete\_cds\_  
 m22382mrna\_1758-  
 2184,mitochondrial\_matrix\_protein\_p1\_(nuclear\_encoded)\_mrna,\_complete\_cds  
 m26880\_2206-2246,ubiquitin\_mrna,\_complete\_cds  
 m29064\_1225-1657,hnrnp\_b1\_protein\_mrna\_  
 m33521exon#2\_2706-3144:in\_reversesequence,\_4118-4148,hla-b-  
 associated\_transcript(bat3)\_gene,\_5'\_end  
 m55531mrna\_1647-2175,glucose\_transport-like(glut5)\_mrna,\_complete\_cds\_  
 m60858mrna\_2193-2481,nucleolin\_gene,\_complete\_cds\_  
 m84739\_1366-1876,autoantigen\_calreticulin\_mrna,\_complete\_cds\_  
 m85169\_2712-3276,homologue\_of\_yeast\_sec7\_mrna,\_complete\_cds  
 m94556\_171-  
 567,mitochondrial\_specific\_single\_stranded\_dna\_binding\_protein\_mrna,\_complete\_c  
 ds\_  
 m96843\_668-  
 1112,striated\_muscle\_contraction\_regulatory\_protein\_(id2b)\_mrna,\_complete\_cds\_  
 m96982\_483-801,u2\_snrnp\_auxiliary\_factor\_small\_subunit,\_complete\_cds  
 s63912\_2442-3018,\_d10s102=fbrnp\_[human,\_fetal\_brain,\_mrna,\_3043\_ntl]  
 u05227\_1078-1564,rar\_protein\_mrna,\_complete\_cds  
 u07550\_139-493,chaperoninmrna,\_complete\_cds  
 u09587\_2261-2330,glycyl-trna\_synthetase\_mrna,\_complete\_cds.  
 u19247mrna\_1469-1939,interferon-gamma\_receptor\_alpha\_chain\_gene\_  
 u24576\_1467-2013,breast\_tumor\_autoantigen\_mrna,\_complete\_sequence  
 u40369mrna\_851-995,spermidine/spermine\_n1-  
 acetyltransferase\_(ssat)\_gene,\_complete\_cds\_  
 u41816\_614-1004,c-1\_mrna,\_complete\_cds\_

u47635\_1921-2353,d13s824e\_locus\_mrna,\_complete\_cds\_  
 u51478\_856-1282,sodium/potassium-transporting\_atpase\_beta-  
 3\_subunit\_mrna,\_complete\_cds\_  
 u63743\_2187-2715,mitotic\_centromere-associated\_kinesin\_mrna,\_complete\_cds\_  
 u69126\_1831-2345,fuse\_binding\_protein(fbp2)\_mrna,\_partial\_cds\_  
 u75308\_3654-4092,tdp-associated\_factor\_(htafii130)\_mrna,\_partial\_cds\_  
 u90552\_2814-  
 3377,butyrophilin\_(btf5)\_mrna,\_complete\_cds,butyrophilin\_(btf5)\_mrna,\_complete\_cds  
 all\_x14684\_629-1150,mrna\_for\_la\_protein\_c-terminal\_region  
 all\_x51755\_8272-8537,\_ig\_light-chain,\_partial\_ke-oz-\_polypeptide;\_author-  
 given\_protein\_sequence\_is\_i  
 x56494mrna#1\_1894-2398,m\_gene\_for\_m1-type\_and\_m2-type\_pyruvate\_kinase  
 all\_x59812\_1586-2025,cyp\_27\_mrna\_for\_vitamin\_d3\_25-hydroxylase\_  
 all\_x60221\_635-1044,mrna\_for\_h+-atp\_synthase\_subunit\_b\_  
 all\_x78627\_2163-2674,mrna\_for\_translin\_  
 all\_x99325\_1482-1927,mrna\_for\_ste20-like\_kinase  
 all\_z29064\_3656-4251,af-1p\_mrna  
 z50022mrna\_2064-2478,mrna\_for\_surface\_glycoprotein\_  
 z74792mrna\_1470-1917,mrna\_for\_ccaat\_transcription\_binding\_factor\_subunit\_gamma.

## Metagene 205

j02973mrna\_3467-  
 4007,\_thbd\_gene\_extracted\_fromthrombomodulin\_gene,\_complete\_cds\_  
 l36069\_1283-  
 1709,high\_conductance\_inward\_rectifier\_potassium\_channel\_alpha\_subunit\_mrna,\_co  
 mplete\_cd  
 u51587\_4262-4772,golgi\_complex\_autoantigen\_golgin-97\_mrna,\_complete\_cds  
 all\_x55666\_1222-1613,usf\_mrna\_for\_late\_upstream\_transcription\_factor\_  
 x58377mrna\_1716-2232,mrna\_for\_adipogenesis\_inhibitory\_factor\_

## Metagene 117

all\_m21642\_180-  
 301,(dysfunctional)\_antithrombin\_iii\_(atiii)\_utah\_gene,(dysfunctional)\_antithro  
 mbin\_i  
 m83772\_1565-2015,flavin-  
 containing\_monooxygenase\_form\_ii\_(fmo2)\_mrna,\_complete\_cds\_  
 y07829exon#1\_7-  
 283,\_exon\_fromgene\_encoding\_ring\_finger\_protein/gb=y07829\_/ntype=dna\_/annot=exo  
 n,\_exo

## Metagene 28

d14822\_570-  
 717,chimeric\_mrna\_derived\_from\_aml1\_gene\_and\_mtg8(eto)\_gene,\_partial\_sequence.  
 d87743\_3861-4323,mrna\_for\_kiaa0267\_gene,\_partial\_cds\_  
 hg3942-ht4212\_at\_hg3942-ht4212\_interferon  
 l14787\_1203-1641,dna-binding\_protein\_mrna,\_3'\_end  
 l15388\_1992-2478,g\_protein-coupled\_receptor\_kinase\_(grk5)\_mrna,\_complete\_cds\_

124564\_854-1400,rad\_mrna,\_complete\_cds\_  
 all\_m61853\_1735-2240,cytochrome\_p4502c18\_(cyp2c18)\_mrna,\_clone\_6b  
 m76482\_2855-3251,130-kd\_pemphigus\_vulgaris\_antigen\_mrna,\_complete\_cds  
 s74683\_848-1268,\_adp-  
 ribosyltransferase\_[human,\_skeletal\_muscle,\_mrna,\_1334\_nt]\_  
 u13369cds\_1792-  
 2248,ribosomal\_dna\_complete\_repeating\_unit/gb=u13369\_/ntype=dna\_/annot=cds  
 all\_x96584\_1444-1961,mrna\_for\_nov\_protein

Metagene 376

all\_ac000061\_18132-  
 57268:in\_ac000061cds#2\_1270,\_wugsc:h\_133k23.1c\_gene\_extracted\_frombac\_clone\_133  
 k2  
 ad000092\_21426-21637:in\_ad000092cds#1\_3369-3688:in\_all\_ad000092\_21396-  
 21427,\_hypotheticalserine-thre  
 af002224\_24-373,angelman\_syndrome\_gene,\_e6-  
 ap\_ubiquitin\_protein\_ligase\_3a\_(ube3a)\_mrna\_from\_promoter  
 d21851\_3680-4148,mrna\_for\_kiaa0028\_gene,\_partial\_cds\_  
 hg3934-ht4204\_at\_hg3934-ht4204\_g1\_phase-specific\_gene  
 hg4272-ht4542\_at\_hg4272-ht4542\_hepatocyte\_growth\_factor\_receptor\_  
 hg4490-ht4876\_f\_at\_hg4490-ht4876\_proline-rich\_protein\_prb4,\_allele\_  
 hg846-ht846\_at\_hg846-ht846\_cyclophilin-related\_protein\_  
 j03069mrna\_2331-2907,mycl2\_gene,\_complete\_cds\_  
 j03634\_1563-1815,erythroid\_differentiation\_protein\_mrna\_(edf),\_complete\_cds  
 j04101\_861-1425,erythroblastosis\_virus\_oncogene\_homolog(ets-  
 1)\_mrna,\_complete\_cds.  
 l02840mrna\_3224-3602:in\_reversesequence,\_3674-  
 3710,potassium\_channel\_kv2.1\_mrna,\_complete\_cds  
 l07540\_721-1159,replication\_factor\_36-kda\_subunit\_mrna,\_complete\_cds  
 m21539\_521-557,small\_proline\_rich\_protein\_(sprii)\_mrna,\_clone\_1292\_  
 m24248exon\_201-220:not\_in\_gb\_record,mlc-1v/sb\_isoform\_gene\_  
 m25296\_82-649,natriuretic\_peptide\_precursor\_mrna,\_complete\_cds\_  
 m37245cds\_272-434:in\_reversesequence,\_113-353,ig\_superfamily\_cytotoxic\_t-  
 lymphocyte-associated\_prote  
 m60165mrna\_571-1069,\_hla-dqb1\_gene\_extracted\_fromguanine\_nucleotide-  
 binding\_regulatory\_protein\_(go-a  
 all\_m62628\_1743-2182,alpha-1\_ig\_germline\_c-region\_membrane-  
 coding\_region,\_3'\_end\_  
 m87499cds\_586-880:in\_reversesequence,\_2927-3041,uracil-  
 dna\_glycosylase\_(ung)\_gene,\_complete\_cds\_  
 m95740exon#12\_279-381,alpha-1-iduronidase\_gene\_  
 m99063\_1942-2452,cytokeratinmrna,\_complete\_cds\_  
 s70348\_55-  
 367,\_integrin\_beta{alternatively\_spliced,\_clone\_beta\_3c}\_[human,\_erythroleukemi  
 a\_cell\_hel,  
 u00951\_1325-1691,clone\_a9a2br11\_(cac)n/(gtg)n\_repeat-containing\_mrna\_  
 u08377\_2654-3134,homolog\_of\_drosophila\_splicing\_regulator\_suppressor-of-white-  
 apricot\_mrna,\_complete  
 u09550\_1597-2149,oviductal\_glycoprotein\_mrna,\_complete\_cds\_  
 u11870mrna\_1901-2411,interleukin-  
 8\_receptor\_type\_a\_(il8rba)\_gene,\_promoter\_and\_complete\_cds\_  
 u16261\_1147-1657,mda-7\_(mda-7)\_mrna,\_complete\_cds  
 u18271exon#3\_51-512,thymopoietin\_(tmpo)\_gene,thymopoietin\_(tmpo)\_gene  
 u19495\_1634-2204,intercrine-alpha\_(hirh)\_mrna,\_complete\_cds

u26914\_3113-3533,ras-responsive\_element\_binding\_protein\_(rreb-  
 1)\_mrna,\_complete\_cds  
 u28150cds\_281-  
 839,adrenoleukodystrophy\_related\_protein\_(haldr)\_gene,\_partial\_cds/gb=u28150\_/n  
 type=dn  
 u36759\_486-1016,pre-t\_cell\_receptor\_alpha-  
 type\_chain\_precursor,\_mrna,\_complete\_cds\_  
 u39905\_2148-2670,vesicular\_monoamine\_transporter\_vmat1\_mrna,\_complete\_cds  
 u54804\_2444-2912,has2\_mrna,\_complete\_cds\_  
 u56976\_1664-  
 2240,calmodulin\_dependent\_phosphodiesterase\_pde1b1\_mrna,\_complete\_cds  
 u61166\_2652-3150,sh3\_domain-containing\_protein\_sh3p17\_mrna,\_complete\_cds\_  
 u64197\_250-658,chemokine\_exodus\_mrna,\_complete\_cds\_  
 u66559\_4812-5244,anaplastic\_lymphoma\_kinase\_receptor\_mrna,\_complete\_cds  
 all\_u66726\_2378-  
 2421,testis\_specific\_rna\_binding\_protein\_(spgyla)\_mrna,\_complete\_cds,testis\_spe  
 cific  
 u67733\_3650-4178,cgmp-stimulated\_3',5'-  
 cyclic\_nucleotide\_phosphodiesterase\_pde2a3\_(pde2a)\_mrna,\_co  
 x16260cds\_2053-2485:in\_reversesequence,\_2508-2631,mrna\_for\_inter-alpha-  
 trypsin\_inhibitor\_subunit\_3  
 all\_x51801\_1415-1824,op-1\_mrna\_for\_osteogenic\_protein  
 x53683mrna\_377-638,lag-1\_mrna  
 all\_x56677\_1103-1584,myod\_mrna\_  
 x74614exon#2\_17-377:in\_reversesequence,\_1279-  
 1387:not\_in\_gb\_record,odf2\_(allele\_2)\_gene\_for\_outer\_de  
 x80590cds\_653-1109,phkg1\_mrna  
 x82634\_1048-1378,partial\_mrna\_for\_hair\_keratin\_acidic\_3-ii\_  
 y10256\_2797-3247,mrna\_for\_serine/threonine\_protein\_kinase,\_nik\_  
 y11710mrna\_2222-  
 2642,mrna\_for\_extracellular\_matrix\_protein\_collagen\_type\_xiv,\_c-terminus  
 z48519exon#3\_11-223,xg\_gene\_(clone\_race5)/gb=z48519\_/ntype=rna\_  
 all\_z50053\_2518-3047,mrna\_for\_alpha2i-subunit\_of\_soluble\_guanylyl\_cyclase  
 z50194cds\_664-856:in\_reversesequence,\_1345-1372,mrna\_for\_pq-rich\_protein  
 all\_z68193\_17672-  
 20477,dna\_sequence\_from\_cosmid\_qc8b6,\_on\_chromosome\_xq28,\_containing\_red\_opsin\_  
 gene  
 z83745exon\_49-367,dna\_sequence\_from\_pac\_453a3\_contains\_est\_and\_sts.

Metagene 302

ab002332\_5132-5666,mrna\_for\_kiaa0334\_gene,\_complete\_cds/gb=ab002332\_/ntype=rna\_  
 k03008\_cds1\_at\_k03008\_k03008,not\_in\_gb\_record,\_gamma-g2-  
 psi\_gene\_extracted\_fromgamma-c-crystallin\_(g  
 l07044\_1420-1762,calcium/calmodulin-  
 dependent\_protein\_kinase\_(camk)\_isoform\_b\_mrna\_sequence\_  
 l36844mrna\_292-  
 808,(clone\_p15ink4b/ha5)\_cdk\_inhibitory\_protein\_mrna,\_complete\_cds\_  
 u35407mrna\_77-  
 193,peroxisomal\_targeting\_signal\_import\_receptor\_(pxr1)\_gene,\_allele\_5,\_partial  
 \_cds/gb  
 y07846exon#7\_92-587,mrna\_for\_gar22\_protein\_  
 all\_y09616\_1443-1948,mrna\_for\_putative\_carboxylesterase

Metagene 423



d38549\_3838-4336,mrna\_for\_kiaa0068\_gene,\_partial\_cds\_  
 d63877\_2386-2908,mrna\_for\_kiaa0241\_gene,\_partial\_cds\_  
 d86967\_5483-5873,mrna\_for\_kiaa0212\_gene,\_complete\_cds  
 hg4063-ht4333\_s\_at\_hg4063-ht4333\_transcription\_factor\_hbf-2  
 j03171\_2250-2700,interferon-alpha\_receptor\_(huifn-alpha-rec)\_mrna,\_complete\_cds  
 j04760mrna\_233-791,slow-twitch\_skeletal\_troponin\_i\_(tnn1)\_mrna,\_complete\_cds\_  
 l07956\_2402-2930,1,4-alpha-glucan\_branching\_enzyme\_(hgbe)\_mrna,\_complete\_cds  
 l35546mrna\_1027-1543,gamma-  
 glutamylcysteine\_synthetase\_light\_subunit\_mrna,\_complete\_cds\_  
 m35128cds\_1044-1320:in\_reversesequence,\_1936-  
 2038,muscarinic\_acetylcholine\_receptor\_gene,\_complete\_c  
 m63582mrna\_1062-1518,preprothyrotropin-releasing\_hormone\_gene  
 u05321mrna\_3734-4220,x-linked\_pest-  
 containing\_transporter\_(xpct)\_gene,\_promoter\_and  
 x13794mrna\_713-  
 1229,lactate\_dehydrogenase\_b\_gene\_exonand(ec\_1.1.1.27)\_(and\_joined\_cds)  
 x82224cds\_733-1165:in\_reversesequence,\_1273-  
 1303,mrna\_for\_glutamine\_transaminase\_k

## Metagene 349

j02943mrna\_869-1373,corticosteroid\_binding\_globulin\_mrna,\_complete\_cds\_  
 m96789\_1026-1548,connexin\_37\_(gja4)\_mrna,\_complete\_cds  
 z81326cds\_913-1189:in\_reversesequence,\_1348-  
 1486,mrna\_for\_protease\_inhibitor(pi12;neuroserpin).

## Metagene 26

d14134\_1646-2192,mrna\_for\_rad51,\_complete\_cds  
 j03778\_520-1075,microtubule-associated\_protein\_tau\_mrna,\_complete\_cds  
 l08096\_314-794,cd27\_ligand\_mrna,\_complete\_cds  
 u17977\_79-379,\_hsu17977cdna\_  
 u39196\_2616-3084,clone\_hgirk1\_g-  
 protein\_coupled\_inwardly\_rectifying\_potassium\_channel\_mrna,\_complete  
 u58090\_1035-1605,hs-cul-4a\_mrna,\_partial\_cds\_  
 u94320\_828-1392,neuropeptide\_y5\_receptor\_(npyy5)\_mrna,\_complete\_cds  
 x00949cds\_65-487,mrna\_for\_prepro-relaxin\_h1/gb=x00949/\_ntype=rna\_  
 x58822mrna\_905-1422,ifn-omegagene\_for\_interferon-omega\_1\_  
 x59841mrna\_2006-2444,pbx3\_mrna\_  
 x97230cds\_782-1274:in\_reversesequence,\_1290-  
 1353,mrna\_for\_nk\_receptor,\_clone\_library\_4m1#6  
 x98001cds\_572-932:in\_reversesequence,\_998-  
 1064,mrna\_for\_geranylgeranyl\_transferase\_ii\_

## Metagene 192

hg3730-ht4000\_s\_at\_hg3730-ht4000\_tyrosine\_kinase\_syk\_  
 l19401\_3716-4220,myosin\_i\_homologue\_(myh12)\_mrna,\_3'\_end\_of\_cds

m96740\_2014-2476, nscl-2\_gene\_sequence  
 all\_s94421\_33-496, tcr\_eta\_#name?\_cell\_receptor\_eta-  
 exon\_[human, \_genomic, \_806\_nt]\_  
 all\_u27333\_2701-  
 2753, alpha\_(1,3)\_fucosyltransferase\_(fut6)\_mrna, \_major\_transcript\_i, \_complete\_c  
 ds, al  
 u33203\_73-282, mdm2-e\_(mdm2)\_mrna, \_complete\_cds/gb=u33203\_/ntype=rna  
 u60975\_6398-6824, hybrid\_receptor\_gp250\_precursor\_mrna, \_complete\_cds  
 x03656mrna\_971-1391, \_g-  
 csf\_protein\_gene\_extracted\_fromgene\_for\_granulocyte\_colony-stimulating\_factor  
 all\_x16281\_402-898, mrna\_for\_zinc\_finger\_protein\_(clone\_431)  
 x66922cds\_362-728:in\_reversesequence, \_848-872, mrna\_for\_myo-  
 inositol\_monophosphatase  
 x80763cds\_202-528:in\_reversesequence, \_663-850, gene\_for\_5-ht2c\_receptor  
 x98307mrna\_13-355, mrna\_for\_uv-b\_repressed\_sequence, \_hur\_7  
 all\_z11685\_1974-2425, mrna\_for\_rna\_helicase\_  
 z29077mrna#1\_3-55, \_un-named-transcript-  
 1\_fromcdc25\_gene\_promoter\_region/gb=z29077\_/ntype=dna\_/annot=

## Metagene 337

d87469\_8413-8899, mrna\_for\_kiaa0279\_gene, \_partial\_cds\_  
 l21934\_3401-3905, acyl\_coenzyme\_a:cholesterol\_acyltransferase\_mrna, \_complete\_cds  
 s60415\_2937-  
 3333, \_myasthenic\_syndrome\_antigen\_b\_[human, \_fetal\_brain, \_mrna, \_3477\_nt]\_  
 u09716\_1621-2124, mannose-specific\_lectin\_(mr60)\_mrna, \_complete\_cds\_  
 u48250\_1490-2030, protein\_kinase\_c-binding\_protein\_rack17\_mrna, \_partial\_cds\_  
 all\_x94612\_2745-3328, mrna\_for\_type\_ii\_cgmp-dependent\_protein\_kinase  
 y11709mrna\_169-709, mrna\_for\_extracellular\_matrix\_protein\_collagen\_type\_xiv, \_n-  
 terminus/gb=y11709\_/nt

## Metagene 12

d14823\_851-  
 1343, chimeric\_mrna\_derived\_from\_aml1\_gene\_and\_mtg8(eto)\_gene, \_partial\_sequence  
 d38076\_322-700, mrna\_for\_ranbp1\_(ran-binding\_protein\_1), \_complete\_cds\_  
 d80004\_6550-6898, mrna\_for\_kiaa0182\_gene, \_partial\_cds\_  
 d87075\_5013-5469, mrna\_for\_kiaa0238\_gene, \_partial\_cds\_  
 d87673\_960-1434, mrna\_for\_heat\_shock\_transcription\_factor\_4, \_complete\_cds\_  
 d87716\_2447-2942, mrna\_for\_kiaa0007\_gene, \_partial\_cds\_  
 hg2271-ht2367\_at\_hg2271-ht2367\_profilaggrin  
 hg3039-ht3200\_at\_hg3039-ht3200\_adp-ribosylation-like\_factor  
 hg3636-ht3846\_at\_hg3636-ht3846\_myosin, \_heavy\_polypeptide\_9, \_non-muscle  
 hg3884-ht4154\_at\_hg3884-ht4154\_homeotic\_protein\_hpx-42\_  
 j02783mrna\_2075-2465, thyroid\_hormone\_binding\_protein\_(p55)\_mrna, \_complete\_cds  
 j03824\_756-1230, uroporphyrinogen\_iii\_synthase\_mrna, \_complete\_cds\_  
 l16782\_1994-2522, putative\_m\_phase\_phosphoprotein(mpp1)\_mrna, \_partial\_cds  
 l18972cds\_1821-2019:in\_reversesequence, \_2065-2305, anonymous\_gene, \_complete\_cds  
 l19711\_4952-5414, dystroglycan\_(dag1)\_mrna, \_complete\_cds  
 l34587\_109-  
 403, rna\_polymerase\_ii\_elongation\_factor\_siii, \_p15\_subunit\_mrna, \_complete\_cds\_  
 l37936\_439-961, nuclear-encoded\_mitochondrial\_elongation\_factor\_ts\_(ef-  
 ts)\_mrna, \_3'\_end\_of\_cds

140407cds\_696-882:in\_reversesequence, 1060-  
 1264,thyroid\_receptor\_interactor\_(trip9)\_gene,\_complete\_c  
 141067\_3380-3884,nf-at4c\_mrna,\_complete\_cds\_  
 176191mrna\_3005-3521,interleukin-1\_receptor-  
 associated\_kinase\_(irak)\_mrna,\_complete\_cds\_  
 177730exon\_529-1009,a3\_adenosine\_receptor\_(adora3)\_gene\_  
 all\_m14158\_1529-1794,\_t-cell\_receptor\_beta-chain\_j1.3\_gene\_extracted\_fromt-  
 cell\_receptor\_germline\_be  
 m19961\_55-469,cytochrome\_c\_oxidase\_subunit\_vb\_(coxvb)\_mrna,\_complete\_cds\_  
 m34338\_626-1197,spermidine\_synthase\_mrna,\_complete\_cds\_  
 m60047\_641-1097,heparin\_binding\_protein\_(hbp17)\_mrna,\_complete\_cds\_  
 m65199\_735-1101,endothelin(et2)\_mrna,\_complete\_cds\_  
 m86752\_1512-2046,transformation-  
 sensitive\_protein\_(ief\_ssp\_3521)\_mrna,\_complete\_cds\_  
 s40719\_2440-2964,\_glial\_fibrillary\_acidic\_protein\_[human,\_glioma\_cell\_line\_u-  
 251\_mg,\_mrna,\_3033\_nt]  
 s66793\_697-1219,\_x-arrestin=s-antigen\_homolog\_[human,\_retina,\_mrna,\_1314\_nt]  
 u05340\_1103-1571,p55cdc\_mrna,\_complete\_cds\_  
 u07424\_1266-1764,putative\_trna\_synthetase-like\_protein\_mrna,\_complete\_cds\_  
 u47621\_1758-2286,nucleolar\_autoantigen\_no55\_mrna,\_complete\_cds\_  
 u55206\_790-1222:not\_in\_gb\_record,gamma-  
 glutamyl\_hydrolase\_(hgh)\_mrna,\_complete\_cds\_  
 u61263\_1603-2077,acetolactate\_synthase\_homolog\_mrna,\_complete\_cds\_  
 u62962\_927-1347,int-6\_mrna,\_complete\_cds\_  
 u68566\_638-1124,hs1\_binding\_protein\_hax-  
 1\_mrna,\_nuclear\_gene\_encoding\_mitochondrial\_protein,\_complet  
 u70735\_507-1005,34\_kda\_mov34\_isologue\_mrna,\_complete\_cds/gb=u70735\_/ntype=rna  
 u79270\_774-1176,clone\_23707\_mrna,\_partial\_cds  
 u85943\_1527-1680,mrna-  
 associated\_protein\_mrnnp41\_mrna,\_complete\_cds/gb=u85943\_/ntype=rna  
 x00368mrna\_7-  
 52,\_exonfromprolactin\_gene\_5'\_region/gb=x00368\_/ntype=dna\_/annot=mrna\_  
 x12794cds\_864-1176:in\_reversesequence, 1905-2139,v-erba\_related\_ear-2\_gene\_  
 x13482cds\_490-712:in\_reversesequence, 870-942,mrna\_for\_u2\_snrnp-  
 specific\_a'\_protein\_  
 x79781cds\_276-546:in\_reversesequence, 675-681,ray\_mrna  
 x92744cds\_6-174:in\_reversesequence, 61-271,mrna\_for\_hbd-1\_protein\_  
 all\_y00285\_8502-8980,mrna\_for\_insuline-like\_growth\_factor\_ii\_receptor

## Metagene 202

d50915\_7282-7750,mrna\_for\_kiaa0125\_gene,\_complete\_cds  
 hg2415-ht2511\_at\_hg2415-ht2511\_transcription\_factor\_e2f-2  
 hg3872-ht4142\_at\_hg3872-  
 ht4142\_immunoglobulin\_gamma\_heavy\_chain,\_v(6)djc\_regions\_  
 hg4460-ht4729\_at\_hg4460-ht4729\_immunoglobulin\_heavy\_chain,\_vdjc\_regions  
 hg4462-ht4731\_at\_hg4462-ht4731\_immunoglobulin\_heavy\_chain,\_vdjc\_regions  
 j00210mrna\_635-735,\_ifna\_gene\_(interferon\_alpha-  
 d)\_extracted\_fromleukocyte\_interferon\_(ifn-alpha)\_al  
 j03068\_2794-3286,dnf1552\_(lung)\_mrna,\_complete\_cds\_  
 l10343cds\_2-308:in\_reversesequence, 476-2076,\_huma\_elafin\_gene,\_complete\_cds\_  
 l29217mrna\_1299-1683,clk3\_mrna,\_complete\_cds\_  
 l34035\_1405-1813,nadp-  
 dependent\_malic\_enzyme\_mrna,\_complete\_cds/gb=l34035\_/ntype=rna

l38025exon#1-3\_30-  
 106:not\_in\_gb\_record,ciliary\_neurotrophic\_factor\_alpha\_receptor\_gene\_  
 all\_m21005\_1803-2524,migration\_inhibitory\_factor-  
 related\_protein(mrp8)\_gene,\_complete\_cds\_  
 all\_u05259\_4343-4740:not\_in\_gb\_record,mb-1\_gene,\_complete\_cds\_  
 u16812cds\_274-601:in\_reversesequence,\_3897-4028,bak-2\_gene,\_complete\_cds\_  
 u18237\_231-759,atp-binding\_cassette\_protein\_mrna\_06b09\_clone,\_partial\_cds\_  
 u39817\_3917-4373,bloom\_syndrome\_protein\_(blm)\_mrna,\_complete\_cds\_  
 u40380\_961-1027,presenilin\_i-374\_(ad3-212)\_mrna,\_complete\_cds\_  
 u58837\_3430-4003,cgmp-  
 gated\_cation\_channel\_beta\_subunit\_(cncg2)\_mrna,\_complete\_cds\_  
 all\_x64878\_3508-3965,mrna\_for\_oxytocin\_receptor\_  
 x82240mrna\_723-  
 1251,\_tcl1\_gene\_(t\_cell\_leukemia)\_extracted\_frommrna\_for\_tcell\_leukemia/lymphom  
 a\_1\_  
 x83412cds\_225-412:in\_reversesequence,\_507-539,b1\_mrna\_for\_mucin\_  
 z00010exon#2\_75-  
 158,germ\_line\_pseudogene\_for\_immunoglobulin\_kappa\_light\_chain\_leader\_peptide\_an  
 d\_var\_  
 z29574exon#3\_1-  
 373:in\_reversesequence,\_3141:not\_in\_gb\_record,gene\_for\_bcma\_peptide\_  
 z49194exon#5\_1962-2256,mrna\_for\_oct-binding\_factor\_

Metagene 278

d00654exon\_127-196:not\_in\_gb\_record,enteric\_smooth\_muscle\_gamma-  
 actin\_gene,\_5'\_flank\_and\_  
 d42085\_2200-2572,mrna\_for\_kiaa0095\_gene,\_complete\_cds\_  
 d76435\_2639-3065,mrna\_for\_zic\_protein,\_complete\_cds\_  
 m37712mrna\_3280-  
 3760,p58/gta\_(galactosyltransferase\_associated\_protein\_kinase)\_mrna,\_complete\_c  
 ds\_  
 u06681\_1348-1774,clone\_cca12\_mrna\_containing\_cca\_trinucleotide\_repeat\_  
 u15552\_1831-2311,acidic\_82\_kda\_protein\_mrna,\_complete\_cds\_  
 u66198\_215-713,fibroblast\_growth\_factor\_homologous\_factor(fhf-  
 2)\_mrna,\_complete\_cds/gb=u66198\_/ntype\_  
 all\_x13293\_2056-2549,mrna\_for\_b-myb\_gene\_  
 x13334cds\_659-1049:in\_reversesequence,\_1234,cd14\_mrna\_for\_myelid\_cell-  
 specific\_leucine-rich\_glycopro\_  
 all\_x87159\_2076-2527,mrna\_for\_beta\_subunit\_of\_epithelial\_amiloride-  
 sensitive\_sodium\_channel\_

Metagene 97

111244mrna\_545-1049,(clone\_a12)\_c4b-binding\_protein\_beta-  
 chain\_mrna,\_complete\_cds\_  
 all\_m29458\_440-1017,carbonic\_anhydrase\_iii\_gene\_  
 m57731mrna\_617-1032,gro-beta\_mrna,\_complete\_cds\_  
 m90657\_581-1163,tumor\_antigen\_(16)\_mrna,\_complete\_cds\_

Metagene 400

hg3085-ht3254\_s\_at\_hg3085-ht3254\_phosphodiesterase\_  
 all\_m60748\_1209-1615,histone\_h1\_(h1f4)\_gene,\_complete\_cds  
 m63623\_2390-2900,oligodendrocyte-myelin\_glycoprotein\_(omgp)\_mrna,\_complete\_cds\_  
 all\_x74837\_2811-3196,humm9\_mrna  
 all\_x78578\_3781-4268,ppp1r3\_mrna\_for\_protein\_phosphatase\_1,\_glycogen-  
 binding\_regulatory\_subunit

Metagene 284

k03021exon#14\_343-853,tissue\_plasminogen\_activator\_(plat)\_gene,\_complete\_cds\_  
 all\_m55998\_2-265,alpha-1\_collagen\_type\_i\_gene,\_3'\_end  
 m88461\_993-1538,neuropeptide\_y\_peptide\_yy\_receptor\_mrna,\_complete\_cds  
 u32907\_1401-1923,p37nb\_mrna,\_complete\_cds  
 u62325\_2343-2805,fe65-like\_protein\_(hfe65l)\_mrna,\_partial\_cds  
 all\_x52947\_2497-2942,mrna\_for\_cardiac\_gap\_junction\_protein\_  
 all\_x54667\_676-706,mrna\_for\_cystatin\_s,mrna\_for\_cystatin\_s  
 all\_x57351\_294-891,1-8d\_gene\_from\_interferon-inducible\_gene\_family,1-  
 8d\_gene\_from\_interferon-inducib  
 all\_x69111\_662-1185,h1h\_1r21\_mrna\_for\_helix-loop-helix\_protein\_  
 all\_z29083\_1644-2023,5t4\_gene\_for\_5t4\_oncofetal\_antigen

Metagene 483

m60094mrna\_196-640,testicular\_h1\_histone\_(h1)\_gene,\_complete\_cds  
 x00948cds\_65-503,mrna\_for\_prepro-relaxin\_h2/gb=x00948\_/ntype=rna\_

Metagene 307

d84454\_2031-2577,mrna\_for\_udp-galactose\_translocator,\_complete\_cds\_  
 l09708mrna\_2255-2795,complement\_component(c2)\_gene\_allele\_b\_  
 u41315mrna#1\_3083-3653,ring\_zinc-finger\_protein\_(znf127-  
 xp)\_gene\_and\_5'\_flanking\_sequence\_  
 x58529mrna\_1754-  
 2276,rearranged\_immunoglobulin\_mrna\_for\_mu\_heavy\_chain\_enhancer\_and\_constant\_re  
 gion  
 x72475cds\_111-  
 343,mrna\_for\_rearranged\_ig\_kappa\_light\_chain\_variable\_region\_(i.114)\_

Metagene 260

d29833\_194-680,mrna\_for\_salivary\_proline\_rich\_peptide\_p-b,\_complete\_cds  
 d87433\_6272-6752,mrna\_for\_kiaa0246\_gene,\_partial\_cds\_  
 u31384\_57-591,g\_protein\_gamma-11\_subunit\_mrna,\_complete\_cds  
 u62801\_935-1481,protease\_m\_mrna,\_complete\_cds

Metagene 126

d38437\_37-604,dna\_mismatch\_repair\_mrna\_  
 hg1604-ht1604\_at\_hg1604-ht1604\_adrenergic,\_beta,\_receptor\_kinase\_2\_  
 hg651-ht5209\_s\_at\_hg651-ht5209\_adducin,\_alpha\_subunit,\_altsplice\_3\_  
 j03915\_1313-1721,chromogranin\_a\_mrna,\_complete\_cds\_  
 k03183cds\_2-326,chorionic\_gonadotropin\_beta\_subunit\_gene\_  
 s75256\_32-  
 446,\_hnl=neutrophil\_lipocalin\_[human,\_ovarian\_cancer\_cell\_line\_oc6,\_mrna\_partia  
 l,\_534\_nt]/  
 u08989\_1383-1857,glutamate\_transporter\_mrna,\_complete\_cds  
 u17280\_1004-  
 1562,steroidogenic\_acute\_regulatory\_protein\_(star)\_mrna,\_complete\_cds  
 all\_u21689\_2955-3116,glutathione\_s-transferase-plc\_gene,\_complete\_cds  
 u31973\_2396-2914,phosphodiesterase\_a'\_subunit\_(pde6c)\_mrna,\_complete\_cds\_  
 u33822\_2053-2563,tax1-binding\_protein\_txbp181\_mrna,\_complete\_cds\_  
 u40372\_1565-  
 2021,3',5'\_cyclic\_nucleotide\_phosphodiesterase\_(hspde1c3a)\_mrna,\_partial\_cds  
 all\_u73167\_4971-  
 35099,\_h\_luca14.2a\_gene\_extracted\_fromcosmid\_luca14,\_h\_luca14.2a\_gene\_extracted  
 \_from  
 all\_x07496\_2066-2268,tangier\_apoa-i\_gene\_  
 x58964cds\_2500-2914,gene\_for\_mhc\_ii\_regulatory\_factor\_rfx  
 x85178\_267-627,surf-5\_mrna\_  
 x98258cds\_481-619:in\_reversesequence,\_625-829,mrna\_for\_m-  
 phase\_phosphoprotein,\_mpp9  
 x99479\_f\_at\_x99479\_x99479,\_40\_in\_x99479cds\_951-  
 1047:\_30\_in\_reversesequence,\_1065-1461,mrna\_for\_nk\_re

Metagene 16

k01396mrna\_769-1201,alpha-1-antitrypsin\_mrna,\_complete\_cds\_  
 m80482\_3922-4324,subtilisin-like\_protein\_(pace4)\_mrna,\_complete\_cds  
 all\_x15422\_3003-3550,mrna\_for\_mannose-binding\_protein\_c  
 all\_x64810\_4454-5019,encoding\_pc1/pc3  
 all\_x81438\_2665-3206,mrna\_for\_amphiphysin  
 z12830cds\_344-764:in\_reversesequence,\_943,mrna\_for\_ssr\_alpha\_subunit  
 all\_z22534\_2132-2637,alk-2\_mrna

Metagene 279

all\_110381\_2086-2579,2-5a-dependent\_rnase\_gene,\_complete\_cds\_  
 m57703\_129-629,melanin\_concentrating\_hormone\_(mch)\_mrna,\_complete\_cds  
 u66359\_1205-1583,t54\_protein\_(t54)\_mrna,\_complete\_cds

Metagene 228

d26535exon#15\_940-  
 1455,gene\_for\_dihydrolipoamide\_succinyltransferase,\_complete\_cds\_(exon\_1-15)\_  
 d78577exon\_853-1391,dna\_for\_14-3-3\_protein\_eta\_chain  
 d86980\_4616-5192,mrna\_for\_kiaa0227\_gene,\_partial\_cds\_  
 hg2743-ht3926\_s\_at\_hg2743-ht3926\_caldesmon\_1,\_altsplice\_6,\_non-muscle

hg4178-ht4448\_at hg4178-ht4448\_af-17\_  
 j03060exon#11\_168-666,glucocerebrosidase\_(gcb)\_gene  
 j03077\_2159-2692,co-beta\_glucosidase\_(proactivator)\_mrna,\_complete\_cds\_  
 l12168\_2032-2476,adenylyl\_cyclase-associated\_protein\_(cap)\_mrna,\_complete\_cds\_  
 m15395\_2621-2736,leukocyte\_adhesion\_protein\_(lfa-1/mac-  
 1/p150,95\_family)\_beta\_subunit\_mrna\_  
 m22898mrna\_2042-2600,phosphoprotein\_p53\_gene\_  
 m33308\_4519-5071,vinculin\_mrna,\_complete\_cds\_  
 m63573\_370-802,secreted\_cyclophilin-like\_protein\_(scylp)\_mrna,\_complete\_cds\_  
 m80563\_133-523,capl\_protein\_mrna,\_complete\_cds\_  
 m94345\_752-1160,macrophage\_capping\_protein\_mrna,\_complete\_cds\_  
 s81439\_2658-  
 3186,\_egr\_alpha=early\_growth\_response\_gene\_alpha\_[human,\_prostate,\_mrna,\_3228\_n  
 t]\_  
 all\_u02020\_1985-2352,pre-b\_cell\_enhancing\_factor\_(pbef)\_mrna,\_complete\_cds\_  
 u22055\_2879-3455,100\_kda\_coactivator\_mrna,\_complete\_cds\_  
 u25165\_1579-  
 2083,fragile\_x\_mental\_retardation\_protein homolog\_fxrl\_mrna,\_complete\_cds\_  
 u56637\_1987-2323,capping\_protein\_alpha\_subunit\_isoform\_mrna,\_complete\_cds\_  
 u57721\_1126-1588,1-kynurenine\_hydrolase\_mrna,\_complete\_cds\_  
 all\_u90546\_1365,tyrophenol\_3-monooxygenase\_(btf4)\_mrna,\_complete\_cds,  
 butyrophilin\_(btf4)\_mrna  
 ,\_complete\_cds\_  
 x12447mrna#13\_1-241:not\_in\_gb\_record,aldolase\_a\_gene\_(ec\_4.1.2.13)  
 x62320cds\_1527-1755:in\_reversesequence,\_1825-2095,mrna\_for\_epithelinand\_2  
 all\_x74262\_1725-2278,rbp48\_mrna\_encoding\_retinoblastoma\_binding\_protein\_  
 all\_x76105\_1661-2208,dap-1\_mrna  
 all\_y00281\_1856-2319,mrna\_for\_ribophorin\_i\_

Metagene 142

d43772\_1616-2168,squamous\_cell\_carcinoma\_of\_esophagus\_mrna\_for\_grb-  
 7\_sh2\_domain\_protein,\_complete\_cd  
 d50920\_2969-3419,mrna\_for\_kiaa0130\_gene,\_complete\_cds  
 l09229\_2642-3099,long-chain\_acyl-  
 coenzyme\_a\_synthetase\_(fac1l)\_mrna,\_complete\_cds  
 l11370\_3486-4038,protocadherin\_42\_mrna,\_complete\_cds\_for\_abbreviated\_pc42  
 all\_m12036\_1553-1732,tyrosine\_kinase-type\_receptor\_(her2)\_gene,\_partial\_cds  
 m24899\_1750-2284,triiodothyronine\_(ear7)\_mrna,\_complete\_cds  
 m80783\_3001-3451,b12\_protein\_mrna,\_complete\_cds  
 u47634\_1341-1623,beta-tubulin\_iii\_isotype\_(beta-3)\_mrna,\_complete\_cds  
 u90914\_1369-1795,clone\_23587\_mrna\_sequence\_  
 all\_x03363\_3873-4408,c-erb-b-2\_mrna  
 x63527cds\_99-549:in\_reversesequence,\_637-655,mrna\_for\_ribosomal\_protein\_l19\_  
 all\_x65233\_1966-2429,mrna\_for\_zinc-finger\_protein\_(znfpt17)  
 all\_x80198\_1398-1939,mln64\_mrna  
 all\_x80199\_3718-4223,mln51\_mrna  
 all\_x80692\_3409-3878,erk3\_mrna\_  
 y09836\_999-1335,mrna\_for\_3'\_utr\_of\_unknown\_protein\_  
 z38026cds\_63-483:in\_reversesequence,\_536-542,mrna\_for\_fall-  
 39\_peptide\_antibiotic

Metagene 450

hg3548-ht3749\_at\_hg3548-  
 ht3749\_ccaat\_displacement\_protein\_cut\_homolog\_altsplice\_1  
 l27559utr#1\_111-166,insulin-like\_growth\_factor\_binding\_protein(igfbp5)\_gene\_  
 m62782\_392-958,insulin-like\_growth\_factor\_binding\_protein(igfbp-  
 5)\_mrna,\_complete\_cds  
 u51336\_2520-3024,inositol\_1,3,4-trisphosphate\_5/6-kinase\_mrna,\_complete\_cds  
 x16665cds\_871-1039:in\_reversesequence,\_1135-  
 1369,hox2h\_mrna\_from\_the\_hox2\_locus\_  
 all\_z48605\_61-326,partial\_mrna\_for\_pyrophosphatase/gb=z48605\_/ntype=rna

Metagene 251

j02874\_63-573,adipocyte\_lipid-binding\_protein,\_complete\_cds  
 m15465\_1955-2384,pyruvate\_kinase\_type\_l\_mrna,\_complete\_cds\_  
 u25128\_2100-2598,pth2\_parathyroid\_hormone\_receptor\_mrna,\_complete\_cds  
 u66616\_3427-3979,swi/snf\_complex\_170\_kda\_subunit\_(baf170)\_mrna,\_complete\_cds\_  
 x82539mrna\_1313-1823,mrna\_for\_mage-xp  
 y08417\_1043-  
 1558,mrna\_for\_nicotinic\_acetylcholine\_receptor\_beta3\_subunit\_precursor\_  
 all\_z11850\_55-  
 416,mrna\_for\_somatotropin\_receptor\_5'\_upstream\_region/gb=z11850\_/ntype=rna\_

Metagene 9

hg371-ht26388\_at\_hg371-ht26388\_mucin\_1\_epithelial\_altsplice\_9  
 j05582mrna\_3910-4100,pancreatic\_mucin\_mrna,\_complete\_cds\_  
 l24893cds\_218-679,myelin\_protein\_zero\_(po)\_gene  
 all\_m30838\_4028-4631,pulmonary\_surfactant\_apoprotein\_(psap)\_gene,\_complete\_cds\_  
 z48633mrna\_1624-2020,mrna\_for\_retrotransposon

Metagene 401

d42055\_5178-5718,mrna\_for\_kiaa0093\_gene,\_partial\_cds\_  
 hg3740-ht4010\_at\_hg3740-ht4010\_basic\_transcription\_factor\_2\_34\_kda\_subunit  
 l15702\_1778-2279,complement\_factor\_b\_mrna,\_complete\_cds  
 l34673mrna\_2853-3381,atpase\_dna-binding\_protein\_(hip116)\_mrna,\_3'\_end\_  
 m11717mrna\_2135-2393,heat\_shock\_protein\_(hsp\_70)\_gene,\_complete\_cds\_  
 m93056\_859-1273,monocyte/neutrophil\_elastase\_inhibitor\_mrna\_sequence  
 u00957\_1638-2136,clone\_kdbl.2\_(cac)n/(gtg)n\_repeat-containing\_mrna\_  
 u09759\_1308-1830,protein\_kinase\_(jnk2)\_mrna,\_complete\_cds  
 u48736\_1195-1693,serine/threonine-  
 protein\_kinase\_prp4h\_(prp4h)\_mrna,\_complete\_cds  
 v00533mrna\_391-915,\_ifna\_gene\_(interferon\_alpha-  
 h2)\_extracted\_fromgene\_for\_leukocyte\_(alpha)\_interfe  
 x99920cds\_6-198:in\_reversesequence,\_31-403,mrna\_for\_s100\_calcium-  
 binding\_protein\_a13

Metagene 39



d26579\_2683-3205,mrna\_for\_transmembrane\_protein,\_complete\_cds  
 hg2663-ht2759\_at\_hg2663-ht2759\_homeotic\_protein\_emx2\_  
 l06797\_1041-1599,(clone\_l5)\_orphan\_g\_protein-  
 coupled\_receptor\_mrna,\_complete\_cds\_  
 l08177\_1042-1606,ebv\_induced\_g-  
 protein\_coupled\_receptor\_(ebi2)\_mrna,\_complete\_cds  
 m30773\_1983-2499,calcineurin\_b\_mrna,\_complete\_cds  
 u20758mrna\_885-1437,osteopontin\_gene,\_complete\_cds  
 all\_x17042\_689-1158,mrna\_for\_hematopoietic\_proteoglycan\_core\_protein

## Metagene 274

af015910\_41-433,unknown\_protein\_mrna,\_partial\_cds/gb=af015910\_/ntype=rna  
 l13800mrna\_4-397,liver\_expressed\_protein\_gene,\_3'\_end/gb=l13800\_/ntype=rna  
 l14269\_1369-1729,synaptic\_vesicle\_amine\_transporter\_(svat)\_mrna,\_complete\_cds\_  
 m74447mrna\_2012-2510,psf-2\_mrna,\_complete\_cds  
 u10693exon#2\_1196-1553,mage-8\_antigen\_(mage8)\_gene,\_complete\_cds\_  
 u11821\_363-907,fas\_ligand\_(fasl)\_mrna,\_complete\_cds  
 x51985cds\_1083-1479:in\_reversesequence,\_1787-1829,lag-3\_mrna\_for\_cd4-  
 related\_protein\_involved\_in\_lym  
 x63454cds\_327-567:in\_reversesequence,\_659-719,hst-2\_(fgf-6)\_mrna  
 y08564cds\_1238-1688,galnac-t4\_gene/gb=y08564\_/ntype=dna\_/annot=cds\_

## Metagene 469

ab002380\_5644-6142,mrna\_for\_kiaa0382\_gene,\_partial\_cds/gb=ab002380\_/ntype=rna  
 ab003103\_2965-3463,mrna\_for\_proteasome\_subunit\_p55,\_complete\_cds\_  
 af007875\_501-  
 1029,dolichol\_monophosphate\_mannose\_synthase\_(dpm1)\_mrna,\_partial\_cds/gb=af0078  
 75\_/ntyp  
 all\_d00596\_15645-16192,thymidylate\_syntase\_(ec\_2.1.1.45)\_gene,\_complete\_cds  
 d10522\_2000-2546,mrna\_for\_80k-l\_protein,\_complete\_cds  
 d11094\_973-1345,mrna\_for\_mss1,\_complete\_cds  
 d13627\_1310-1778,mrna\_for\_kiaa0002\_gene,\_complete\_cds  
 d13641\_2748-3216,mrna\_for\_kiaa0016\_gene,\_complete\_cds  
 d26069\_5879-6455,mrna\_for\_kiaa0041\_gene,\_partial\_cds\_  
 d43951\_4874-5264,mrna\_for\_kiaa0099\_gene,\_complete\_cds  
 d49493exon#3\_403-811,gene\_forbone\_morphogenetic\_protein-3b  
 d49738\_456-990,cytoskeleton\_associated\_protein\_(cg22)\_mrna,\_complete\_cds\_  
 d78132\_373-907,mrna\_for\_ras\_homologue\_enriched\_in\_brain\_(rheb)\_gene,\_ras-  
 related\_gtp\_binding\_protein  
 d86956\_3139-3589,mrna\_for\_kiaa0201\_gene,\_complete\_cds  
 d87127\_2088-2448,mrna\_for\_translocation\_protein-1,\_complete\_cds  
 d87684\_3222-3696,mrna\_for\_kiaa0242\_gene,\_partial\_cds\_  
 j03473mrna\_3212-3752,poly(adp-ribose)\_synthetase\_mrna,\_complete\_cds  
 l40357mrna\_7-463,thyroid\_receptor\_interactor\_(trip7)\_mrna,\_3'\_end\_of\_cds  
 l41887mrna#1\_1773-2277,splicing\_factor,\_arginine/serine-  
 rich(sfrs7)\_gene,\_complete\_cds  
 l43631\_2189-2753,scaffold\_attachment\_factor\_(saf-b)\_gene,\_partial\_cds\_  
 m11353\_707-1226,h3.3\_histone\_c\_mrna,\_complete\_cds  
 m14764mrna\_2785-3337,nerve\_growth\_factor\_receptor\_mrna,\_complete\_cds\_  
 m93425\_2577-3111,protein\_tyrosine\_phosphatase\_(ptp-pest)\_mrna,\_complete\_cds  
 u14575\_1842-2328,(ard-1)\_mrna,\_complete\_cds

u28042\_2726-3104,dead\_box\_rna\_helicase-like\_protein\_mrna,\_complete\_cds\_  
 u31814\_1366-1876,transcriptional\_regulator\_homolog\_rpd3\_mrna,\_complete\_cds\_  
 u34252\_2177-2579,gamma-aminobutyraldehyde\_dehydrogenase\_mrna,\_complete\_cds\_  
 u37547\_2931-3477,iap\_homolog\_b\_(mihb)\_mrna,\_complete\_cds\_  
 u41815\_3037-3559,nucleoporin\_98\_(nup98)\_mrna,\_complete\_cds\_  
 u49844\_7699-8095,frap-related\_protein\_(frp1)\_mrna,\_complete\_cds\_  
 u50534\_10101-10671,brca2\_region,\_mrna\_sequence\_cg003\_  
 u59863\_1541-2039,traf-interacting\_protein\_i-traf\_mrna,\_complete\_cds\_  
 u61234\_986-1490,tubulin-folding\_cofactor\_c\_mrna,\_complete\_cds\_  
 u73737mrna\_4359-4785,hmsh6\_gene,\_5'\_utr\_and  
 u78575\_3124-3634,68\_kda\_type\_i\_phosphatidylinositol-4-phosphate\_5-  
 kinase\_alpha\_mrna,\_clone\_pip5kia1,  
 u79291\_756-1287,clone\_23721\_mrna\_sequence  
 all\_x65488\_2664-3169,u21.1\_mrna  
 y14140exon\_13-  
 185,g\_protein\_gene\_encoding\_betasubunit\_exonand\_promoter/gb=y14140\_/ntype=dna\_  
 annot=e  
 all\_z29066\_1451-2035,nek2\_mrna\_for\_protein\_kinase

Metagene 244

all\_m55419\_2275-2470,amelogenin\_(amely)\_gene,\_3'\_end\_of\_cds  
 s41458\_3026-3200,\_rod\_cgmp\_phosphodiesterase\_beta-  
 subunit\_[human,\_mrna,\_3231\_nt]  
 u11036\_121-553,ibd1\_mrna,\_partial\_cds/gb=u11036\_/ntype=rna\_  
 all\_z37987\_2052-2198,mrna\_for\_mxr7\_

Metagene 233

m24283mrna\_2420-2954,major\_group\_rhinovirus\_receptor\_(hrv)\_mrna,\_complete\_cds  
 s62027\_21-320,\_transducin\_gamma\_subunit\_[human,\_mrna,\_408\_nt]  
 u37546\_2477-3012,iap\_homolog\_c\_(mihc)\_mrna,\_complete\_cds\_  
 u46569mrna\_1025-1241:in\_reversesequence,\_300-498,aquaporin-5\_(aqp5)\_gene

Metagene 8

all\_d00003\_1681-1721,liver\_cytochrome\_p-  
 450\_mrna,\_complete\_cds,liver\_cytochrome\_p-450\_mrna,\_complete  
 d17408\_906-1481,mrna\_for\_calponin,\_complete\_cds  
 d49490\_1092-1644,mrna\_for\_protein\_disulfide\_isomerase-  
 related\_protein\_(pdir),\_complete\_cds\_  
 d64053\_3337-3467,mrna\_for\_protein-tyrosine\_phosphatase\_  
 d70830\_1610-2018,mrna\_for\_doc2\_beta,\_complete\_cds  
 hg174-ht174\_at\_hg174-ht174\_desmoplakin\_i\_  
 hg2147-ht2217\_at\_hg2147-ht2217\_mucin\_3,\_intestinal\_  
 hg3502-ht3696\_at\_hg3502-ht3696\_homeotic\_protein\_hox5.4\_  
 hg363-ht363\_at\_hg363-ht363\_epidermal\_growth\_factor\_receptor-related\_protein  
 hg37-ht37\_at\_hg37-ht37\_iron-responsive\_element-binding\_protein\_  
 j05158mrna\_2315-2825,carboxypeptidase\_n\_mrna,\_3'\_end\_  
 all\_j05412\_3866-4062:in\_j05412cds\_411-  
 439,regenerating\_protein\_(reg)\_gene,\_complete\_cds\_

k03207mrna\_286-748:in\_reversesequence,\_772-848,prb4\_locus\_salivary\_proline-rich\_protein\_mrna,\_comple  
 102648\_1312-1852,(clone\_v6)\_transcobalamin\_ii\_(tcn2)\_mrna,\_complete\_cds\_  
 110377\_879-1441,(clone\_ctg-b37)\_mrna\_sequence  
 113266\_4056-4630,n-methyl-d-aspartate\_receptor\_(nr1-1)\_mrna,\_complete\_cds\_  
 116464\_440-752,ets\_oncogene\_(pep1)\_mrna,\_complete\_cds  
 128175\_1375-1933,prostaglandin\_e2\_receptor\_ep2\_subtype\_mrna,\_complete\_cds\_  
 131584exon\_1488-1986,g\_protein-coupled\_receptor\_(ebi\_1)\_gene\_  
 m19878cds\_3-  
 125:in\_reversesequence,\_1964,calbindin\_27\_gene,\_exonsand\_2,\_and\_alu\_repeat/gb=m  
 19878\_/nt  
 m23197\_848-1388,differentiation\_antigen\_(cd33)\_mrna,\_complete\_cds  
 m26657\_1861-2430,testicular\_angiotensin\_converting\_enzyme\_mrna,\_complete\_cds\_  
 m27318\_365-878,interferon\_(ifn-alpha-m1)\_mrna,\_complete\_cds  
 all\_m28439\_261-360,keratin\_typegene  
 m30625\_1154-1554,dopamine\_d2\_receptor,\_mrna,\_complete\_cds  
 m35531\_2832-3318,gdp-1-fucose:beta-d-galactoside\_2-alpha-1-  
 fucosyltransferase\_mrna,\_complete\_cds\_  
 m55621\_2074-2452,n-acetylglucosaminyltransferase\_i\_(glcnac-  
 ti)\_mrna,\_complete\_cds  
 m58600mrna\_1634-2168,heparin\_cofactor\_ii\_(hcf2)\_gene,\_exonsthrough\_5\_  
 all\_m60331\_669-1094:in\_m60331cds\_116,protaminegene,\_complete\_cds\_  
 m62783\_3069-3453,alpha-n-acetylgalactosaminidase\_mrna,\_complete\_cds  
 m64930\_2982-3366,protein\_phosphatase\_2a\_beta\_subunit\_mrna,\_complete\_cds  
 m68907\_2-187,tachykinin-a\_(gamma-ppt-a)\_gene,\_partial\_cds/gb=m68907\_/ntype=rna\_  
 m83181cds\_918-1206:in\_reversesequence,\_1639-  
 1867,serotonin\_receptor\_gene,\_complete\_cds\_  
 s78723mrna#1\_565-991,\_5-ht2ar=serotonin\_5-  
 ht2a\_receptor\_{promoter}\_{human,\_genomic,\_1678\_nt}]\_  
 s80905\_f\_at\_s80905\_s80905\_4040\_in\_s80905cds\_17-  
 1067,\_prb2\_(prb2l\_con1+)=con1\_{exon\_3}\_{human,\_perip  
 s82075\_115-283,\_pa4=candidate\_oncogene\_{3'\_region}\_{human,\_hen-16,\_hen-  
 16t\_transformed\_endocervical\_  
 s83308\_920-1400,\_sox5=sry-  
 related\_hmg\_box\_gene\_{alternatively\_spliced}\_{human,\_testis,\_mrna,\_1473\_nt  
 u02566\_2456-2990,receptor\_tyrosine\_kinase\_tif\_mrna,\_partial\_cds  
 u09117\_2164-2536,phospholipase\_c\_deltamrna,\_complete\_cds  
 u10099\_938-1435,pom-zp3\_mrna,\_complete\_cds\_  
 u11791\_662-1160,cyclin\_h\_mrna,\_complete\_cds  
 u25041\_at\_u25041\_u25041,not\_in\_gb\_record,5c5\_mrna,\_putative\_complete\_cds  
 u27699\_2929-3349,pephbgt-1\_betaine-gaba\_transporter\_mrna,\_complete\_cds\_  
 u31216\_3168-  
 3641,metabotropic\_glutamate\_receptorbeta\_(mglur1beta)\_mrna,\_complete\_cds  
 all\_u33447\_1311-1888,putative\_g-protein-  
 coupled\_receptor\_(gpr17)\_gene,\_complete\_cds  
 u40279cds\_70-574,beta-2\_integrin\_alphad\_subunit\_(itgad)\_gene,\_exons\_25-  
 30,\_and\_partial\_cds/gb=u40279  
 u46752\_1476-1872,phosphotyrosine\_independent\_ligand\_p62b\_b-  
 cell\_isoform\_for\_the\_lck\_sh2\_domain\_mrna,  
 u47334\_7-307,gamma\_aminobutyric\_acid\_receptor\_beta4\_subunit-  
 like\_mrna,\_partial\_cds/gb=u47334\_/ntype=  
 u57650\_4714-5224,sh2-containing\_inositol\_5-  
 phosphatase\_(hship)\_mrna,\_complete\_cds  
 u77975\_1042-1420,hepatocyte\_nuclear\_factor(hnf-6)\_mrna,\_partial\_cds\_  
 u79725\_2240-2744,a33\_antigen\_precursor\_mrna,\_complete\_cds  
 all\_x02958\_1064-1245,interferon\_alpha\_gene\_ifn-alpha\_6\_  
 all\_x13444\_852-1357,mrna\_for\_cd8\_beta-chain\_glycoprotein\_(cd8\_beta.1)

x56687cds\_1698-2154:in\_reversesequence,\_2348,mrna\_for\_autoantigen\_nor-90  
 x57110mrna\_2510-2998,mrna\_for\_c-cbl\_proto-oncogene.  
 all\_x60299\_3486-4065,kalig-1\_mrna\_for\_neural\_cell\_adhesion\_and\_axonal\_path-  
 finding\_molecule\_homologu  
 x70083mrna\_166-460,abp-280-like\_mrna\_for\_filamin\_(695\_bps)/gb=x70083\_/ntype=rna  
 x76132mrna\_4097-4583,dcc\_mrna  
 x79510cds\_3165-3459:in\_reversesequence,\_3839-3971,mrna\_for\_protein-tyrosine-  
 phosphatase\_d1  
 all\_x80026\_1785-2363,b-cam\_mrna  
 all\_x81882\_2153-  
 2682,mrna\_for\_for\_vasopressin\_activated\_calcium\_mobilizing\_receptor-  
 like\_protein\_  
 x82324cds\_866-1055:in\_reversesequence,\_1096-1450,brainmrna\_  
 x82877cds\_1533-1809:in\_reversesequence,\_3974-4118,na+-d-  
 glucose\_cotransport\_regulator\_gene  
 x86371cds\_2629-3129,mrna\_for\_tumour\_suppressor\_protein,\_hugl\_  
 x91348mrna\_893-1211,predicted\_non\_coding\_cdna\_(dgcr5)  
 y10936\_637-1027,mrna\_for\_hypothetical\_protein\_downstream\_of\_dmpk\_and\_dmahp\_  
 y13153\_1404-1950,mrna\_for\_kynurenine\_3-monooxygenase/gb=y13153\_/ntype=rna\_  
 all\_z80787\_563-700,h4/j\_gene.

## Metagene 348

ab005535\_1056-1635,mrna\_for\_clock,\_partial\_cds/gb=ab005535\_/ntype=rna\_  
 ad000684cds#1\_934-1252:in\_reversesequence,\_16809-17037,\_lisch7\_gene\_(liver-  
 specific\_bhlh-zip\_transcr  
 d26068\_2056-2398,mrna\_for\_kiaa0038\_gene,\_partial\_cds\_  
 d26362\_2475-2985,mrna\_for\_kiaa0043\_gene,\_complete\_cds  
 d26561cds#4\_3-  
 237:in\_reversesequence,\_4010:not\_in\_gb\_record,\_orf\_for\_l1\_protein\_gene\_extrac  
 t\_d\_fromp  
 d29013\_664-1234,mrna\_for\_dna\_polymerase\_beta,\_complete\_cds\_  
 d31886\_3076-3592,mrna\_for\_kiaa0066\_gene,\_partial\_cds\_  
 d38293\_2926-3400,mrna\_for\_clathrin-like\_protein,\_complete\_cds  
 d44466\_2575-3115,mrna\_for\_proteasome\_subunit\_p112,\_complete\_cds  
 d50525mrna\_3316-3886,mrna\_for\_ti-227h/gb=d50525\_/ntype=rna\_  
 d63486\_5877-6267,mrna\_for\_kiaa0152\_gene,\_complete\_cds  
 d63881\_3840-4278,mrna\_for\_kiaa0160\_gene,\_partial\_cds\_  
 d64154\_786-1254,mrna\_for\_mr\_110,000\_antigen,\_complete\_cds  
 d78156cds\_888-1140:in\_reversesequence,\_2058-  
 2292,mrna\_for\_rasgtpase\_activating\_protein,\_partial\_cds\_  
 d80002\_4430-4938,mrna\_for\_kiaa0180\_gene,\_partial\_cds\_  
 d82348\_1479-1947,mrna\_for\_5-aminoimidazole-4-carboxamide-1-beta-d-  
 ribonucleoti\_de\_transformylase/ino  
 d85758\_214-748,mrna\_forprotein\_homologous\_to\_droer\_protein,\_complete\_cds  
 d86979\_5308-5842,mrna\_for\_kiaa0226\_gene,\_complete\_cds  
 d90084exon#10-8\_36-  
 41,pyruvate\_dehydrogenase\_(ec\_1.2.4.1)\_alpha\_subunit\_gene,\_exons\_11-jan\_  
 hg110-ht110\_s\_at\_hg110-ht110\_heterogeneous\_nuclear\_ribonucleoprotein\_a/b\_  
 hg1869-ht1904\_at\_hg1869-ht1904\_male\_enhanced\_antigen\_  
 hg2274-ht2370\_at\_hg2274-ht2370\_rna\_polymerase\_ii,\_14.5\_kda\_subunit\_  
 hg662-ht662\_at\_hg662-ht662\_epstein-barr\_virus\_small\_rna-associated\_protein\_  
 j04611\_1533-2061,lupus\_p70\_(ku)\_autoantigen\_protein\_mrna,\_complete\_cds\_  
 k03515mrna\_1392-1938,neuroleukin\_mrna,\_complete\_cds  
 l02426\_1040-1556,26s\_protease\_(s4)\_regulatory\_subunit\_mrna,\_complete\_cds\_

l16896\_1717-2257,zinc\_finger\_protein\_mrna,\_complete\_cds  
 l20773\_1025-1517,mrna\_in\_the\_region\_near\_the\_btk\_gene\_involved\_in\_a-gamma-globulinemia  
 l25851\_3332-3812,integrin\_alpha\_e\_mrna,\_complete\_cds  
 l37127mrna\_73-553,(clone\_mf.18)\_rna\_polymerase\_ii\_mrna,\_complete\_cds  
 m24398mrna\_522-970,parathymosin\_mrna,\_complete\_cds\_  
 m25077mrna\_1310-1712:in\_reversesequence,\_1760-1826,ss-a/ro\_ribonucleoprotein\_autoantigen\_60\_kd\_subun  
 m58028mrna\_2999-3401,ubiquitin-activating\_enzyme\_e1\_(ube1)\_mrna,\_complete\_cds  
 m84332exon#4\_764-1226:in\_reversesequence,\_2337-2397,adp-ribosylation\_factorgene  
 u12465\_19-367,ribosomal\_protein\_l35\_mrna,\_complete\_cds\_  
 u21090\_1109-1541,dna\_polymerase\_delta\_small\_subunit\_mrna,\_complete\_cds\_  
 u56418\_785-1313,lysophosphatidic\_acid\_acyltransferase-beta\_mrna,\_complete\_cds  
 u79716\_11015-11537,reelin\_(reln)\_mrna,\_complete\_cds  
 u81554\_431-839,cam\_kinase\_ii\_isoform\_mrna,\_complete\_cds/gb=u81554\_/ntype=rna\_  
 u86602\_772-1240,nucleolar\_protein\_p40\_mrna,\_complete\_cds\_  
 u90426\_959-1439,nuclear\_rna\_helicase,\_complete\_cds\_  
 u90915\_122-674,clone\_23600\_cytochrome\_c\_oxidase\_subunit\_iv\_mrna,\_complete\_cds  
 all\_x14346\_1969-2534,mrna\_for\_eosinophil\_peroxidase  
 x52851mrna\_152-  
 692,\_peptidylprolyl\_isomerase\_gene\_extracted\_fromcyclophilin\_gene\_for\_cyclophil  
 in\_(ec  
 x58401mrna\_356-900,l2-  
 9\_transcript\_of\_unrearranged\_immunoglobulin\_v(h)5\_pseudogene.  
 x59543mrna\_2500-3016,mrna\_for\_m1\_subunit\_of\_ribonucleotide\_reductase\_  
 all\_x60486\_394-737,h4/g\_gene\_for\_h4\_histone  
 all\_x69141\_1444-1997,mrna\_for\_squalene\_synthase  
 z21507cds\_424-802:in\_reversesequence,\_901-955,ef-  
 1delta\_gene\_encodingelongation\_factor-1-delta\_

Metagene 220

d13631\_2795-3373,mrna\_for\_kiaa0006\_gene,\_complete\_cds  
 d16581\_42-552,mrna\_for\_8-oxo-dgtpase,\_complete\_cds\_  
 d30755\_1189-1633,mrna\_for\_kiaa0113\_gene,\_partial\_cds\_  
 d38048\_391-919,mrna\_for\_proteasome\_subunit\_z,\_complete\_cds\_  
 d49818\_1445-1919,mrna\_for\_fructose\_6-phosphate,2-kinase/fructose\_2,6-bisphosphatase,\_partial\_cds\_  
 d63487\_2889-3369,mrna\_for\_kiaa0153\_gene,\_partial\_cds\_  
 hg3989-ht4259\_at\_hg3989-ht4259\_cpg-enriched\_dna,\_clone\_e14\_  
 j04948mrna\_1898-2432,alkaline\_phosphatase\_(alp-1)\_mrna,\_complete\_cds\_  
 l16862\_2289-2763,g\_protein-coupled\_receptor\_kinase\_(grk6)\_mrna,\_complete\_cds  
 l19605\_1483-1915,56k\_autoantigen\_annexin\_xi\_gene\_mrna,\_complete\_cds\_  
 l33801\_860-1334,protein\_kinase\_mrna,\_complete\_cds  
 l38593mrna#1\_2-200,integral\_membrane\_protein\_(nrampl)\_gene,\_exon\_5  
 l42243exon#2\_2604-  
 3066,\_ifnar2\_gene\_(interferon\_receptor)\_extracted\_from(clone\_q-2od3)\_interferon\_re  
 m15796\_660-1152,cyclin\_protein\_gene,\_complete\_cds  
 m25897mrna\_40-359,platelet\_factor(pf4)\_mrna,\_complete\_cds\_  
 m28211\_176-650,gtp-binding\_protein\_(rab4)\_mrna,\_complete\_cds  
 all\_m32639\_3894-4064,salivary\_statherin\_gene,\_5'\_flank\_  
 m55671mrna\_968-1448,protein\_z\_(plus\_66\_bp\_insertion)\_mrna,\_complete\_cds  
 m63589mrna#1\_4159-4573,stem\_cell\_leukemia\_gene\_product\_

s66431\_5869-6361,\_rbp2=retinoblastoma\_binding\_protein[human,\_nalm-6\_pre-  
b\_cell\_leukemia,\_mrna,\_6455\_  
s74221\_317-  
695,\_ik=ik\_factor\_[human,\_leukemic\_cells\_k562,\_chronic\_myeloid\_leukemia\_patient  
,\_mrna,\_75  
u03634\_1244-1652,p47\_lbc\_oncogene\_mrna,\_complete\_cds\_  
u05255\_159-  
261,glycophorin\_hep2\_mrna,\_partial\_cds,glycophorin\_hep2\_mrna,\_partial\_cds  
u20499exon#10\_185-  
431,thermolabile\_phenol\_sulfotransferase\_(stm)\_gene,\_complete\_cds  
u27325\_712-1266,thromboxane\_a2\_receptor\_mrna,\_complete\_cds\_  
u32315\_1374-1842,syntaxinmrna,\_complete\_cds\_  
u43203\_1561-2060,thyroid\_transcription\_factor(ttf-1)\_mrna,\_complete\_cds\_  
u43753exon\_9-237:not\_in\_gb\_record,frataxin\_(frda)\_gene,\_promoter\_region\_and  
u56085\_2568-3048,periodic\_tryptophan\_protein(pwp2)\_mrna,\_complete\_cds\_  
u79299\_988-1462,neuronal\_olfactomedin-  
related\_er\_localized\_protein\_mrna,\_partial\_cds.  
u82306\_135-225,unknown\_protein\_mrna,\_partial\_cds/gb=u82306\_/ntype=rna  
u86782\_591-1077,26s\_proteasome-  
associated\_pad1\_homolog\_(poh1)\_mrna,\_complete\_cds/gb=u86782\_/ntype=rn  
u88871\_910-1312,hspex7p\_(hspex7)\_mrna,\_complete\_cds  
u89606\_521-917,pyridoxal\_kinase\_mrna,\_complete\_cds.  
u96094\_193-667,sarcosine\_(sln)\_mrna,\_complete\_cds.  
x56253mrna\_1914-2274,mpr46\_gene\_for\_46kd\_mannose\_6-phosphate\_receptor\_  
x61587mrna\_701-1259,rhog\_mrna\_for\_gtpase\_  
all\_x78549\_1912-2186,brk\_mrna\_for\_tyrosine\_kinase  
x95384\_435-807,mrna\_for\_unknown\_14kda\_protein  
x99720mrna\_1458-1944,tprc\_gene  
z18948exon#3\_69-465,mrna\_for\_s100e\_calcium\_binding\_protein\_  
z48804mrna\_1006-1528,mrna\_(ocular\_albinism\_typerelated)\_

Metagene 147

all\_ac000061\_18132-57268:in\_ac000061cds#1\_720-  
760,\_wugsc:h\_133k23.1c\_gene\_extracted\_frombac\_clone\_13  
ac000062\_110059-110206:in\_all\_ac000062\_109961-109993,pac\_clone\_2g3a\_from\_13q12-  
13q13  
d50640exon\_700-1132,dna\_for\_phosphodiesterase\_3b\_

Metagene 412

d87462\_3013-3403,mrna\_for\_kiaa0272\_gene,\_partial\_cds\_  
d89858\_671-1157,mrna\_for\_d-aspartate\_oxidase,\_complete\_cds\_  
m10050mrna\_25-424,liver\_fatty\_acid\_binding\_protein\_(fabp)\_mrna,\_complete\_cds\_  
u63717\_402-852,osteoclast\_stimulating\_factor\_mrna,\_complete\_cds

Metagene 128

d31765\_3735-4191,mrna\_for\_kiaa0061\_gene,\_partial\_cds\_  
d84239\_15949-16339,mrna\_for\_igg\_fc\_binding\_protein,\_complete\_cds\_

hg36-ht4101\_s\_at\_hg36-ht4101\_polymyositis/scleroderma\_(pm-scl)\_autoantigen,\_altsplice\_2  
 l10665mrna\_1623-2049,gtp-binding\_protein\_superfamily,\_g\_protein\_alpha-olf\_subunit\_(olfactory)\_mrna,\_  
 l13203\_1536-2064,hnf-3/fork-head\_homolog-3\_hfh-3\_mrna,\_complete\_cds  
 l34075\_7342-7912,fkbp-rapamycin\_associated\_protein\_(frap)\_mrna,\_complete\_cds\_  
 all\_m10942\_421-1762,metallothionein-ie\_gene\_(hmt-ie)\_  
 m21389mrna\_1754-2192,keratin\_type\_ii\_(58\_kd)\_mrna,\_complete\_cds  
 m21812\_61-592,(clone\_pwhlc2-24)\_myosin\_light\_chainmrna,\_complete\_cds  
 m57399\_434-998,nerve\_growth\_factor\_(hbnf-1)\_mrna,\_complete\_cds\_  
 m96803\_6960-7482,general\_beta-spectrin\_(sptbn1)\_mrna,\_complete\_cds\_  
 u06863\_1416-1938,follistatin-related\_protein\_precursor\_mrna,\_complete\_cds  
 u08815\_2346-2676,splicesomal\_protein\_(sap\_61)\_mrna,\_complete\_cds\_

Metagene 460

m62994\_1478-1964,thyroid\_autoantigen\_(truncated\_actin-binding\_protein)\_mrna,\_complete\_cds\_  
 u00968\_3595-4069,srebp-1\_mrna,\_complete\_cds  
 u53468\_862-  
 1390,nadh:ubiquinone\_oxidoreductase\_subunit\_b13\_(b13)\_mrna,\_complete\_cds  
 u79751\_2171-2615,basic-leucine\_zipper\_nuclear\_factor\_(jem-1)\_mrna,\_complete\_cds/gb=u79751\_/ntype=rna  
 x14885mrna\_2506-2558,gene\_for\_transforming\_growth\_factor-beta(tgf-beta\_3)\_exon(and\_joined\_cds)

Metagene 179

d42138\_1371-1833,mrna\_for\_pig-b,\_complete\_cds  
 d45132\_5577-6099,kidney\_mrna\_for\_zinc-finger\_dna-binding\_protein,\_complete\_cds\_  
 hg3914-ht4184\_s\_at\_hg3914-ht4184\_cell\_division\_cycle\_protein\_2-related\_protein\_kinase\_(pisslre)  
 hg4144-ht4414\_at\_hg4144-ht4414\_zinc\_finger\_protein\_hzf6  
 l10333mrna\_2590-3166,neuroendocrine-specific\_protein\_a\_(nsp)\_mrna,\_complete\_cds\_  
 m31328mrna\_1054-1480,guanine\_nucleotide-binding\_protein\_beta-3\_subunit\_mrna,\_complete\_cds  
 m96944\_2724-3252,b-cell\_specific\_transcription\_factor\_(bsap)\_mrna,\_complete\_cds  
 u25138\_676-1168,maxik\_potassium\_channel\_beta\_subunit\_mrna,\_complete\_cds  
 u57629\_2195-  
 2735,retinitis\_pigmentosa\_gtpase\_regulator\_(rpgr)\_mrna,\_complete\_cds\_  
 u68494\_1290-1764,hbc647\_mrna\_sequence  
 u80457\_2243-2645,transcription\_factor\_sim2\_short\_form\_mrna,\_complete\_cds\_  
 x59842mrna\_2321-2861,pbx2\_mrna  
 all\_y07759\_5956-6377,mrna\_for\_myosin\_heavy\_chain\_12  
 all\_y08976\_956-1548,mrna\_for\_fev\_protein\_  
 z50115cds\_1782-2011:in\_reversesequence,\_2181-  
 2473,mrna\_for\_thimet\_oligopeptidase\_(metalloproteinase)

Metagene 438

ab000115\_1469-1973,\_complete\_cds  
 d14664\_3255-3639,mrna\_for\_kiaa0022\_gene,\_complete\_cds  
 d26361\_5991-6543,mrna\_for\_kiaa0042\_gene,\_complete\_cds  
 l38951mrna\_3611-4151,importin\_beta\_subunit\_mrna,\_complete\_cds\_  
 l40399mrna\_993-1467,(clone\_s240ii117/zap112)\_mrna,\_complete\_cds\_  
 m15353mrna\_1277-1769,cap-binding\_protein\_mrna,\_complete\_cds\_  
 m69043\_985-1459,mad-3\_mrna\_encoding\_ikb-like\_activity,\_complete\_cds\_  
 u05040\_1814-2282,fuse\_binding\_protein\_mrna,\_complete\_cds\_  
 u08998\_962-1280,tar\_rna\_binding\_protein(trbp2)\_mrna,\_complete\_cds\_  
 u22431\_3070-3644,hypoxia-inducible\_factoralpha\_(hif-  
 1\_alpha)\_mrna,\_complete\_cds\_  
 u41515\_61-397,deleted\_in\_split\_hand/split\_foot(dss1)\_mrna,\_complete\_cds\_  
 u43522\_3580-4072,cell\_adhesion\_kinase\_beta\_(cakbeta)\_mrna,\_complete\_cds\_  
 u44111mrna\_1108-1642,histamine\_n-methyltransferase\_(hnmt)\_gene\_  
 u51166\_2941-3361,g/t\_mismatch-  
 specific\_thymine\_dna\_glycosylase\_mrna,\_complete\_cds  
 u70063\_1750-2266,acid\_ceramidase\_mrna,\_complete\_cds  
 all\_x83228\_3359-3561,mrna\_for\_li-cadherin  
 z79581exon\_19-226,laz3/bcl6\_gene,\_first\_non\_coding\_exon

## Metagene 297

l41690\_906-1332,tnf\_receptor-1\_associated\_protein\_(tradd)\_mrna,\_3'\_end\_of\_cds\_  
 s78693\_2-40,\_alpha\_creb-1=cyclic\_amp\_response\_element-binding\_protein-  
 1\_alpha\_isoform\_{alternatively  
 x05153mrna\_264-678,\_alpha-lactalbumin\_precursor\_gene\_extracted\_fromalpha-  
 lactalbumin\_gene\_  
 all\_x06956\_5299-5359,halpha44\_gene\_for\_alpha-tubulin,\_exons\_3-jan

## Metagene 471

d21852\_3671-4241,mrna\_for\_kiaa0029\_gene,\_partial\_cds\_  
 d25303\_2993-3539,mrna\_for\_integrin\_alpha\_subunit,\_complete\_cds\_  
 d25538\_5613-6147,mrna\_for\_kiaa0037\_gene,\_complete\_cds  
 d28791exon\_1763-2267,pig-a\_gene,\_5'\_flanking\_region\_and  
 d30758\_1965-2469,mrna\_for\_kiaa0050\_gene,\_complete\_cds  
 d42041\_3435-3771,mrna\_for\_kiaa0088\_gene,\_partial\_cds\_  
 d50911\_3298-3718,mrna\_for\_kiaa0121\_gene,\_complete\_cds  
 d63506\_1940-2435,mrna\_for\_unc-18homologue,\_complete\_cds  
 d79983\_5024-5498,mrna\_for\_kiaa0161\_gene,\_complete\_cds  
 d80003\_6029-6395,mrna\_for\_kiaa0181\_gene,\_partial\_cds\_  
 d83032\_6016-6364,mrna\_for\_nuclear\_protein,\_np220,\_complete\_cds\_  
 d83777\_4475-5003,mrna\_for\_kiaa0193\_gene,\_complete\_cds  
 d86962\_5028-5328,mrna\_for\_kiaa0207\_gene,\_complete\_cds  
 d86969\_4436-4886,mrna\_for\_kiaa0215\_gene,\_complete\_cds  
 j03161mrna\_3636-4122,serum\_response\_factor\_(srf)\_mrna,\_complete\_cds  
 j03779mrna\_4985-  
 5459,common\_acute\_lymphoblastic\_leukemia\_antigen\_(calla)\_mrna,\_complete\_cds  
 l19067\_2335-2419,nf-kappa-b\_transcription\_factor\_p65\_subunit\_mrna,\_complete\_cds  
 l29218mrna\_1408-1894,clk2\_mrna,\_complete\_cds  
 l35035mrna\_629-1079,ribose\_5-phosphate\_isomerase\_(rpi)\_mrna\_  
 l35240cds\_1065-1323:in\_reversesequence,\_1431-1533,enigma\_gene,\_complete\_cds\_  
 all\_m16505\_6015-6520,steroid\_sulfatase\_(sts)\_mrna,\_complete\_cds



m23161\_3287-3791,transposon-like\_element\_mrna  
 m29550\_2005-2317,calcineurin\_a1\_mrna,\_complete\_cds\_  
 m33552mrna\_1042-1546,lymphocyte-specific\_protein(lsp1)\_mrna,\_complete\_cds\_  
 m34057\_4720-5044,transforming\_growth\_factor-  
 betabinding\_protein\_mrna,\_complete\_cds  
 m87770\_3759-4125,fibroblast\_growth\_factor\_receptor\_(k-sam)\_mrna,\_complete\_cds  
 u02031\_3660-4182,sterol\_regulatory\_element\_binding\_protein-2\_mrna,\_complete\_cds  
 u16660\_685-1153,peroxisomal\_enoyl-coa\_hydratase-  
 like\_protein\_(hpxel)\_mrna,\_complete\_cds  
 u35376\_2006-2254,repressor\_transcriptional\_factor\_(znf85)\_mrna,\_complete\_cds\_  
 u58048\_1891-2431,metallopeptidase\_prsm1\_mrna,\_complete\_cds\_  
 u73524\_1866-2304,putative\_atp/gtp-binding\_protein\_(heab)\_mrna,\_complete\_cds  
 u78556\_2774-  
 3248,cisplatin\_resistance\_associated\_alpha\_protein\_(hcra\_alpha)\_mrna,\_complete\_  
 cds\_  
 all\_x16396\_1543-2102,mrna\_for\_nad-  
 dependent\_methylene\_tetrahydrofolate\_dehydrogenase\_cyclohydrolase\_  
 all\_x77744\_1467-1750,f11\_mrna  
 x90780mrna\_255-765,cardiac\_troponin\_i\_gene,\_exonsto\_5  
 all\_z48481\_2878-3347,mrna\_for\_membrane-type\_matrix\_metalloproteinase\_1\_

## Metagene 439

d13645\_1517-2027,mrna\_for\_kiaa0020\_gene,\_complete\_cds  
 v00542mrna\_375-902,messenger\_rna\_forleukocyte\_(alpha)\_interferon  
 all\_x62822\_2104-2645,gene\_encoding\_beta-galactoside\_alpha-2,6-sialyltransferase

## Metagene 256

hg210-ht210\_s\_at\_hg210-ht210\_galactokinase  
 j02923\_2574-3132,65-kilodalton\_phosphoprotein\_(p65)\_mrna,\_complete\_cds\_  
 104270\_1613-  
 2111,(clone\_cd18)\_tumor\_necrosis\_factor\_receptorrelated\_protein\_mrna,\_complete\_  
 cds\_  
 106633\_1153-1669,transcription\_factor\_mrna,\_complete\_cds\_  
 m14219\_1375-  
 1753,chondroitin/dermatan\_sulfate\_proteoglycan\_(pg40)\_core\_protein\_mrna,\_comple  
 te\_cds  
 m21624mrna\_603-1149,t-cell\_receptor\_delta\_chain\_mrna\_(vjc-region),\_complete\_cds  
 m76766\_679-1129,transcription\_factor\_(tfiib)\_mrna,\_complete\_cds  
 u88964\_130-568,hem45\_mrna,\_complete\_cds

## Metagene 235

hg67-ht67\_f\_at\_hg67-ht67\_zinc\_finger\_protein\_  
 m18728mrna\_1932-2460,nonspecific\_crossreacting\_antigen\_mrna,\_complete\_cds  
 m29540\_2616-2949,carcinoembryonic\_antigen\_mrna\_(cea),\_complete\_cds\_  
 m36803exon\_142-352:not\_in\_gb\_record,hemopexin\_gene  
 m55284\_1800-2364,protein\_kinase\_c-1\_(prkcl)\_mrna,\_complete\_cds\_  
 u13913\_3871-4120,large-conductance\_calcium-  
 activated\_potassium\_channel\_(hslo)\_mrna,\_complete\_cds\_

u34879mrna\_1628-2073,17-beta-  
hydroxysteroid\_dehydrogenase\_(edh17b2)\_gene,\_complete\_cds  
u69140\_297-846,zygini\_mrna,\_partial\_cds\_

Metagene 375

m37981\_1751-1829,alpha-  
3\_neuronal\_nicotinic\_acetylcholine\_receptor\_subunit\_mrna,\_complete\_cds  
m74290\_1261-1741,substance\_p\_receptor\_protein\_mrna\_  
m76729\_6573-7077,pro-alpha-1(v)\_collagen\_mrna,\_complete\_cds\_  
s46622\_1569-  
2055,\_calcineurin\_a\_catalytic\_subunit\_[human,\_testis,\_mrna,\_2134\_nt]  
u10473\_333-895,clone\_p4betagt/3\_beta-1,4-  
galactosyltransferase\_mrna,\_partial\_cds/gb=u10473\_/ntype=rn  
u16720mrna\_959-1508,interleukin(il10)\_gene,\_complete\_cds  
u28015\_1201-1351,cysteine\_protease\_(icerel-iii)\_mrna,\_complete\_cds\_  
u80184mrna\_3661-4093,flil\_gene,\_complete\_cds\_  
u89336exon#46-49\_2-  
143:in\_fullsequence,\_26932:,\_unknown\_gene\_extracted\_fromhla\_iii\_region\_containi  
ng  
x52221mrna\_1674-2244,ercc2\_gene,\_exons&(partial)\_  
x69090\_4322-4880,mrna\_for\_skeletal\_muscle\_190kd\_protein  
x76302exon#3\_386-923,ry-1\_mrna\_for\_putative\_nucleic\_acid\_binding\_protein\_  
x91141mrna\_2412-2904,mrna\_for\_rabaptin-5\_protein\_  
all\_x91249\_2428-2855,mrna\_for\_white\_gene\_protein\_

Metagene 107

d00591exon#14\_597-1041,rcc1\_gene,\_complete\_cds\_  
d28114\_780-1278,mrna\_for\_mobp\_(myelin-  
associated\_oligodendrocytic\_basic\_protein),\_complete\_cds,\_clon  
d50532\_839-1283,mrna\_for\_macrophage\_lectin\_2,\_complete\_cds\_  
d56495\_1102-1600,mrna\_for\_reg-related\_sequence\_derived\_peptide-2\_  
l21993\_1527-2013,adenylyl\_cyclase\_mrna,\_3'\_end\_of\_cds  
m32313mrna\_1537-2047,steroid\_5-alpha-reductase\_mrna,\_complete\_cds  
all\_z46788\_1637-2082,mrna\_for\_cylicin\_ii\_

Metagene 209

all\_d11139\_1902-  
2407,gene\_for\_tissue\_inhibitor\_of\_metalloproteinases,\_partial\_sequence\_  
d12775\_3124-3662,mrna\_for\_erythrocyte-specific\_AMP\_deaminase,\_complete\_cds\_  
d88799\_43-379,mrna\_for\_cadherin,\_partial\_cds/gb=d88799\_/ntype=rna\_  
hg4263-ht4533\_at\_hg4263-ht4533\_nkr-pla\_protein\_  
m32598cds\_2214-2448:in\_reversesequence,\_146-  
368,muscle\_glycogen\_phosphorylase\_(pygm)\_gene\_  
m80397\_2847-3368,dna\_polymerase\_delta\_catalytic\_subunit\_mrna,\_complete\_cds\_  
s42457\_2418-2814,\_cncg=rod\_photoreceptor\_cgmp-  
gated\_channel\_[human,\_retina,\_mrna,\_2857\_nt]

s81916\_98-  
 146, phosphoglycerate\_kinase\_{alternatively\_spliced}\_[human, phosphoglycerate\_k  
 inase\_defic  
 u40371\_2129-  
 2591,3',5'\_cyclic\_nucleotide\_phosphodiesterase\_(hspdelc1a)\_mrna,\_complete\_cds\_  
 u41813\_816-1290,i\_homeoprotein\_(hoxa9)\_mrna,\_partial\_cds\_  
 u72514\_405-837,c2f\_mrna,\_complete\_cds  
 x62055cds\_1413-1767:in\_reversesequence,\_2028-2232,ptplc\_mrna\_for\_protein-  
 tyrosine\_phosphatase\_1c\_

Metagene 341

u17033\_5092-5578,180\_kda\_transmembrane\_pla2\_receptor\_mrna,\_complete\_cds  
 u77949\_2079-2622,cdc6-related\_protein\_(hscdc6)\_mrna,\_complete\_cds

Metagene 82

ab000460\_4262-4724,\_clone\_res4-22b,\_complete\_cds  
 af007551\_16-  
 574,bet1p\_homolog\_(hbet1)\_mrna,\_complete\_cds/gb=af007551\_/ntype=rna\_  
 d12763\_882-1314,mrna\_for\_st2\_protein  
 d21337\_5825-6353,mrna\_for\_collagen\_  
 d31797exon\_752-1274,cd40\_ligand\_(cd40l)\_gene,\_5'\_flanking\_region\_and\_  
 d84276\_909-1185:in\_reversesequence,\_1299-1305,mrna\_for\_cd38,\_complete\_cds\_  
 d87024cds#5\_85-283:in\_reversesequence,\_2475-  
 39492,(lambda)\_dna\_for\_immunoglobulin\_light\_chain\_  
 d87119\_3614-4160,cancellous\_bone\_osteoblast\_mrna\_for\_gs3955,\_complete\_cds  
 l14542\_664-982,lectin-like\_type\_ii\_integral\_membrane\_protein\_(nkg2-  
 e)\_mrna,\_complete\_cds\_  
 l32140\_1681-2227,afamin\_mrna,\_complete\_cds\_  
 l41870\_4412-  
 4814,retinoblastoma\_susceptibility\_protein\_(rb1)\_mrna\_and\_mutations\_  
 m27394cds\_459-860:in\_reversesequence,\_1054-1101,b-lymphocyte\_cell-  
 surface\_antigen\_b1\_(cd20)\_  
 m77698\_1764-2310,gli-kruppel\_related\_protein\_(yy1)\_mrna,\_complete\_cds\_  
 u03105\_1538-1916,b4-2\_protein\_mrna,\_complete\_cds\_  
 u41344mrna\_1478-1988,prolargin\_(prelp)\_gene,\_5'\_flanking\_sequence\_and\_  
 u73499mrna\_29-200,hepatic\_nuclear\_factor\_1-alpha\_(tcf-1-  
 alpha)\_gene,\_promoter\_region\_and\_partial\_cds  
 x51804cds\_400-532:in\_reversesequence,\_820-  
 1162,pmi\_gene\_for\_a\_putative\_receptor\_protein\_  
 y10204mrna\_49-505,mrna\_for\_cd77\_protein/gb=y10204\_/ntype=rna\_

Metagene 440

d10925\_1613-2123,mrna\_for\_hm145  
 u29680\_251-659,a1\_protein\_mrna,\_complete\_cds\_  
 u45878\_2591-2689,inhibitor\_of\_apoptosis\_proteinmrna,\_complete\_cds\_

Metagene 485

d87682\_5800-6286,mrna\_for\_kiaa0241\_gene,\_partial\_cds\_  
d87742\_5513-5921,mrna\_for\_kiaa0268\_gene,\_partial\_cds\_  
d89050\_691-1219,mrna\_for\_lectin-like\_oxidized\_ldl\_receptor,\_complete\_cds\_  
l20688\_864-1188,gdp-dissociation\_inhibitor\_protein\_(ly-gdi)\_mrna,\_complete\_cds\_  
m31158\_2670-3216,camp-dependent\_protein\_kinase\_subunit\_rii-  
beta\_mrna,\_complete\_cds\_  
u63542\_303-750,putative\_fap\_protein\_mrna,\_partial\_cds\_  
u95740mrna#2\_1995-  
2457,\_362g6.1\_gene\_(unknown\_protein\_cit987sk\_362g6\_1)\_extracted\_fromchromosome\_  
16p  
all\_x05409\_1388-  
1965,rna\_for\_mitochondrial\_aldehyde\_dehydrogenase\_i\_aldh\_i\_(ec\_1.2.1.3)

Metagene 308

u14518\_859-1315,centromere\_protein-a\_(cenp-a)\_mrna,\_complete\_cds\_  
u31116\_1448-2012,beta-sarcoglycan\_a3b\_mrna,\_complete\_cds\_  
all\_u58675\_25626-39844,\_or17-  
228\_gene\_extracted\_fromolfactory\_receptor\_gene\_cluster\_on\_chromosome\_17  
u64573exon\_58-  
164,connexin43\_gap\_junction\_protein\_(connexin43)\_gene,\_exonand\_promoter\_region/  
gb=u645  
all\_x99142\_1281-1702,mrna\_for\_hair\_keratin,\_hkb6\_

Metagene 140

ab002365\_5053-5617,mrna\_for\_kiaa0367\_gene,\_partial\_cds/gb=ab002365\_/ntype=rna  
hg3729-ht3999\_f\_at\_hg3729-ht3999\_homeotic\_protein\_hpx-5  
l07077\_3277-3661,enyol-coa:\_hydratase\_3-hydroxyacyl-  
coa\_dehydrogenase\_(ehhadh)\_mrna,\_complete\_cds\_wi  
l11353\_1698-2202:in\_reversesequence,\_2208-2214,moesin-ezrin-radixin-  
like\_protein\_mrna,\_complete\_cds\_  
all\_l12052\_3408-3871,camp\_phosphodiesterase\_mrna,\_3'\_end\_  
l27050\_1166-1508,apolipoprotein\_f\_(apof)\_mrna,\_complete\_cds\_  
l36847cds\_1044-1578,(clone\_p17/90)\_rearranged\_iduronate-2-  
sulphatase\_homologue\_gene/gb=l36847\_/ntype  
l76569mrna\_6762-  
7284,(clones\_cyg3,\_b5p6c4)\_fragile\_x\_e\_mental\_retardation\_syndrome\_protein\_(fmr  
2)\_mr  
m21535\_2603-3101,\_m17390erg\_protein\_(ets-related\_gene)\_mrna,\_complete\_cds\_  
u28687\_1710-  
1983,zinc\_finger\_containing\_protein\_znf157\_(znf157)\_mrna,\_complete\_cds\_  
u34380\_rna1\_s\_at\_u34380\_u34380,not\_in\_gb\_record,\_tec\_gene\_extracted\_fromprotein\_  
\_tyrosine\_kinase\_tec\_  
z35309cds\_3385-3727,mrna\_for\_adenylyl\_cyclase  
all\_z79693\_2421-3018,mrna\_for\_protein-tyrosine\_phosphatase\_nc-ptpcom1

Metagene 286

d14446\_794-1166,hfrep-1\_mrna\_for\_unknown\_protein,\_complete\_cds\_  
 d21262\_3210-3663,mrna\_for\_kiaa0035\_gene,\_partial\_cds\_  
 d28383\_4-  
 37,mrna\_for\_atp\_synthase\_b\_chain,\_5'\_utr\_(sequence\_from\_the\_5'\_cap\_to\_the\_start  
 \_codon)/gb=d  
 d42063\_9590-9962,mrna\_for\_ranbp2\_(ran-binding\_protein\_2),\_complete\_cds\_  
 d87453\_2046-2586,mrna\_for\_kiaa0264\_gene,\_partial\_cds\_  
 hg3088-ht3263\_at\_hg3088-ht3263\_splicing\_factor\_sc35,\_alt\_splice\_form\_3\_  
 l48692\_581-1067,(clone\_p5-23-3)\_mrna  
 m74558\_4849-5170,sil\_mrna,\_complete\_cds  
 u28251exon\_1192-1642,krueppel-  
 type\_zinc\_finger\_protein\_(znf169)\_gene,\_partial\_cds\_  
 u33632\_1401-1839,two\_p-domain\_k+\_channel\_twik-1\_mrna,\_complete\_cds\_  
 u41745\_296-794,pdgf\_associated\_protein\_mrna,\_complete\_cds  
 u96131\_1638-  
 2130,hpv16\_e1\_protein\_binding\_protein\_mrna,\_complete\_cds/gb=u96131/\_ntype=rna\_  
 x82206cds\_769-1107:in\_reversesequence,\_1192-1410,mrna\_for\_alpha-centractin  
 z15005cds\_7614-7968:in\_reversesequence,\_8076-8184,cenp-e\_mrna\_

Metagene 95

d13630\_2433-2919,mrna\_for\_kiaa0005\_gene,\_complete\_cds  
 d14530\_55-403,homolog\_of\_yeast\_ribosomal\_protein\_s28,\_complete\_cds\_  
 d14658\_859-1285,mrna\_for\_kiaa0102\_gene,\_complete\_cds\_  
 d21090\_2298-2868,mrna\_for\_xp-  
 c\_repair\_complementing\_protein\_(p58/hhr23b),\_complete\_cds\_  
 d25218\_1125-1575,mrna\_for\_kiaa0112\_gene,\_partial\_cds\_  
 d43948\_6033-6549,mrna\_for\_kiaa0097\_gene,\_complete\_cds  
 d45248\_389-773,mrna\_for\_proteasome\_activator\_hpa28\_subunit\_beta,\_complete\_cds  
 d50663\_235-625,mrna\_for\_tctel1\_gene,\_complete\_cds  
 d61380\_258-762,mrna\_for\_dj-1\_protein,\_complete\_cds\_  
 d63480\_2623-3187,mrna\_for\_kiaa0146\_gene,\_partial\_cds\_  
 d76444mrna\_2828-3362,hkf-1\_mrna,\_complete\_cds  
 d80005\_4364-4862,mrna\_for\_kiaa0183\_gene,\_partial\_cds\_  
 d87076\_5065-5581,mrna\_for\_kiaa0239\_gene,\_partial\_cds\_  
 d87440\_3807-4245,mrna\_for\_kiaa0252\_gene,\_partial\_cds\_  
 d87466\_3602-4124,mrna\_for\_kiaa0276\_gene,\_partial\_cds\_  
 d87470\_6278-6794,mrna\_for\_kiaa0280\_gene,\_partial\_cds\_  
 d88378\_2857-3157,mrna\_for\_proteasome\_inhibitor\_hpi31\_subunit,\_complete\_cds\_  
 d90086exon#10\_9-  
 489:not\_in\_gb\_record,pyruvate\_dehydrogenase\_(ec\_1.2.4.1)\_beta\_subunit\_gene,\_exo  
 ns\_10  
 j04543\_1215-1725,synexin\_mrna,\_complete\_cds  
 j04615mrna\_833-  
 1265,lupus\_autoantigen\_(small\_nuclear\_ribonucleoprotein,\_snrnp,\_sm-  
 d)\_mrna,\_complete  
 all\_j04982\_4001-  
 5444,heart/skeletal\_muscle\_atp/adp\_translocator\_(ant1)\_gene,\_complete\_cds  
 l06132\_1325-1721,voltage-  
 dependent\_anion\_channel\_isoform(vdac)\_mrna,\_complete\_cds\_  
 l10284\_3582-  
 4038,integral\_membrane\_protein,\_calnexin,\_ (ip90)\_mrna,\_complete\_cds\_  
 l13977\_1675-2017,prolylcarboxypeptidase\_mrna,\_complete\_cds\_  
 l19527\_31-415,ribosomal\_protein\_l27\_(rpl27)\_mrna,\_complete\_cds

l32977mrna\_680-  
 1124,(clone\_f17252)\_ubiquinol\_cytochrome\_c\_reductase\_rieske\_iron-  
 sulphur\_protein\_(uqc  
 all\_m12783\_3467-3780,c-sis/platelet-  
 derived\_growth\_factor(sis/pdgf2)\_mrna,\_complete\_cds\_  
 all\_m19645\_4941-5470,78\_kdalton\_glucose-  
 regulated\_protein\_(grp78)\_gene,\_complete\_cds\_  
 m21259\_at\_m21259\_m21259,not\_in\_gb\_record,alu\_repeats\_in\_the\_region\_5'\_to\_the\_sm  
 all\_nuclear\_ribonucle  
 m22760\_142-586,nuclear-  
 encoded\_mitochondrial\_cytochrome\_c\_oxidase\_va\_subunit\_mrna,\_complete\_cds\_  
 m23613\_701-1217,nucleophosmin\_mrna,\_complete\_cds\_  
 all\_m32405\_2395-2832:in\_m32405cds\_316-  
 347,homologue\_of\_rat\_insulinoma\_gene\_(rig),\_exons\_4-jan  
 m80335\_574-886,protein\_kinase\_a\_catalytic\_subunit\_mrna,\_3'\_end  
 m86667\_1037-1517,nap\_(nucleosome\_assembly\_protein)\_mrna,\_complete\_cds\_  
 m93036mrna\_987-1353:in\_reversesequence,\_527-545,(clone\_21726)\_carcinoma-  
 associated\_antigen\_ga733-2\_(  
 u07231\_2329-2647,g-rich\_sequence\_factor-1\_(grsf-1)\_mrna,\_complete\_cds\_  
 u07857\_173-677,\_humankda\_alu\_rna\_binding\_protein\_mrna,\_complete\_cds\_  
 u09813mrna\_225-  
 765,mitochondrial\_atp\_synthase\_subunit\_9,\_p3\_gene\_copy,\_mrna,\_nuclear\_gene\_enco  
 ding\_m  
 u12595\_1663-  
 2083,tumor\_necrosis\_factor\_tyrosereceptor\_associated\_protein\_(trap1)\_mrna,\_partia  
 l\_cds  
 u18062\_1678-2152,tfiid\_subunit\_tafii55\_(tafi55)\_mrna,\_complete\_cds  
 u44772\_1738-2176,palmitoyl\_protein\_thioesterase\_mrna,\_complete\_cds\_  
 u50733\_1132-1642,dynamitin\_mrna,\_complete\_cds  
 u58089\_1599-1941,hs-cul-3\_mrna,\_partial\_cds  
 u62800\_181-535,cystatin\_m\_(cst6)\_mrna,\_complete\_cds  
 u66879\_394-928,bcl-2\_binding\_component(bbc6)\_mrna,\_complete\_cds.  
 x02317cds\_251-371:in\_reversesequence,\_531-  
 831,mrna\_for\_cu/zn\_superoxide\_dismutase\_(sod)  
 all\_x52979\_759-  
 895:not\_in\_gb\_record,\_smb\_protein\_gene\_extracted\_fromgene\_for\_small\_nuclear\_rib  
 onucle  
 x56468mrna\_1303-1789,mrna\_for\_14.3.3\_protein,\_a\_protein\_kinase\_regulator\_  
 x59417cds\_319-709:in\_reversesequence,\_813-861,pros-27\_mrna  
 all\_x75252\_1083-1408,phosphatidylethanolamine\_binding\_protein\_mrna\_  
 all\_x91809\_980-1533,mrna\_for\_gaip\_protein  
 z50749cds\_689-1055:in\_reversesequence,\_1088-1274,sds22-like\_mrna

Metagene 476

d00763\_609-1035,mrna\_for\_proteasome\_subunit\_hc9  
 d14661\_1027-1579,mrna\_for\_kiaa0105\_gene,\_complete\_cds  
 d43949\_2627-3143,mrna\_for\_kiaa0082\_gene,\_partial\_cds\_  
 d63879\_3065-3599,mrna\_for\_kiaa0156\_gene,\_complete\_cds  
 d86973\_7230-7716,mrna\_for\_kiaa0219\_gene,\_partial\_cds\_  
 hg2460-ht2556\_at\_hg2460-ht2556\_integrin\_beta  
 hg4194-ht4464\_at\_hg4194-ht4464\_sodium/hydrogen\_exchanger  
 hg4716-ht5158\_at\_hg4716-ht5158\_guanosine\_5'\_-monophosphate\_synthase  
 j02963\_641-1049,platelet\_glycoprotein\_iib\_mrna,\_3'\_end\_  
 j05448\_1173-1665,rna\_polymerase\_subunit\_hrp33,\_mrna

all\_k01383\_2141-2388,metallothionein-i-a\_gene,\_complete\_coding\_sequence  
 l05500\_2226-2688,fetal\_brain\_adenylyl\_cyclase\_mrna,\_3'\_end\_  
 all\_l15440\_5674-  
 5845,tyrosine\_hydroxylase\_(th)\_gene,\_3'\_end;\_insulin\_(ins)\_gene,\_complete\_cds;\_  
 insul  
 l38941mrna\_19-343,ribosomal\_protein\_l34\_(rpl34)\_mrna,\_complete\_cds  
 m18185mrna\_206-656,gastric\_inhibitory\_polypeptide\_(gip)\_mrna,\_complete\_cds\_  
 m20471\_512-1066,brain-type\_clathrin\_light-chain\_a\_mrna,\_complete\_cds\_  
 m77232mrna\_329-  
 773,ribosomal\_protein\_s6\_gene,\_complete\_cds\_and\_flanking\_regions\_  
 u23803\_1125-1659,heterogeneous\_ribonucleoprotein\_a0\_mrna,\_complete\_cds  
 u31120mrna\_802-1234:in\_reversesequence,\_5052,interleukin-13\_(il-  
 13)\_precursor\_gene,\_complete\_cds\_  
 u37408\_1514-2078,ctbp\_mrna,\_complete\_cds\_  
 u41371\_2249-2777,spliceosome\_associated\_protein\_(sap\_145)\_mrna,\_complete\_cds\_  
 u68018\_1512-1890,rad\_protein\_homolog\_(hmad-2)\_mrna,\_complete\_cds\_  
 u90547\_2553-2811,ro/ssa\_ribonucleoprotein\_homolog\_(roret)\_mrna,\_complete\_cds\_  
 u96915\_165-693,sin3\_associated\_polypeptide\_p18\_(sap18)\_mrna,\_complete\_cds.  
 x77584cds\_5-215:in\_reversesequence,\_43-481,mrna\_for\_atl-  
 derived\_factor/thiredoxin\_  
 x85237cds\_1957-2311:in\_reversesequence,\_2480-  
 2588,mrna\_for\_splicing\_factor\_sf3a120  
 all\_x85373\_43-404,mrna\_for\_sm\_protein\_g  
 y00764cds\_85-235:in\_reversesequence,\_331-  
 463,mrna\_for\_mitochondrial\_hinge\_protein\_  
 all\_z26634\_11848-12401,mrna\_for\_ankyrin\_b\_(440\_kda)

Metagene 403

d90276\_757-1156,cgm7\_gene\_for\_nonspecific\_cross-reacting\_antigen\_(nca)\_  
 m92642\_5127-5311,alpha-1\_type\_xvi\_collagen\_(col16a1)\_mrna,\_complete\_cds\_  
 u68233\_1565-2063,farnesol\_receptor\_hrr-1\_(hrr-1)\_mrna,\_complete\_cds\_  
 u90911\_1165-1549,clone\_23652\_mrna\_sequence\_  
 x61070mrna\_61-379,mrna\_for\_t\_cell\_receptor,\_clone\_igra15.  
 all\_x72012\_2495-3060,end\_mrna\_for\_endoglin\_  
 y12394\_1326-1770,mrna\_for\_srpl-like\_protein

Metagene 138

af003743\_28-235,delayed\_rectifier\_potassium\_channel\_(kvlqt1-  
 iso5)\_mrna,\_5'\_utr\_and\_partial\_cds/gb=af  
 d10495\_1562-2054,mrna\_for\_protein\_kinase\_c\_delta-type  
 all\_d13897\_1402-  
 1545,\_peptide\_yy\_precursor\_gene\_extracted\_fromdna\_for\_peptide\_yy,\_complete\_cds  
 d16583exon#12\_473-1001,gene\_for\_l-histidine\_decarboxylase,\_complete\_cds  
 d17532\_3624-4104,mrna\_for\_rck,\_complete\_cds  
 d28416\_5-  
 55,mrna\_for\_esterase\_d,\_5'\_utr\_(sequence\_from\_the\_5'\_cap\_to\_the\_start\_codon)/gb  
 =d28416\_/nty  
 d42044\_5131-5635,mrna\_for\_kiaa0090\_gene,\_partial\_cds\_  
 d42046\_3648-4077,mrna\_for\_kiaa0083\_gene,\_partial\_cds\_  
 d55696\_1285-1807,mrna\_for\_cysteine\_protease,\_complete\_cds  
 d63484\_2642-3188,mrna\_for\_kiaa0150\_gene,\_partial\_cds\_

d83542\_2250-2808,mrna\_for\_cadherin-15,\_complete\_cds  
 d83780\_3502-4060,mrna\_for\_kiaa0196\_gene,\_complete\_cds  
 d83784\_5115-5445,mrna\_for\_kiaa0198\_gene,\_partial\_cds\_  
 d87937\_88-  
 502,mrna\_for\_alpha(1,2)fucosyltransferase,\_5'\_utr\_partial\_sequence/gb=d87937\_/n  
 type=rna  
 hg1602-ht1602\_at\_hg1602-ht1602\_utrophin  
 hg2247-ht2332\_at\_hg2247-ht2332\_major\_intrinsic\_protein\_  
 hg2348-ht2444\_s\_at\_hg2348-ht2444\_peptide\_yy  
 hg2994-ht4850\_s\_at\_hg2994-ht4850\_elastin,\_altsplice\_2  
 hg3148-ht3324\_s\_at\_hg3148-  
 ht3324\_major\_histocompatibility\_complex,\_iii,\_rpl,\_altsplice\_1\_  
 hg3437-ht3628\_s\_at\_hg3437-ht3628\_myelin\_proteolipid\_protein,\_altsplice\_2\_  
 hg3565-ht3768\_r\_at\_hg3565-ht3768\_zinc\_finger\_protein\_  
 hg3566-ht3769\_at\_hg3566-ht3769\_zinc\_finger\_protein\_  
 hg4018-ht4288\_at\_hg4018-ht4288\_opioid-binding\_cell\_adhesion\_molecule\_  
 hg4264-ht4534\_s\_at\_hg4264-ht4534\_guanine\_nucleotide-binding\_protein\_rab5c-  
 like\_protein\_  
 hg4638-ht5050\_at\_hg4638-ht5050\_spliceosomal\_protein\_sap\_49\_  
 hg4724-ht5166\_at\_hg4724-ht5166\_atp-binding\_cassette\_protein\_  
 hg4749-ht5197\_at\_hg4749-ht5197\_calmitine\_calcium-binding\_protein,\_mitochondrial  
 hg880-ht880\_at\_hg880-ht880\_mucin\_6,\_gastric  
 j02871\_1475-1931,lung\_cytochrome\_p450\_(iv\_subfamily)\_bi\_protein,\_complete\_cds  
 j02947mrna\_839-1349,extracellular-  
 superoxide\_dismutase\_(sod3)\_mrna,\_complete\_cds\_  
 j03241\_1918-2438,transforming\_growth\_factor-beta(tgf-beta3)\_mrna,\_complete\_cds  
 l22454\_2803-2944,nuclear\_respiratory\_factor-1\_(nrf-1)\_mrna,\_complete\_cds  
 l33799\_1065-1455,procollagen\_c-  
 proteinase\_enhancer\_protein\_(pcolce)\_mrna,\_complete\_cds\_  
 l40402mrna\_593-1157,(clone\_zap2)\_mrna\_fragment  
 ml1749cds\_141-405:in\_reversesequence,\_1501-1747,thy-  
 1\_glycoprotein\_gene,\_complete\_cds\_  
 ml3929mrna\_421-974,c-myc-  
 p64\_mrna,\_initiating\_from\_promoter\_p0,\_ (hlmyc2.5)\_partial\_cds\_  
 ml6336mrna\_923-1463,t-  
 cell\_surface\_antigen\_cd2\_(t11)\_mrna,\_complete\_cds,\_clone\_pb1\_  
 m28882\_2907-3186,muc18\_glycoprotein\_mrna,\_complete\_cds\_  
 m29932cds\_637-1180,beta-3-adrenergic\_receptor\_gene\_  
 m31211mrna\_150-714,myosin\_light\_chainslow\_a\_(mlc1sa)\_mrna,\_complete\_cds\_  
 m37238mrna\_3630-4187,phospholipase\_c\_mrna,\_complete\_cds  
 m37763cds\_350-740:in\_reversesequence,\_965-989,neurotrophin-3\_(nt-  
 3)\_gene,\_complete\_cds  
 m59916\_1784-2300,acid\_sphingomyelinase\_(asm)\_mrna,\_complete\_cds  
 m64673\_1541-2084,heat\_shock\_factor(tcf5)\_mrna,\_complete\_cds\_  
 m79463\_2979-3514,pml-2\_mrna,\_complete\_cds  
 m85085\_1449-1953,cleavage\_stimulation\_factor,\_complete\_cds\_  
 m93284\_879-1407,pancreatic\_lipase\_related\_protein(plrp2)\_mrna,\_complete\_cds\_  
 m95627mrna\_1227-1587,angio-  
 associated\_migratory\_cell\_protein\_(aamp)\_mrna,\_complete\_cds  
 s39329\_948-1368,glandular\_kallikrein-  
 1\_{alternatively\_spliced}\_[human,\_prostate,\_mrna,\_1541\_nt]  
 s83309\_1291-  
 l856,\_germ\_cell\_nuclear\_factor\_[human,\_embryonal\_carcinoma\_nt2/d1,\_mrna,\_1916\_n  
 t]  
 u01038\_1649-2123,plk\_mrna,\_complete\_cds  
 u07664exon#2\_535-973,hb9\_homeobox\_gene\_



u08198mrna\_313-  
 805, complement\_c8\_gamma\_subunit\_precursor\_(c8g)\_gene, \_complete\_cds\_  
 u09937mrna\_1176-1581, \_urokinase-  
 type\_plasminogen\_activator\_receptor\_gene\_extracted\_fromurokinase-typ  
 u11877\_7-139, interleukin-  
 8\_receptor\_type\_b\_(il8rb)\_mrna, \_splice\_variant\_il8rb9, \_partial\_cds/gb=u1187  
 u14187\_824-962, receptor\_tyrosine\_kinase\_ligand\_lerk-  
 3\_(eplg3)\_mrna, \_complete\_cds.  
 all\_u15637\_1727-2315, cd40\_binding\_protein\_(cd40bp)\_mrna, \_complete\_cds  
 u18018\_1732-2290, ela\_enhancer\_binding\_protein\_(ela-f)\_mrna, \_partial\_cds  
 u18235\_61-493, atp-  
 binding\_cassette\_protein\_(abc2)\_mrna\_hfbcd04\_clone, \_partial\_cds  
 u18300\_1231-1657, damage-  
 specific\_dna\_binding\_protein\_p48\_subunit\_(ddb2)\_mrna, \_complete\_cds\_  
 u19261\_1792-2320, epstein-barr\_virus-induced\_protein\_mrna, \_complete\_cds\_  
 u32645\_3566-4112, myeloid\_elf-1\_like\_factor\_(mef)\_mrna, \_complete\_cds\_  
 u38372\_13-331, huntingtin\_associated\_protein\_(hhap1)\_mrna, \_partial\_cds  
 u40998\_760-1312, retinal\_protein\_(hrq4)\_mrna, \_complete\_cds  
 u43965\_3313-3389, ankryrin\_g119\_(ank3)\_mrna, \_complete\_cds  
 u46570\_974-1364, tetratricopeptide\_repeat\_protein\_(tpr1)\_mrna, \_complete\_cds\_  
 u49070\_411-951, peptidyl-  
 prolyl\_isomerase\_and\_essential\_mitotic\_regulator\_(pin1)\_mrna, \_complete\_cds\_  
 u50079\_1013-1569, histone\_deacetylase\_hd1\_mrna, \_complete\_cds  
 u50136mrna\_106-640, leukotriene\_c4\_synthase\_(ltc4s)\_gene, \_complete\_cds\_  
 u52100\_167-605, xmp\_mrna, \_complete\_cds  
 u56417\_1673-2063, lysophosphatidic\_acid\_acyltransferase-alpha\_mrna, \_complete\_cds  
 all\_u57450\_305-546, epc-1\_gene  
 u67674exon\_2279-2813, ileal\_sodium\_dependent\_bile\_acid\_transporter  
 u70426\_1863-2301, a28-rgs14p\_mrna, \_complete\_cds\_  
 u73377\_3059-3363, p66shc\_(shc)\_mrna, \_complete\_cds.  
 u76456\_587-1145, tissue\_inhibitor\_of\_metalloproteinasemrna, \_complete\_cds.  
 u83192\_3401-3905, post-synaptic\_density\_protein\_95\_(psd95)\_mrna, \_complete\_cds\_  
 u83410\_2256-2772, cul-2\_(cul-2)\_mrna, \_complete\_cds  
 u83598\_519-  
 790, death\_domain\_receptorsoluble\_form\_(ddr3)\_mrna, \_partial\_cds, death\_domain\_rec  
 eptorsolub  
 u85611\_385-919, dna-pk\_interaction\_protein\_(kip)\_mrna, \_complete\_cds\_  
 u86409cds\_61-  
 523, hyaluronan\_synthase(has3)\_gene, \_partial\_cds/gb=u86409\_/ntype=dna\_/annot=cds  
 u88629cds\_1508-  
 1898, rna\_polymerase\_ii\_elongation\_factor\_ell2, \_complete\_cds/gb=u88629\_/ntype=dn  
 a\_/ann  
 u89278\_1958-2402, polyhomeotichomolog\_(hph2)\_mrna, \_complete\_cds  
 u89355\_3288-3618, clone\_crt16\_creb-binding\_protein\_mrna, \_partial\_cds.  
 all\_x04828\_1116-1702, mrna\_for\_g(i)\_protein\_alpha-  
 subunit\_(adenylate\_cyclase\_inhibiting\_gtp-binding\_p  
 all\_x07315\_341-864, gene\_for\_pp15\_(placental\_protein\_15)  
 x52192cds\_2144-2426:in\_reversesequence, \_2525-2717, rna\_for\_c-fes\_  
 x52611cds\_962-1273:in\_reversesequence, \_1441-  
 1555, mrna\_for\_transcription\_factor\_ap-2\_  
 all\_x52638\_1152-1723, mrna\_for\_6-phosphofructo-2-kinase/fructose-2,6-  
 biphosphatase\_(ec\_2.7.1.105, \_ec  
 x59373mrna\_531-1071, hox4d\_mrna\_for\_a\_homeobox\_protein  
 all\_x60104\_1532-2110, mrna\_for\_zinc\_finger\_protein  
 x62025mrna\_877-1180, rod\_cg-pde\_g\_gene\_for\_3', \_5'-  
 cyclic\_nucleotide\_phosphodiesterase  
 x62153cds\_1930-2398:in\_reversesequence, \_2459-2494, mrna\_for\_p1\_protein\_(p1.h)

x63380\_1061-1613,mrna\_for\_rsrfr2\_  
 all\_x65463\_1187-1734,mrna\_for\_mhc\_i\_promoter\_binding\_protein\_  
 x68688mrna\_111-134,znf33b\_gene  
 x70991\_1597-2089,mader\_mrna  
 all\_x74295\_178-695,mrna\_for\_alpha\_7b\_integrin  
 x77588cds\_154-679,te2\_mrna\_for\_ard-1\_n-acetyltransferase\_homologue.  
 x86428cds\_626-  
 920:not\_in\_gb\_record,gene\_for\_phosphotyrosyl\_phosphatase\_activator\_(exon\_1)\_  
 x92715\_3170-3701,mrna\_for\_znf74\_protein  
 x95463cds\_793-1222,mrna\_for\_ox19\_protein\_  
 y00970cds\_756-1236:in\_reversesequence,\_1264-  
 1312,mrna\_for\_acrosin\_(ec\_3.4.21.10)  
 y08302cds\_807-1122:in\_reversesequence,\_1385-  
 1445,mrna\_for\_map\_kinase\_phosphatase\_4  
 y08836mrna\_37-181,mrna\_for\_hrx-like\_protein/gb=y08836\_/ntype=rna\_  
 y09022cds\_805-1291:in\_reversesequence,\_1328-1406,mrna\_for\_not56-like\_protein  
 y11416mrna\_1639-2209,mrna\_for\_p73  
 all\_z14978\_1422-1673,mrna\_for\_actin-related\_protein  
 z33905mrna\_1190-1598,gene\_for\_43kd\_acetylcholine\_receptor-  
 associated\_protein\_(rapsyn)

Metagene 99

ac002450cds\_13-535,bac\_clone\_gs244b22\_from\_7q21-  
 q22,\_complete\_sequence/gb=ac002450\_/ntype=dna\_/annot  
 af006041\_300-762,fas-  
 binding\_protein\_(daxx)\_mrna,\_partial\_cds/gb=af006041\_/ntype=rna  
 d80006\_4068-4596,mrna\_for\_kiaa0184\_gene,\_partial\_cds\_  
 d83779\_4499-4967,mrna\_for\_kiaa0195\_gene,\_complete\_cds  
 hg4310-ht4580\_at\_hg4310-ht4580\_cellular\_retinol\_binding\_protein\_ii\_  
 j04501\_3032-3482,muscle\_glycogen\_synthase\_mrna,\_complete\_cds\_  
 j04513mrna\_6156-  
 6714,basic\_fibroblast\_growth\_factor\_(bfgf)\_22.5\_kd,\_21\_kd\_andkd\_protein\_mrna,\_c  
 omple  
 m16276mrna\_1281-1569,mhc\_ii\_hla-dr2-dw12\_mrna\_dqw1-beta,\_complete\_cds  
 m74099\_4835-5327,displacement\_protein\_(ccat)\_mrna\_  
 m97388\_786-1332,tata\_binding\_protein-  
 associated\_phosphoprotein\_(dr1)\_mrna,\_complete\_cds  
 s77575\_11-  
 59,\_erv9\_reverse\_transcriptase\_homolog\_{clone\_rt11}\_[human,\_multiple\_sclerosis,  
 \_brain\_plaq  
 u75679\_1214-1622,histone\_stem-loop\_binding\_protein\_(slbp)\_mrna,\_complete\_cds\_  
 u91616\_1484-1988,i\_kappa\_b\_epsilon\_(ikbe)\_mrna,\_complete\_cds\_  
 all\_x54925\_1537-1904,mrna\_for\_type\_i\_interstitial\_collagenase  
 all\_x73882\_2585-3120,e-map-115\_mrna

Metagene 14

d16532exon\_123-  
 561,gene\_for\_very\_low\_density\_lipoprotein\_receptor,\_5'\_flanking\_and\_  
 d49354\_769-1293,mrna\_for\_enhancer\_protein\_in\_hsp70\_gene,\_partial\_cds\_  
 d79984\_5275-5836,mrna\_for\_kiaa0162\_gene,\_complete\_cds  
 d79999\_4526-4922,mrna\_for\_kiaa0177\_gene,\_partial\_cds\_

d82346\_944-1316,mrna\_for\_hnspec,\_complete\_cds\_  
 d83597\_2108-2612,mrna\_for\_rp105,\_complete\_cds\_  
 d84361\_1601-2135,mrna\_for\_p52\_and\_p64\_isoforms\_of\_n-shc,\_complete\_cds\_  
 d87435\_5153-5591,mrna\_for\_kiaa0248\_gene,\_partial\_cds\_  
 d87454\_4950-5490,mrna\_for\_kiaa0265\_gene,\_partial\_cds\_  
 d87455\_4996-5542,mrna\_for\_kiaa0266\_gene,\_complete\_cds\_  
 d87957cds\_549-825:in\_reversesequence,\_1148-  
 1256,male\_foreskin\_fibroblast\_dna\_for\_protein\_involved\_in  
 hg1699-ht1704\_s\_at\_hg1699-ht1704\_epimorphin  
 hg1751-ht1768\_at\_hg1751-ht1768\_chorionic\_somatotropin\_hormone\_cs-5  
 hg2228-ht2305\_at\_hg2228-ht2305\_crystallin,\_beta\_b  
 hg2936-ht3080\_at\_hg2936-ht3080\_immunoglobulin\_heavy\_chain,\_enhancer\_element  
 hg3132-ht3308\_at\_hg3132-ht3308\_cea\_family,\_bi-like\_domain  
 hg3227-ht3404\_at\_hg3227-ht3404\_guanine\_nucleotide-binding\_protein\_hsr1\_  
 hg3286-ht3463\_at\_hg3286-ht3463\_crystallin,\_alpha\_a\_  
 hg721-ht4828\_s\_at\_hg721-  
 ht4828\_placental\_protein\_14,\_endometrial\_alphaglobulin,\_altsplice\_3\_  
 hg907-ht907\_at\_hg907-ht907\_mg44  
 hg921-ht3995\_at\_hg921-ht3995\_serine/threonine\_kinase,\_receptor\_2-2,\_altsplice\_3  
 all\_j00301\_342-715,parathyroid\_(pth)\_gene,\_3'\_end  
 j03910mrna\_31-319,(clone\_14vs)\_metallothionein-ig\_(mt1g)\_gene,\_complete\_cds\_  
 j04809mrna\_1742-2216,cytosolic\_adenylate\_kinase\_(ak1)\_gene,\_complete\_cds\_  
 l05624\_910-1418,map\_kinase\_kinase\_mrna,\_complete\_cds\_  
 l10386\_2036-2498,transglutaminase\_e3\_(tgase3)\_mrna,\_complete\_cds\_  
 l11238\_2922-3445,platelet\_membrane\_glycoprotein\_v\_mrna,\_complete\_cds\_  
 l18920exon#4\_970-1461,mage-2\_gene\_exons\_1-4,\_complete\_cds\_  
 l19267\_2335-2755,59\_protein\_mrna,\_3'\_end  
 l22005\_797-1349,ubiquitin\_conjugating\_enzyme\_mrna,\_partial\_cds\_  
 l39874exon#5\_778-1198,deoxycytidylate\_deaminase\_gene,\_complete\_cds\_  
 m17754\_1298-1838,bn51\_mrna,\_complete\_cds\_  
 m19684cds\_912-1212:in\_reversesequence,\_3443-3539,alpha-1-antitrypsin-  
 related\_protein\_gene\_  
 m19720mrna#2\_2659-3217,\_l-myc\_gene\_(l-myc\_protein)\_extracted\_froml-  
 myc\_protein\_gene,\_complete\_cds,\_l  
 m19722\_1843-2245,fgr\_proto-oncogene\_encoded\_p55-c-fgr\_protein,\_complete\_cds\_  
 m21142cds#1\_889-1109:in\_reversesequence,\_1884-2122,\_guanine\_nucleotide-  
 binding\_protein\_g-s-alpha-3\_g  
 m24594mrna\_1077-1593,interferon-inducible\_56\_kd\_protein\_mrna,\_complete\_cds\_  
 m25393\_1686-2253,protein\_tyrosine\_phosphatase\_(ptpase)\_mrna,\_complete\_cds\_  
 m30607mrna\_2131-2301:in\_reversesequence,\_2607,zinc\_finger\_protein\_y-  
 linked\_(zfy)\_mrna,\_complete\_cds\_  
 m36542mrna\_1437-1832,lymphoid-specific\_transcription\_factor\_mrna,\_complete\_cds\_  
 m37457cds\_2823-2990,na+,k+\_#name?\_catalytic\_subunit\_alpha-  
 iii\_isoform\_gene,na+,k+\_#name?\_catalytic\_s  
 m58597\_2260-2806,elam-1\_ligand\_fucosyltransferase\_(elft)\_mrna,\_complete\_cds\_  
 m63391mrna\_1637-2189,desmin\_gene,\_complete\_cds\_  
 m64752\_2904-3150,glutamate\_receptor\_subunit\_(gluh1)\_mrna,\_complete\_cds\_  
 m67439cds\_941-1355,d5\_dopamine\_receptor\_(drd5)\_gene,\_complete\_cds\_  
 m76665mrna\_792-1332,11-beta-hydroxysteroid\_dehydrogenase\_(hsd11)\_gene  
 m77836\_1239-1749,pyrroline\_5-carboxylate\_reductase\_mrna,\_complete\_cds\_  
 m81780cds#4\_49-265:in\_fullsequence,\_3676-  
 3940,\_smpd1\_gene\_(acid\_sphingomyelinase)\_extracted\_fromacid  
 m83667mrna\_713-1143,nf-il6-beta\_protein\_mrna,\_complete\_cds\_  
 m88579\_1225-1615,zinc\_finger\_protein\_(sre-zbp)\_mrna,\_3'\_end  
 m89796mrna\_3128-3671,high\_affinity\_ige\_receptor\_beta\_chain\_gene,\_complete\_cds\_  
 m94065\_1051-1417,dihydroorotate\_dehydrogenase\_mrna,\_3'\_end\_

m94856\_163-619,fatty\_acid\_binding\_protein\_homologue\_(pa-  
 fabp)\_mrna,\_complete\_cds\_  
 m97796\_88-595,helix-loop-helix\_protein\_(id-2)\_mrna,\_complete\_cds\_  
 m97936\_2354-2564,transcription\_factor\_isgf-3\_mrna\_sequence\_  
 s45630\_108-612,\_alpha\_b-  
 crystallin=rosenthal\_fiber\_component\_[human,\_glioma\_cell\_line,\_mrna,\_691\_nt]  
 s62696\_39-  
 119,\_ebv/c3d\_receptor\_{alternatively\_spliced,\_exons\_8a,9,10}\_[human,\_jurkat\_t\_c  
 ells,\_mrna\_  
 s79639\_2588-  
 3068,\_ext1=putative\_tumour\_suppressor/hereditary\_multiple\_exostoses\_candidate\_g  
 ene\_[huma  
 s82597mrna\_9-507,\_description:\_udp-galnac:polypeptide\_n-  
 acetylgalactosaminyltransferase\_gene\_extract  
 u00946\_1382-1916,clone\_a9a2brb5\_(cac)n/(gtg)n\_repeat-containing\_mrna\_  
 all\_u01317\_19502-63478:in\_u01317cds#1\_82-113,\_epsilon-  
 globin\_gene\_extracted\_frombeta\_globin\_region\_o  
 u05572\_2563-3028,lysosomal\_alpha-mannosidase\_(manb)\_mrna,\_complete\_cds\_  
 u09366\_2042-2540,zinc\_finger\_protein\_znf133  
 u10689exon#3\_939-1505,mage-5a\_antigen\_(mage5a)\_gene,\_complete\_cds  
 u16126\_2216-2684,glutamate/kainate\_receptor\_subunit\_(eaa4)\_mrna,\_complete\_cds  
 u23435\_832-1319,abl\_interactor(abi-2)\_mrna,\_complete\_cds  
 u28811\_3404-3866,cysteine-rich\_fibroblast\_growth\_factor\_receptor\_(cfr-  
 1)\_mrna,\_complete\_cds  
 u36922\_19-136:in\_reversesequence,\_205-  
 220,fork\_head\_domain\_protein\_(fkhr)\_mrna,\_3'\_end/gb=u36922\_/nt  
 u37055mrna\_1680-2195,hepatocyte\_growth\_factor-like\_protein\_gene,\_complete\_cds\_  
 u37139mrna#1\_596-998,beta\_3-  
 endonexin\_mrna,\_long\_form\_and\_short\_form,\_complete\_cds\_  
 u38175\_719-1205,hur\_rna\_binding\_protein\_(hur)\_mrna,\_complete\_cds\_  
 u42408\_1997-2393,ladinin\_(lad)\_mrna,\_complete\_cds  
 u43030\_1121-1484,cardiotrophin-1\_(ctf1)\_mrna,\_complete\_cds\_  
 all\_u44429\_1151-1626,d53\_(hd53)\_mrna,\_partial\_cds  
 u49082\_1830-2370,transporter\_protein\_(gl7)\_mrna,\_complete\_cds  
 u49188\_1187-1685,placenta\_(diff33)\_mrna,\_complete\_cds  
 u53442\_1615-2131,p38beta\_map\_kinase\_mrna,\_complete\_cds\_  
 u59111\_892-1444,dermatan\_sulfate\_proteoglycan(dspg3)\_mrna,\_complete\_cds\_  
 all\_u63842\_423-1018,neurogenic\_basic-helix-loop-  
 helix\_protein\_(neurod3)\_gene,\_complete\_cds\_  
 u70732mrna\_1335-1899,glutamate\_pyruvate\_transaminase\_(gpt)\_gene,\_complete\_cds\_  
 u72512\_4-196,b-  
 cell\_receptor\_associated\_protein\_(hbap)\_alternatively\_spliced\_mrna,\_partial\_3'\_  
 utr/gb  
 u79259\_1214-1610,clone\_23945\_mrna,\_complete\_cds  
 u82169\_1613-2135,frizzled\_homolog\_(fzd3)\_mrna,\_complete\_cds  
 u83601mrna\_58-  
 136,calpastatin\_gene,\_exonsand\_15,\_partial\_cds/gb=u83601\_/ntype=dna\_/annot=mrna  
 v01514mrna\_1440-1986,mrna\_encoding\_alpha-  
 fetoprotein\_(afp)afp\_is\_a\_major\_serum\_protein\_(mg:\_70000)\_s  
 x12517cds\_261-441:in\_reversesequence,\_480-660,mrna\_for\_u1\_small\_nuclear\_rnp-  
 specific\_c\_protein  
 x15875cds\_1176-1476:in\_reversesequence,\_1604-  
 1622,mrna\_for\_camp\_response\_element\_(cre-bp1)\_binding\_p  
 all\_x52889\_24339-24440,gene\_for\_cardiac\_beta\_myosin\_heavy\_chain  
 all\_x53390\_2839-3093,mrna\_for\_upstream\_binding\_factor\_(hubf)\_  
 x53795mrna\_1868-2003,r2\_mrna\_for\_an\_inducible\_membrane\_protein\_  
 all\_x60487\_686-948,h4/h\_gene\_for\_h4\_histone

all\_x63131\_1996-2179,myl\_(pml)\_mrna  
 all\_x64037\_1887-2200,mrna\_for\_rna\_polymerase\_ii\_associated\_protein\_rap74\_  
 x72879cds\_3-52:in\_reversesequence,\_76-208,14a2ak\_dna\_sequence\_  
 all\_x73874\_3675-4156,phkamrna\_  
 x79067utr#1\_1631-2165,erf-1\_mrna\_3'\_end  
 all\_x82434\_589-1112,mrna\_for\_emerin  
 all\_x86401\_1686-2217,mrna\_for\_l-arginine:glycine\_amidinotransferase  
 x90976\_26-185,mrna\_for\_an\_acute\_myeloid\_leukaemia\_protein\_(3917bp)\_  
 x92098cds\_368-560:in\_reversesequence,\_635-  
 737,mrna\_for\_transmembrane\_protein\_rnp24  
 x92972cds\_585-885:in\_reversesequence,\_968-1148,mrna\_for\_protein\_phosphatase\_6\_  
 x93499cds\_285-591:in\_reversesequence,\_1241-1451,mrna\_for\_rab7\_protein\_  
 all\_x93920\_1520-2031,mrna\_for\_protein-tyrosine-  
 phosphatase\_(tissue\_type:\_foreskin)\_  
 all\_x95876\_1330-1415,mrna\_for\_g-protein\_coupled\_receptor\_  
 x99699cds\_603-855:in\_reversesequence,\_939-1131,mrna\_for\_xiap\_associated\_factor-  
 1  
 y08837\_275-473:not\_in\_gb\_record,mrna\_for\_rad51-  
 like\_protein/gb=y08837\_/ntype=rna  
 y10210mrna\_55-433,mrna\_for\_cd22\_protein/gb=y10210\_/ntype=rna\_  
 z23090cds\_277-589:in\_reversesequence,\_1086-  
 1098,mrna\_for\_28\_kda\_heat\_shock\_protein  
 all\_z35307\_2215-2636,mrna\_for\_endothelin-converting-enzyme\_1\_  
 z83806\_25-283,mrna\_for\_axonemal\_dynein\_heavy\_chain\_(partial,\_id\_hdhc9).

## Metagene 342

j00139cds\_68-506,dihydrofolate\_reductase\_gene  
 s76942\_5-  
 311,\_dopamine\_d4\_receptor\_{exon\_1}\_[human,\_brain\_tumor\_tissue,\_mrna\_partial\_mut  
 ant,\_386\_nt]  
 u09477\_2707-3175,clone\_53bp1\_p53-binding\_protein\_mrna,\_partial\_cds\_  
 u56102\_1973-2537,adhesion\_molecule\_dnam-1\_mrna,\_complete\_cds\_  
 all\_x04706\_1122-1295,homeobox\_gene\_(clone\_hho.cl3)\_  
 x69398cds\_898-927,mrna\_for\_oa3\_antigenic\_surface\_determinant\_  
 all\_x83301\_1254-1471,sma5\_mrna.  
 x83705mrna\_67-535,mrna\_for\_c-sis\_proto-oncogene

## Metagene 122

af000234\_1038-1578,p2x\_purinoreceptor\_mrna,\_complete\_cds  
 d79989\_3469-3919,mrna\_for\_kiaa0167\_gene,\_complete\_cds  
 d87463\_2511-2997,mrna\_for\_kiaa0273\_gene,\_complete\_cds  
 hg1071-ht1071\_at\_hg1071-ht1071\_bone\_morphogenetic\_protein\_  
 hg2028-ht2082\_at\_hg2028-ht2082\_laminin,\_a\_polypeptide  
 hg3790-ht4060\_at\_hg3790-ht4060\_immunoglobulin\_heavy\_chain,\_fd\_fragment\_  
 hg884-ht884\_s\_at\_hg884-ht884\_oncogene\_e6-ap,\_papillomavirus  
 j04605mrna\_1389-1833,prolidase\_(imidodipeptidase)\_mrna,\_complete\_cds\_  
 l05425\_1712-2162,autoantigen\_mrna,\_complete\_cds\_  
 l13258\_2109-2463,renal\_na/pi-cotransporter\_mrna,\_complete\_cds\_  
 l20316\_1565-2003,glucagon\_receptor\_mrna,\_complete\_cds

l40387cds\_31-  
 433,thyroid\_receptor\_interactor\_(trip14)\_gene,\_3'\_end\_of\_cds/gb=l40387\_/ntype=d  
 na\_/anno  
 l40395mrna\_861-1395,(clone\_s20iii15)\_mrna,\_3'\_end\_of\_cds  
 m21985\_1548-2004,steroid\_receptor\_tr2\_mrna,\_complete\_cds\_  
 m24461exon#11\_528-780,pulmonary\_surfactant-associated\_protein\_sp-  
 b\_(sftp3)\_mrna,\_complete\_cds  
 m32373mrna\_2201-2753,arylsulfatase\_b\_(asb)\_mrna,\_complete\_cds  
 m33374mrna\_19-427,cell\_adhesion\_protein\_(sqm1)\_mrna,\_complete\_cds  
 m34667\_3969-4305,phospholipase\_c-gamma\_mrna,\_complete\_cds  
 m35416mrna\_864-1302,gtp-binding\_protein\_(ralb)\_mrna,\_complete\_cds  
 m62958\_2486-2942,retinal\_degradation\_slow\_(rds)\_mrna\_  
 m64497\_1307-1559,apolipoprotein\_ai\_regulatory\_protein\_(arp-  
 l)\_mrna,\_complete\_cds\_  
 m65214\_492-997,(hela)\_helix-loop-helix\_protein\_he47\_(e2a)\_mrna,\_3'\_end\_  
 m76125\_2612-3170,tyrosine\_kinase\_receptor\_(axl)\_mrna,\_complete\_cds\_  
 m77144mrna\_1332-1630,\_3-beta-  
 hydroxysteroid\_dehydrogenase\_gene\_extracted\_fromtype\_ii\_3-beta\_hydroxys  
 m91463mrna\_2634-3168,glucose\_transporter\_(glut4)\_gene,\_complete\_cds\_  
 s69189\_2575-3007,\_peroxisomal\_acyl-  
 coenzyme\_a\_oxidase\_[human,\_liver,\_mrna,\_3086\_nt]\_  
 s76965\_1718-2066,\_protein\_kinase\_inhibitor\_[human,\_neuroblastoma\_cell\_line\_sh-  
 sy-5y,\_mrna,\_2147\_nt]\_  
 s77361\_25-  
 184,\_transcript\_ch132\_[human,\_rf1,rf48\_stomach\_cancer\_cell\_lines,\_mrna,\_216\_nt]  
 /gb=s77361\_  
 u04840\_3088-3646,onconeural\_ventral\_antigen-1\_(nova-1)\_mrna,\_complete\_cds  
 u09414\_1994-2462,zinc\_finger\_protein\_znf137\_mrna,\_complete\_cds\_  
 u16282\_2336-2744,ell\_mrna,\_complete\_cds  
 u17163\_1086-1644,transcription\_factor\_etv1\_mrna,\_complete\_cds  
 u21551\_728-1076,eca39\_mrna,\_complete\_cds/gb=u21551\_/ntype=rna  
 u28749\_3491-4033,high-mobility\_group\_phosphoprotein\_isoform\_i-  
 c\_(hmgic)\_mrna,\_complete\_cds\_  
 u32519\_1294-1708,gap\_sh3\_binding\_protein\_mrna,\_complete\_cds  
 u60060\_1090-1540,fez1\_mrna,\_complete\_cds\_  
 u64520\_308-650,synaptobrevin-3\_mrna,\_complete\_cds  
 u87459\_331-703,autoimmunogenic\_cancer/testis\_antigen\_ny-eso-  
 l\_mrna,\_complete\_cds\_  
 u93553\_1729-2251,alpha1-  
 fetoprotein\_transcription\_factor\_(hftf)\_mrna,\_complete\_cds.  
 x15376mrna\_1216-1684,mrna\_for\_gaba-a\_receptor,\_gamma\_subunit\_  
 all\_x51405\_1974-2413,mrna\_for\_carboxypeptidase\_e\_(ec\_3.4.17.10)  
 all\_x51435\_8408-8982,prdii-bf1\_gene\_for\_a\_dna-binding\_protein  
 x56411mrna\_1990-  
 2470,adh4\_gene\_for\_ii\_alcohol\_dehydrogenase\_(pi\_subunit),\_exon\_1  
 x56465cds\_1607-  
 2069:in\_reversesequence,\_3400,znf6\_mrna\_for\_zinc\_finger\_transcription\_factor\_  
 x59065exon\_2834-3254,fgf\_gene,\_exon\_3  
 all\_x63097\_2195-2670,mrna\_for\_rhesus\_polypeptide\_(rhxiil)  
 all\_x64624\_2881-3429,mrna\_for\_rdc-1\_pou\_domain\_containing\_protein  
 y10659cds\_1011-1239:in\_reversesequence,\_1342-1552,il-13ra\_mrna  
 all\_z18956\_3398-3951,mrna\_for\_taurine\_transporter

Metagene 31

d26155\_4647-5214,mrna\_for\_transcriptional\_activator\_hsnf2a,\_complete\_cds\_  
 hg3412-ht3593\_s\_at\_hg3412-ht3593\_blue\_cone\_photoreceptor\_pigment\_  
 j02758exon#3\_568-980:in\_reversesequence,\_3307-3464,apolipoprotein\_a-  
 iv\_gene,\_complete\_cds\_  
 m13982mrna\_7-508,interleukin(il-4)\_mrna,\_complete\_cds\_  
 m26901cds\_808-1187:in\_reversesequence,\_218-293,renin\_gene\_  
 u03056\_1988-2468,tumor\_suppressor\_(luca-1)\_mrna,\_complete\_cds\_  
 u16120\_2267-2833,placental\_taurine\_transporter\_mrna,\_complete\_cds\_  
 x68285cds\_886-976,mrna\_for\_glycerol\_kinase\_

Metagene 475

d31889\_2835-3279,mrna\_for\_kiaa0072\_gene,\_partial\_cds\_  
 d82326\_2784-3312,mrna\_for\_na+-  
 independent\_neutral\_and\_basic\_amino\_acid\_transporter,\_complete\_cds\_  
 d82347\_1949-2459,mrna\_for\_neurod,\_complete\_cds\_  
 all\_j03756\_527-783,growth\_hormone-variant\_(gh1)\_and\_growth\_hormone-variant-  
 2\_(gh2)\_mrna,\_complete\_cd\_  
 l25270\_5352-5856,xel169\_mrna,\_complete\_cds\_  
 all\_m13934\_834-  
 1309,\_rps14\_gene\_(unknown\_protein)\_extracted\_fromribosomal\_protein\_s14\_gene,\_co  
 mplete  
 all\_m16405\_1994-2553,m4\_muscarinic\_acetylcholine\_receptor\_gene\_  
 all\_m20543\_2890-3542,skeletal\_alpha-actin\_gene,\_complete\_cds\_  
 m90359\_2039-2519,camp-dpendent\_protein\_kinase\_(akap\_79)\_mrna,\_complete\_cds\_  
 s81893\_13-  
 331,\_mesi3/15=extracellular\_matrix\_induced\_gene\_[human,\_endometrial\_adenocarcin  
 oma\_cells\_h  
 u03851\_1800-2220,capping\_protein\_alpha\_mrna,\_partial\_cds\_  
 u30998\_43-166,(nmd)\_mrna,\_3'\_utr/gb=u30998\_/ntype=rna  
 u90910\_1208-1724,clone\_23564\_mrna\_sequence\_  
 x00129cds\_332-566:in\_reversesequence,\_671-  
 851,mrna\_for\_retinol\_binding\_protein\_(rbp)  
 x99101cds\_1121-1409:in\_reversesequence,\_1439-1535,mrna\_for\_estrogen\_receptor  
 all\_y09858\_1990-2483,mrna\_for\_unknown\_protein  
 y12856\_182-668,mrna\_for\_amp-activated\_protein\_kinase\_alpha-  
 1,\_partial/gb=y12856\_/ntype=rna\_

Metagene 436

d31884\_2579-3023,mrna\_for\_kiaa0063\_gene,\_complete\_cds\_  
 d63998\_3542-4046,mrna\_for\_golgi\_alpha-mannosidaseii,\_complete\_cds\_  
 l13740\_2002-2047,tr3\_orphan\_receptor\_mrna,\_complete\_cds\_  
 l13852\_2790-3270,ubiquitin-  
 activating\_enzyme\_e1\_related\_protein\_mrna,\_complete\_cds\_  
 l13972\_1930-2224,beta-galactoside\_alpha-2,3-  
 sialyltransferase\_(sialt4a)\_mrna,\_complete\_cds\_  
 l35475cds\_642-888:in\_reversesequence,\_1441-1675,olfactory\_receptor-  
 like\_gene,\_complete\_cds\_  
 l40366mrna\_31-  
 223,thyroid\_receptor\_interactor\_(trip2)\_mrna,\_partial\_cds/gb=l40366\_/ntype=rna  
 m18391\_2780-3147,tyrosine\_kinase\_receptor\_(eph)\_mrna,\_complete\_cds\_  
 m27826mrna\_464-1025,endogenous\_retroviral\_protease\_mrna,\_complete\_cds\_

m31165mrna\_843-1353,tumor\_necrosis\_factor-inducible\_(tsg-  
 6)\_mrna\_fragment,\_adhesion\_receptor\_cd44\_pu  
 m59371mrna\_3386-3878,protein\_tyrosine\_kinase\_mrna,\_complete\_cds  
 m83308\_31-343,mitochondrial\_cytochrome-  
 c\_oxidase\_subunit\_via\_(cox6a)\_mrna,\_complete\_cds  
 s80335\_2197-2719,\_integrin\_betasubunit\_[human,\_mrna,\_2798\_nt]  
 s82024\_20-548,\_scg10=neuron-specific\_growth-  
 associated\_protein/stathmin\_homolog\_[human,\_embryo,\_mrna  
 all\_s83366\_910-  
 2840,\_region\_centromeric\_to\_t(12;17)\_brakepoint:\_orf1/unknown\_43\_amino\_acid\_tra  
 nscrip  
 u15172\_619-967,nip1\_(nip1)\_mrna,\_complete\_cds  
 u56998\_1628-  
 2048,putative\_serine/threonine\_protein\_kinase\_prk\_(prk)\_mrna,\_complete\_cds\_  
 u89336exon#30-33\_48-  
 208:in\_reversesequence,\_22261:not\_in\_gb\_record,\_unknown\_gene\_extracted\_fromhla\_  
 i  
 all\_x51602\_7115-7680,flt\_mrna\_for\_receptor-related\_tyrosine\_kinase\_  
 all\_x52005\_476-969,skeletal\_embryonic\_myosin\_light\_chain(mlc1)\_mrna\_  
 x62535mrna\_1975-2515,mrna\_for\_diacylglycerol\_kinase  
 all\_x89985\_1010-1389,mrna\_for\_bcl7b\_protein  
 x90761mrna\_1365-1683,hha2\_gene\_  
 all\_x92762\_1360-1883,mrna\_for\_tafazzins\_protein

Metagene 310

hg3319-ht3496\_s\_at\_hg3319-ht3496\_split\_geneenhancer,\_tup1-like  
 hg4480-ht4833\_at\_hg4480-ht4833\_collagen\_type\_vi,\_alpha\_2,\_n-terminal\_domain\_  
 l32163\_1998-2380,zinc\_finger\_protein\_mrna,\_3'\_end\_  
 l34219exon#7\_26-452:not\_in\_gb\_record,retinaldehyde-  
 binding\_protein\_(cralbp)\_gene,\_complete\_cds\_  
 m34181\_2356-2872,testis-specific\_camp-  
 dependent\_protein\_kinase\_catalytic\_subunit\_(c-beta\_isoform)\_mr  
 u17195\_1567-2143,a-kinase\_anchor\_protein\_(akap100)\_mrna,\_complete\_cds  
 u20647\_232-736,zinc\_finger\_protein\_(znf151)\_mrna,\_partial\_cds  
 u22815\_3771-3923,lar-interacting\_protein\_1a\_mrna,\_complete\_cds\_  
 u25265\_1758-2052,mek5\_mrna,\_complete\_cds\_  
 all\_u48405\_1076-1650,g\_protein\_coupled\_receptor\_ogr1\_gene,\_complete\_cds  
 u48730\_2629-2690,transcription\_factor\_stat5b\_(stat5b)\_mrna,\_complete\_cds.  
 u79280\_795-1359,clone\_23575\_mrna,\_partial\_cds  
 u82320\_546-1050,unknown\_protein\_mrna,\_partial\_cds/gb=u82320\_/ntype=rna\_  
 u89717\_635-1151,9-cis-retinol\_specific\_dehydrogenase\_mrna,\_complete\_cds  
 u89896\_1184-1688,casein\_kinase\_i\_gammamrna,\_complete\_cds  
 x56654mrna\_3221-3641,dsg1\_mrna\_for\_desmoglein\_type\_1\_  
 all\_x96849\_49-323,5'\_mrna\_of\_pecam-1\_molecule/gb=x96849\_/ntype=rna\_

Metagene 159

d78514cds\_73-409:in\_reversesequence,\_511-565,mrna\_for\_ubiquitin-  
 conjugating\_enzyme,\_complete\_cds  
 m30448mrna\_1936-2447,casein\_kinase\_ii\_beta\_subunit\_mrna,\_complete\_cds  
 all\_x74794\_2662-2906,p1-cdc21\_mrna\_



## Metagene 91

d50402\_1972-2533,mrna\_for\_nramp1,\_complete\_cds\_  
d64159\_2585-2828,mrna  
m98399\_1688-2165,antigen\_cd36\_(clone\_21)\_mrna,\_complete\_cds  
u29343\_2203-2731,hyaluronan\_receptor\_(rhamm)\_mrna,\_complete\_cds  
u52960\_186-630,rna\_polymerase\_ii\_complex\_component\_srb7\_mrna,\_complete\_cds\_  
all\_x82835\_5995-6350,mrna\_for\_voltage-activated\_sodium\_channel\_

## Metagene 81

d78335\_242-770,mrna\_for\_5'-terminal\_region\_of\_umk,\_complete\_cds\_  
hg2724-ht2820\_at\_hg2724-ht2820\_oncogene\_tls/chop,\_fusion\_activated\_  
109234\_2517-3075,vacuolar\_atpase\_(isoform\_ho68)\_mrna,\_complete\_cds\_  
all\_x02751\_1835-2430,n-ras\_mrna\_and\_flanking\_regions\_

## Metagene 394

d38537\_1174-1689,mrna\_for\_protoporphyrinogen\_oxidase,\_complete\_cds.  
d50692\_31-469,mrna\_for\_c-myc\_binding\_protein,\_complete\_cds\_  
d86062\_286-862,mrna\_for\_knp-ib,\_complete\_cds\_  
107548\_886-1390,aminoacylase-1\_(acy1)\_mrna,\_complete\_cds\_  
148546exon#1-4\_54-264:not\_in\_gb\_record,tuberin\_(tsc2)\_gene\_  
176517\_2497-2977,(clone\_cc44)\_senilin(ps1;s182)\_mrna,\_complete\_cds  
u79252\_1026-1530,clone\_23679\_mrna,\_complete\_cds  
u80040\_2167-  
2647,nuclear\_aconitase\_mrna,\_encoding\_mitochondrial\_protein,\_complete\_cds  
x12492cds\_1087-1474:in\_reversesequence,\_1544-1718,mrna\_for\_caat-  
box\_binding\_transcription\_factor\_ctf  
x57398mrna\_3503-4007,mrna\_for\_pm5\_protein  
all\_x59766\_583-1166,mrna\_for\_zn-alpha2-glycoprotein  
all\_x77794\_1678-2171,mrna\_for\_cyclin\_g1  
all\_z31695\_2159-2592,mrna\_for\_43\_kda\_inositol\_polyphosphate\_5-phosphatase

## Metagene 231

k02215mrna#2\_1510-2026,angiotensinogen\_mrna,\_complete\_cds  
138969cds\_2517-2835:in\_reversesequence,\_2946-  
2964,thrombospondin(thbs3)\_gene,\_complete\_cds  
all\_u33838\_62-95,nf-kappa-  
b\_p65delta3\_mrna,\_spliced\_transcript\_lacking\_exonsand\_7,\_partial\_cds/gb=u3  
u79241\_849-1347,clone\_23759\_mrna,\_partial\_cds

## Metagene 468

107594\_3847-4159,transforming\_growth\_factor-beta\_type\_iii\_receptor\_(tgf-  
beta)\_mrna,\_complete\_cds\_

all\_u18422\_1719-2254,dp2\_(humdp2)\_mrna,\_complete\_cds\_

Metagene 292

l20814\_2826-3306,glutamate\_receptor(hbgr2)\_mrna,\_complete\_cds\_  
u79260\_1035-1341,clone\_23745\_mrna,\_complete\_cds

Metagene 40

d49487\_32-512,mrna\_for\_obese\_gene,\_complete\_cds  
hg2148-ht2218\_f\_at\_hg2148-ht2218\_mucin\_3,\_intestinal\_  
hg2239-ht2324\_r\_at\_hg2239-ht2324\_potassium\_channel\_protein\_  
hg3725-ht3981\_s\_at\_hg3725-ht3981\_insulin-like\_leydig\_hormone\_  
hg406-ht406\_at\_hg406-ht406\_p97\_antigen,\_melanoma-specific  
hg4113-ht4383\_s\_at\_hg4113-ht4383\_olfactory\_receptor\_or17-201\_  
hg4593-ht4998\_at\_hg4593-ht4998\_sodium\_channel\_  
hg960-ht960\_at\_hg960-ht960\_guanine\_nucleotide\_exchange\_factor\_  
k03498cds#1\_2-163,\_pol\_protein\_fromendogenous\_retrovirus\_herv-  
k22\_pol\_and\_envelope\_orf\_region/gb=k03  
l10615mrna\_502-528,beta\_casein\_(csn2)\_gene,\_complete\_cds  
l38490mrna\_785-1319,adp-ribosylation\_factor\_mrna,\_complete\_cds  
all\_m13485\_188-243:in\_m13485cds\_47:not\_in\_gb\_record,metallothionein\_i-b\_gene\_  
all\_m55418\_2452-2650,amelogenin\_(amelx)\_gene,\_3'\_end\_of\_cds  
m84820\_1155-1709,retinoid\_x\_receptor\_beta\_(rxr-beta)\_mrna,\_complete\_cds  
all\_m86406\_3670-4169,skeletal\_muscle\_alphaactinin\_(actn20\_mrna,\_complete\_cds\_  
m92424\_1822-2209,p53-associated\_mrna,\_complete\_cds\_  
s57212\_1561-2027,hmef2c=myocyte\_enhancer-  
binding\_factor[human,\_skeletal\_muscles,\_mrna,\_2161\_nt]\_  
s72493\_617-  
819,\_keratin=keratinhomolog\_[human,\_tracheobronchial\_epithelial\_cells,\_mrna\_par  
tial,\_976\_  
s77893\_121-  
203,\_gpsat=glycophorin\_sat\_[human,\_peripheral\_bloods,\_mrna\_partial,\_407\_nt]  
all\_s78653\_1782-2347,\_mrg=mas-related\_[human,\_genomic,\_2416\_nt]\_  
u14577\_974-1504,microtubule-associated\_protein\_1a\_(map1a)\_mrna,\_complete\_cds\_  
u16296\_4938-5478,t-  
lymphoma\_invasion\_and\_metastasis\_inducing\_tiam1\_protein\_(tiam1)\_mrna,\_complete\_  
cd  
u23852\_1523-2066,t-  
lymphocyte\_specific\_protein\_tyrosine\_kinase\_p56lck\_(lck)\_abberant\_mrna,\_complet  
e\_  
all\_u28055\_2678-3165,hepatocyte\_growth\_factor-  
like\_protein\_homolog\_(dlf15s1a)\_mrna,\_partial\_cds  
u40002\_3192-3701,hormone-sensitive\_lipase\_testicular\_isoform\_mrna,\_complete\_cds  
u48865cds\_400-  
807:in\_reversesequence,\_3499,c/ebp\_epsilon\_(cebpe)\_gene,\_complete\_cds\_  
u52077cds\_428-  
982,mariner1\_transposase\_gene,\_complete\_consensus\_sequence/gb=u52077\_/ntype=dna  
\_/annot  
u57971\_3646-4130,calcium\_atpase\_isoform\_3x/a\_mrna,\_complete\_cds  
u59058\_8-508,beta-a3/a1\_crystallin\_(cyrba3/a1)\_mrna,\_partial\_cds\_  
u74667\_1599-2067,tat\_interactive\_protein\_(tip60)\_mrna,\_complete\_cds  
u79275\_509-989,clone\_23947\_mrna,\_partial\_cds.

u80226\_1440-1476,gamma-  
 aminobutyric\_acid\_transaminase\_mrna,\_partial\_cds/gb=u80226\_/ntype=rna\_  
 u82467\_2667-3213,tub\_homolog\_(tub)\_mrna,\_complete\_cds  
 u89336exon#54\_51-  
 369:not\_in\_gb\_record,\_unknown\_gene\_extracted\_fromhla\_iii\_region\_containing\_notc  
 h4\_g  
 u89336exon#65\_12-282:in\_reversesequence,\_54136-  
 54166:not\_in\_gb\_record,\_unknown\_gene\_extracted\_fromhl  
 u92436\_2591-  
 3077,mutated\_in\_multiple\_advanced\_cancers\_protein\_(mmacl)\_mrna,\_complete\_cds.  
 x03072cds\_765-1089:in\_reversesequence,\_3505-3649,int-1\_mammary\_oncogene\_  
 x04707cds\_815-1343:in\_reversesequence,\_1649-1673,c-erb-  
 a\_mrna\_for\_thyroid\_hormone\_receptor  
 all\_x07203\_1419-1576,mrna\_for\_cd20\_receptor\_(s7)\_  
 all\_x16866\_688-1280,mrna\_for\_cytochrome\_p-450iid\_(clone\_pmp33)\_  
 all\_x51823\_2-51,mrna\_for\_b-  
 subunit\_of\_coagulation\_factor\_xiii\_(fxiiib)\_(partial)/gb=x51823\_/ntype=rn  
 x52008cds\_899-1325:in\_reversesequence,\_1748-1814,alpha-  
 2\_strychnine\_binding\_subunit\_of\_inhibitory\_gl  
 x58431mrna#1\_1781-  
 2299,\_hox\_2.2\_gene\_extracted\_fromhox2.2\_gene\_for\_a\_homeobox\_protein\_  
 x61072mrna\_43-325,mrna\_for\_t\_cell\_receptor,\_clone\_igra17.  
 all\_x62466\_25-410,mrna\_for\_campath-1\_(cdw52)\_antigen\_  
 all\_x68314\_466-923,mrna\_for\_glutathione\_peroxidase-gi  
 x80923mrna\_31-361,nov\_gene/gb=x80923\_/ntype=dna\_/annot=mrna  
 all\_x89059\_722-1203,mrna\_for\_unknown\_protein\_expressed\_in\_macrophages  
 x90763\_1272-1632,mrna\_for\_type\_i\_keratin,\_hha5\_  
 x91103cds\_587-965:in\_reversesequence,\_1055-  
 1097,mrna\_for\_hr44\_protein/gb=x91103\_/ntype=rna  
 all\_z11737\_1537-2120,mrna\_for\_flavin-containing\_monooxygenase\_4  
 z15114cds\_1319-1589:in\_reversesequence,\_1595-  
 1805,mrna\_for\_protein\_kinase\_c\_gamma\_(partial)\_  
 all\_z48482\_2998-3401,mrna\_for\_membrane-type\_matrix\_metalloproteinase\_2\_  
 all\_z80783\_510-565,h2b/l\_gene  
 all\_z83336\_618-702,hh2b/d\_gene.  
 z83821cds#2\_1428-1668:in\_reversesequence,\_39964-  
 40156,dna\_sequence\_from\_pac\_296k21\_on\_chromosome\_x\_c

Metagene 433

af000573mrna\_1162-1666,homogentisate\_1,2-dioxygenase\_gene,\_complete\_cds  
 d45399mrna\_155-  
 629,adult\_neural\_retina\_mrna\_forcone\_cgmp\_phosphodiesterase\_gamma\_subunit,\_comp  
 lete\_c  
 hg4557-ht4962\_r\_at\_hg4557-ht4962\_small\_nuclear\_ribonucleoprotein\_u1,\_lsnrp\_  
 k03189cds\_2-404,chorionic\_gonadotropin\_beta\_subunit\_gene\_  
 all\_l43579\_398-  
 428,(clone\_110298)\_mrna/gb=l43579\_/ntype=rna,(clone\_110298)\_mrna/gb=l43579\_/nty  
 pe=rna  
 all\_m17236\_1896-2224,mhc\_ii\_hla-dq-alpha\_gene\_(dr4,w6),mhc\_ii\_hla-dq-  
 alpha\_gene\_(dr4,w6)  
 all\_m17236\_1896-2224,mhc\_ii\_hla-dq-alpha\_gene\_(dr4,w6),mhc\_ii\_hla-dq-  
 alpha\_gene\_(dr4,w6)  
 m60828\_3252-3720,keratinocyte\_growth\_factor\_mrna,\_complete\_cds\_

s76853\_1683-2244,\_cerebrin-  
 50=cerebrospinal\_fluid\_protein\_[human,\_cerebral\_brain,\_mrna,\_2295\_nt]  
 u43189\_2384-2942,ets\_transcription\_factors\_nerf-1a\_and\_nerf-1b\_(nerf-  
 1a,b)\_mrna,\_complete\_cds  
 v00571mrna\_714-  
 1218,gene\_encoding\_prepro\_form\_of\_corticotropin\_releasing\_factor\_  
 all\_x04571\_4306-4835,mrna\_for\_kidney\_epidermal\_growth\_factor\_(egf)\_precursor\_  
 x61755mrna\_1020-1562,hox3d\_gene\_for\_homeoprotein\_hox3d  
 all\_x66403\_1856-2301,mrna\_for\_acetylcholine\_receptor\_(epsilon\_subunit)\_  
 x80695cds\_938-1250:in\_reversesequence,\_1298-1496,oxalhs\_mrna\_  
 all\_z22535\_2433-2932,alk-3\_mrna  
 z50781cds\_100-205:in\_reversesequence,\_346-394,mrna\_for\_leucine\_zipper\_protein\_

## Metagene 320

d17400\_196-622,mrna\_for\_6-pyruvoyl-tetrahydropterin\_synthase,\_complete\_cds\_  
 d38498\_37-  
 604,pms5\_mrna\_(yeast\_mismatch\_repair\_gene\_pms1\_homologue),\_partial\_cds\_(c-  
 terminal\_region)  
 hg3991-ht4261\_r\_at\_hg3991-ht4261\_cpg-enriched\_dna,\_clone\_e18\_  
 j05500mrna#1\_6200-6740,beta-spectrin\_(sptb)\_mrna,\_complete\_cds\_  
 l13689mrna\_2674-3076,prot-oncogene\_(bmi-1)\_mrna,\_complete\_cds\_  
 u18291\_1439-1973,cdc16hs\_mrna,\_complete\_cds  
 u22662\_1017-1473,nuclear\_orphan\_receptor\_lxr-alpha\_mrna,\_complete\_cds  
 u35100\_330-915,complexin\_ii\_mrna,\_complete\_cds.  
 x05855cds\_12-  
 65:not\_in\_gb\_record,histone\_h3.3\_gene\_exon\_2,histone\_h3.3\_gene\_exon\_2\_  
 all\_x63597\_5486-5979,si\_mrna\_for\_sucrase-isomaltase  
 all\_x68486\_2465-2934,mrna\_for\_a2a\_adenosine\_receptor\_  
 all\_z23091\_6853-7358,gpv\_gene\_encoding\_platelet\_glycoprotein\_v\_precursor

## Metagene 246

hg2380-ht2476\_s\_at\_hg2380-ht2476\_adp-ribosylarginine\_hydrolase\_  
 m35252\_602-998,co-029  
 u59325\_2353-2815,cadherin-14\_mrna,\_complete\_cds  
 y12812cds\_486-768:in\_reversesequence,\_914-1130,rfxap\_mrna\_

## Metagene 46

af000424\_214-610,lst1\_mrna,\_clst1/c\_splice\_variant,\_complete\_cds  
 d30036\_1743-2283,mrna\_for\_phosphatidylinositol\_transfer\_protein\_(pi-  
 tpalpha),\_complete\_cds\_  
 d64109\_642-1152,mrna\_for\_tob\_family,\_complete\_cds  
 l11672\_3266-  
 3562,kruppel\_related\_zinc\_finger\_protein\_(htf10)\_mrna,\_complete\_cds,kruppel\_rel  
 ated\_zinc  
 l15326\_2760-3323,endoperoxide\_synthase\_type\_ii\_mrna,\_complete\_cds  
 m27543mrna\_2548-3070,guanine\_nucleotide-  
 binding\_protein\_(gi)\_alpha\_subunit\_mrna,\_complete\_cds

m29335\_2-180,mhc\_ii\_do-alpha\_mrna,\_partial\_cds,mhc\_ii\_do-  
 alpha\_mrna,\_partial\_cds  
 m95178\_2567-2996,non-muscle\_alpha-actinin\_mrna,\_complete\_cds\_  
 u37248\_848-1304,alpha-mannosidase\_(6a8)\_mrna,\_complete\_cds\_  
 u42387\_1180-1642,pancreatic\_polyptide\_receptor\_mrna,\_complete\_cds\_  
 u49957\_5044-5581,lim\_protein\_(lpp)\_mrna,\_partial\_cds\_  
 u66661\_2656-3082,gaba-a\_receptor\_epsilon\_subunit\_mrna,\_complete\_cds\_  
 u77665\_393-873,رناسهپروتين\_p30\_(rpp30)\_mrna,\_complete\_cds.  
 u78524\_1571-1967,gu\_binding\_protein\_mrna,\_partial\_cds  
 u90904\_1102-1342,clone\_23773\_mrna\_sequence\_  
 x01630cds\_883-1213:in\_reversesequence,\_1312-  
 1468,mrna\_for\_argininosuccinate\_synthetase  
 x04143cds\_49-265:in\_reversesequence,\_1430-1592,gene\_for\_bone\_gla\_protein\_(bpg)  
 all\_x16832\_840-1381,mrna\_for\_cathepsin\_h\_(ec\_3.4.22.16)  
 all\_x54936\_1140-1627,mrna\_for\_placenta\_growth\_factor\_(plgf)  
 all\_x70683\_2322-2752,mrna\_for\_sox-4\_protein  
 all\_x85545\_1122-1591,mrna\_for\_protein\_kinase,\_pkx1\_  
 all\_x90392\_2058-2545,mrna\_for\_dnase\_x\_gene\_  
 z32765exon\_79-159,cd36\_gene\_exon/gb=z32765\_/ntype=dna\_/annot=exon

Metagene 318

hg3111-ht3287\_at\_hg3111-ht3287\_autoantigen\_  
 m57230\_2652-3000,membrane\_glycoprotein\_gp130\_mrna,\_complete\_cds\_  
 all\_x68487\_1174-1667,mrna\_for\_a2b\_adenosine\_receptor\_  
 all\_x89430\_1828-2333,mrna\_for\_methyl\_cpg\_binding\_protein\_2\_  
 z18951cds\_311-509:in\_reversesequence,\_627-813,mrna\_for\_caveolin\_

Metagene 424

hg311-ht311\_at\_hg311-ht311\_ribosomal\_protein\_l30\_  
 m26167mrna\_385-730,platelet\_factorvariation(pf4var1)\_gene,\_complete\_cds  
 m28219\_7-  
 253,low\_density\_lipoprotein\_receptor\_(fhmutant\_causing\_familial\_hypercholesterole-  
 mia)\_mrna,  
 m57892mrna\_775-1267,carbonic\_anhydrase\_isozyme\_vi\_(ca6)\_mrna,\_complete\_cds\_  
 u09303\_2354-2870,t\_cell\_leukemia\_lerk-2\_(eplg2)\_mrna,\_complete\_cds\_  
 v00594mrna\_15-316,mrna\_for\_metallothionein\_from\_cadmium-  
 treated\_cells,mrna\_for\_metallothionein\_from\_  
 x59871mrna\_2672-2836,tcf-1\_mrna\_for\_t\_cell\_factor(splice\_form\_c)  
 z47556mrna#2\_1596-  
 1866,\_semenogelin\_ii\_gene\_extracted\_fromgenes\_for\_semenogelin\_i\_and\_semenogelin\_  
 \_ii

Metagene 324

d29810\_835-1363,mrna\_for\_unknown\_product,\_partial\_cds  
 l76224\_3424-3970,nmda\_receptor\_mrna,\_complete\_cds\_  
 all\_m24349\_838-1316,parathyroid\_hormone-  
 like\_protein\_(plp)\_gene,\_exon\_4,\_clones\_lambda-plpg(1,3,7-2)

s81944\_1173-1689, gamma-aminobutyric acid type a receptor alphasubunit [human, cerebellum, mrna\_part  
 all\_u03642\_1060-1565, g\_protein-coupled\_receptor\_apj\_gene, complete\_cds\_  
 all\_u06155\_512-  
 660, chromosome\_1q\_subtelomeric\_sequence\_d1s553/gb=u06155\_/ntype=dna\_/annot=cds,  
 chromo  
 u19557\_998-1104, squamous\_cell\_carcinoma\_antigen(scca2)\_mrna, complete\_cds\_  
 u32659\_1393-1825, il-17\_mrna, complete\_cds  
 u43519\_2976-3474, dystrophin-related\_protein(drp2)\_mrna, complete\_cds  
 u88902\_cds1\_f\_at\_u88902\_u88902, 40\_in\_u88902cds#1\_19-  
 247: 21\_in\_reversesequence, 289-499, integrase\_  
 x80915mrna\_1908-2322, gdf5\_gene  
 y10205mrna\_146-548, mrna\_for\_cd88\_protein/gb=y10205\_/ntype=rna

Metagene 204

d42040\_4334-4623, mrna\_for\_kiaa9001\_gene, complete\_cds  
 u07695\_3362-3770, tyrosine\_kinase(htk)\_mrna, complete\_cds  
 u19252\_4495-5045, putative\_transmembrane\_protein\_mrna, complete\_cds\_  
 u32680\_1088-1664, cln3\_mrna, complete\_cds\_  
 u80073\_1289-  
 1655, tip\_associating\_protein(tap)\_mrna, complete\_cds/gb=u80073\_/ntype=rna\_  
 x06745mrna\_4850-5288, mrna\_for\_dna\_polymerase\_alpha-subunit\_  
 all\_x52896\_1629-2195, rna\_for\_dermal\_fibroblast\_elastin\_  
 x53742mrna\_1930-2470, mrna\_for\_fibulin-1\_b  
 x54667cds\_110-326, mrna\_for\_cystatin\_s, mrna\_for\_cystatin\_s\_  
 x59303cds\_3274-3773, g7a\_mrna\_for\_valyl-trna\_synthetase\_  
 x64728cds\_1694-1946:in\_reversesequence, 2140-2278, chml\_mrna  
 x79440cds\_1303-1759:in\_reversesequence, 1827-1851, mrna\_for\_nadp+-  
 dependent\_malic\_enzyme\_  
 all\_x97198\_5010-5545, mrna\_for\_receptor\_phosphate\_pcp-2\_  
 all\_x99975\_3672-4243, mrna\_for\_hrtr/hgcnf\_protein\_  
 y08612cds\_1849-2197:in\_reversesequence, 2257-2269, mrna\_for\_nup88\_protein  
 y10514mrna\_6-270, mrna\_for\_cd152\_protein/gb=y10514\_/ntype=rna\_  
 all\_z80788\_607-1040, h4/l\_gene

Metagene 101

d13814\_960-1532, mrna\_for\_angiotensin\_ii\_type\_1b\_receptor, complete\_cds\_  
 m63175\_1221-1689, autocrine\_motility\_factor\_receptor\_mrna\_  
 u22029\_1690-2227, cytochrome\_p450(cyp2a7)\_mrna, complete\_cds\_  
 x13930cds\_1147-1454:in\_reversesequence, 1650-1695, cyp2a4\_mrna\_for\_p-  
 450\_iaa4\_protein  
 x63187mrna\_91-511, he4\_mrna\_for\_extracellular\_proteinase\_inhibitor\_homologue

Metagene 177

hg1148-ht1148\_at\_hg1148-ht1148\_lipopolysaccharide-binding\_protein  
 hg2309-ht2405\_at\_hg2309-ht2405\_insulin-like\_growth\_factor\_ib\_  
 u70370\_1511-  
 2012, hindlimb\_expressed\_homeobox\_protein\_backfoot\_(bft)\_mrna, complete\_cds\_

all\_x15573\_2313-2800,liver-type\_1-phosphofructokinase\_(pfkl)\_mrna,\_complete\_cds  
 x66365cds\_543-957:in\_reversesequence,\_1080-  
 1206,mrna\_plstire\_for\_serine/threonine\_protein\_kinase  
 all\_x85786\_1751-2262,mrna\_for\_dna\_binding\_regulatory\_factor  
 x86564cds\_417-446:not\_in\_gb\_record,fhr-2\_gene,\_exon\_1\_  
 all\_x95240\_1487-2056,mrna\_for\_cysteine-rich\_secretory\_protein-3

Metagene 52

hg2841-ht2969\_s\_at\_hg2841-  
 ht2969\_albumin,\_altsplice\_3,\_missplicing\_in\_alloalbumin\_venezia  
 hg3417-ht3600\_s\_at\_hg3417-ht3600\_gtp\_cyclohydrolase\_i,\_altsplice\_1\_  
 j05008exon#5\_637-1183,endothelin-1\_(edn1)\_gene,\_complete\_cds  
 u44105\_314-574,rab9\_expressed\_pseudogene\_mrna,\_complete\_cds  
 all\_x04602\_920-1086,mrna\_for\_interleukin\_bsf-2\_(b-cell\_differentiation\_factor)\_

Metagene 93

d85423\_133-439,mrna\_for\_cdc5,\_partial\_cds/gb=d85423\_/ntype=rna\_  
 u23070\_938-1460,putative\_transmembrane\_protein\_(nma)\_mrna,\_complete\_cds  
 all\_x52001\_1770-2281,endothelinmrna\_  
 x83863cds\_1151-1241,mrna\_for\_prostaglandin\_e\_receptor\_(ep3f)\_  
 z34822\_f\_at\_z34822\_z34822,\_4040\_in\_z34822\_6145-6595,(hlcc85)\_mrna\_for\_voltage-  
 dependent\_l-type\_ca\_ch

Metagene 421

hg3255-ht3432\_at\_hg3255-ht3432\_gamma-  
 aminobutyric\_acid\_(gaba)\_a\_receptor\_betasubunit  
 hg4108-ht4378\_at\_hg4108-ht4378\_olfactory\_receptor\_or17-24  
 m22490\_1282-1630,bone\_morphogenetic\_protein-2b\_(bmp-2b)\_mrna\_  
 m95925\_1366-1852,leucine\_zipper\_on\_the\_d14s46e\_locus\_mrna,\_complete\_cds  
 u27333\_2523-  
 2728,alpha\_(1,3)\_fucosyltransferase\_(fut6)\_mrna,\_major\_transcript\_i,\_complete\_c  
 ds,alpha\_  
 u35735\_2115-2442;rach1\_(rach1)\_mrna,\_complete\_cds  
 u44799\_299-860,u1-snrnp\_binding\_protein\_homolog\_mrna,\_complete\_cds\_

Metagene 371

d86096\_cds6\_at\_d86096\_d86096,not\_in\_gb\_record,\_ep3-  
 iv\_gene\_extracted\_fromdna\_for\_prostaglandin\_e\_rec  
 s62907\_1577-2136,\_gamma-  
 aminobutyric\_acida\_receptor\_alphasubunit\_[human,\_fetal\_brain,\_mrna,\_2189\_nt]  
 u33920\_2564-2644,clone\_lambdasemaphorin\_mrna,\_complete\_cds  
 u87309\_4315-4843,hvps41p\_(hvps41)\_mrna,\_complete\_cds\_  
 u96114\_2964-3390,nedd-4-like\_ubiquitin-protein\_ligase\_wwp2\_mrna,\_complete\_cds.  
 all\_x82018\_2942-3459,mrna\_for\_zid\_protein

## Metagene 306

hg3238-ht4861\_s\_at\_hg3238-ht4861\_prostaglandin\_ep3\_receptor,\_altsplice\_8\_s72904\_1884-  
 2322,\_apk1\_antigen=mab\_ki\_recognized\_[human,\_ovarian\_carcinoma\_cell\_line\_ovcar-3,\_mrna,\_  
 u45285\_2099-2579,specific\_116-kda\_vacuolar\_proton\_pump\_subunit\_(oc-116kda)\_mrna,\_complete\_cds  
 u80017mrna#1\_412-  
 673,\_btf2p44\_gene\_(basic\_transcription\_factorp44)\_extracted\_frombasic\_transcription  
 x01057mrna\_1492-1738,mrna\_for\_interleukin-2\_receptor\_  
 x95592\_558-1122,mrna\_for\_cld\_protein\_  
 x97301mrna\_13-148,mrna\_for\_ptg-11\_protein/gb=x97301\_/ntype=rna\_

## Metagene 479

ab002318\_6384-6786,mrna\_for\_kiaa0320\_gene,\_partial\_cds/gb=ab002318\_/ntype=rna  
 ac000099\_12194-12426:in\_ac000099cds\_519-  
 556:in\_all\_ac000099\_12207,\_cosmid\_g0771a003\_  
 af010193\_2552-3044,mad-related\_gene\_smad7\_(smad7)\_mrna,\_complete\_cds  
 d13634\_1915-2419,mrna\_for\_kiaa0009\_gene,\_complete\_cds  
 d17516\_1075-1615,mrna\_for\_pacap\_receptor,\_complete\_cds\_  
 d61391\_1169-1685,mrna\_for\_phosphoribosypyrophosphate\_synthetase-associated\_protein\_39,\_complete\_cds  
 d78011\_1552-2098,mrna\_for\_dihydropyrimidinase,\_complete\_cds  
 d83920\_732-1158,uterus\_mrna\_forficolin-1,\_complete\_cds  
 hg1723-ht1729\_at\_hg1723-ht1729\_macrophage\_scavenger\_receptor,\_altsplice\_2  
 hg315-ht315\_at\_hg315-ht315\_beta-1-glycoprotein\_11,\_pregnancy-specific  
 hg3242-ht3419\_s\_at\_hg3242-ht3419\_calcium\_channel,\_voltage-gated,\_alpha\_1e\_subunit,\_altsplice\_2\_  
 j03798\_1026-1536,autoantigen\_small\_nuclear\_ribonucleoprotein\_sm-d\_mrna,\_complete\_cds\_  
 l01664\_43-529,eosinophil\_charcot-  
 leyden\_crystal\_(clc)\_protein\_(lysophospholipase)\_mrna,\_complete\_cds  
 l03411\_798-1260,rd\_protein\_(rd)\_mrna,\_complete\_cds\_  
 all\_l05512\_1285-1313:not\_in\_gb\_record,histatin(his1)\_gene  
 l25441\_1410-1890,geranylgeranyltransferase\_type\_i\_beta-subunit\_mrna,\_complete\_cds  
 l26081\_1959-2487,semaphorin-iii\_(hsema-i)\_mrna,\_complete\_cds  
 l38929mrna\_5668-6190,protein\_tyrosine\_phosphatase\_delta\_mrna,\_complete\_cds  
 l40586\_1123-1255,iduronate-2-sulphatase\_(ids)\_mrna,\_complete\_cds  
 l41066\_2321-2831,nf-at3\_mrna,\_complete\_cds  
 l76670\_502-1071,nkat7\_mrna,\_complete\_cds  
 m58297\_2215-2653,zinc\_finger\_protein\_42\_(mzf-1)\_mrna,\_complete\_cds\_  
 m91036mrna#1\_37-529,\_g-gamma\_globin\_gene\_extracted\_fromg-gamma\_globin\_and\_a-gamma\_globin\_genes,\_comp  
 m95724\_2549-2939,centromere\_autoantigen\_c\_(cenpc)\_mrna,\_complete\_cds\_  
 s78203\_2096-  
 2660,\_pept\_2=h+/peptide\_cotransporter\_[human,\_kidney,\_mrna\_partial,\_2685\_nt]  
 s83365\_109-343,\_putative\_rab5-interacting\_protein\_{clone\_l1-94}\_[human,\_hela\_cells,\_mrna\_partial,\_36  
 u07223mrna\_1930-2410,beta2-chimaerin\_mrna,\_complete\_cds



u18932\_4216-4756,heparan\_sulfate-n-deacetylase/n-  
 sulfotransferase\_mrna,\_clone\_hsst3',\_3'\_utr  
 u26032\_2176-2596,translation\_initiation\_factor\_eif-2alpha\_mrna,\_3'\_utr\_  
 u32581\_2488-2884,lambda/iota-protein\_kinase\_c-  
 interacting\_protein\_mrna,\_complete\_cds\_  
 u52700\_70-328,tenascin-  
 x\_(xb)\_mrna,\_race\_clone\_n1,\_partial\_cds/gb=u52700\_/ntype=rna  
 u62438\_1545-  
 1875,nicotinic\_acetylcholine\_receptor\_beta3\_subunit\_precursor,\_mrna,\_complete\_c  
 ds  
 u67932mrna\_1128-  
 1700,camp\_phosphodiesterase\_(pde7a2)\_mrna,\_complete\_cds/gb=u67932\_/ntype=rna\_  
 u68488\_1013-1397,5-hydroxytryptamine7\_receptor\_isoform\_d\_mrna,\_complete\_cds  
 u85267\_7-  
 145,down\_syndrome\_critical\_region(dscrl)\_gene,\_alternative\_exon\_1,\_partial\_cds/  
 gb=u85267\_/n  
 all\_x16667\_1634-1917,hox2g\_mrna\_from\_the\_hox2\_locus  
 all\_x74987\_2208-2684,mrna\_for\_2'-5'\_oligoadenylate\_binding\_protein  
 all\_x76040\_2954-3309,mrna\_for\_lon\_protease-like\_protein  
 x76498exon#3\_63-369:in\_reversesequence,\_2899-  
 3043,gene\_for\_uterine\_bombesin\_receptor  
 all\_x78520\_3490-3935,\_hsapiens\_rna\_for\_clcn3  
 all\_x81636\_2127-2329,clathrin\_light\_chain\_a\_gene\_  
 all\_x81637\_5805-5938,clathrin\_light\_chain\_b\_gene\_  
 all\_x91992\_1340-1929,mrna\_for\_alkb\_protein\_homolog\_  
 x93017exon\_1293-1797,ncx2\_gene\_(exon\_2)/gb=x93017\_/ntype=dna\_/annot=exon\_  
 all\_x96753\_7313-7896,mrna\_for\_melanoma-  
 associated\_chondroitin\_sulfate\_proteoglycan\_(mcsp)  
 all\_y00064\_1931-2418,mrna\_for\_secretogranin\_i\_(chromogranin\_b)\_  
 y08991cds\_3846-4038:in\_reversesequence,\_4743-  
 4845,mrna\_for\_adaptor\_protein\_p150\_  
 z34897\_1138-1654,mrna\_for\_h1\_histamine\_receptor

## Metagene 239

ab000409\_2046-2538,mrna\_for\_mnk1,\_complete\_cds\_  
 af000430\_1941-2427,dynamin-like\_protein\_mrna,\_complete\_cds  
 af009426\_7540-8044,clone\_22\_mrna,\_alternative\_splice\_variant\_beta-  
 1,\_complete\_cds/gb=af009426\_/ntype  
 d14660\_739-1249,mrna\_for\_kiaa0104\_gene,\_complete\_cds\_  
 d14878\_1001-1499,mrna\_for\_protein\_d123,\_complete\_cds\_  
 d38251\_642-1149,mrna\_for\_rpb5\_(xap4),\_complete\_cds\_  
 d50678\_3909-4413,mrna\_for\_apolipoprotein\_e\_receptor\_2,\_complete\_cds  
 d87448\_4763-5183,mrna\_for\_kiaa0259\_gene,\_partial\_cds\_  
 hg1102-ht1102\_at\_hg1102-ht1102\_ras-related\_c3\_botulinum\_toxin\_substrate  
 hg3400-ht3579\_at\_hg3400-ht3579\_nestin  
 hg4120-ht4392\_s\_at\_hg4120-ht4392\_protein\_kinase\_pitslre,\_alpha,\_altsplice\_1-feb  
 hg944-ht944\_s\_at\_hg944-ht944\_dopamine\_receptor\_d4  
 j03626mrna#1\_1151-  
 1653,\_umps\_gene\_extracted\_fromump\_synthase\_mrna,\_complete\_cds\_  
 l02547\_1290-1752,(clone\_pz50-  
 19)\_cleavage\_stimulation\_factor\_50kda\_subunit,\_complete\_cds  
 l77864\_2060-2618,stat-like\_protein\_(fe65)\_mrna,\_complete\_cds\_  
 m29580mrna\_1813-2326,zinc-finger\_protein(zfp7)\_mrna,\_complete\_cds\_

m81181\_2360-2731,sodium/potassium\_atpase\_beta-  
 2\_subunit\_(atpb2)\_mrna,\_complete\_cds\_  
 s81221\_2246-  
 2546,\_lanosterol\_synthase\_[human,\_fetal\_liver,\_mrna\_partial,\_2637\_nt]\_  
 u07349\_2331-  
 2805,b\_lymphocyte\_serine/threonine\_protein\_kinase\_mrna,\_complete\_cds\_  
 u36221\_1562-1814,pancreatic\_zymogen\_granule\_membrane\_protein\_gp-  
 2\_mrna,\_complete\_cds\_  
 u36787\_491-995,putative\_holocytochrome\_c-type\_synthetase\_mrna,\_complete\_cds\_  
 u38864\_1766-2186,zinc-finger\_protein\_c2h2-150\_mrna,\_complete\_cds\_  
 u40271\_3598-3999,transmembrane\_receptor\_precursor\_(ptk7)\_mrna,\_complete\_cds\_  
 u41804\_882-  
 1254,putative\_tl/st2\_receptor\_binding\_protein\_precursor\_mrna,\_complete\_cds\_  
 u51903\_5202-5712,rasgap-related\_protein\_(iqgap2)\_mrna,\_complete\_cds\_  
 u52969\_19-505,pep19\_(pcp4)\_mrna,\_complete\_cds\_  
 u71207\_1846-2224,eyes\_absent\_homolog\_(eab1)\_mrna,\_complete\_cds.  
 u79256\_655-1033,clone\_23719\_mrna\_sequence  
 all\_v00594\_15-75,mrna\_for\_metallothionein\_from\_cadmium-  
 treated\_cells,mrna\_for\_metallothionein\_from\_c  
 all\_x04434\_4484-4971,mrna\_for\_insulin-like\_growth\_factor\_i\_receptor  
 x07438exon#2\_11-  
 166,dna\_for\_cellular\_retinol\_binding\_protein\_(crbp)\_exonsand/gb=x07438\_/ntype=d  
 na\_/a  
 x58199mrna\_2491-2573,mrna\_for\_beta\_adducin\_  
 all\_x72304\_1456-1688,mrna\_for\_corticotrophin\_releasing\_factor\_receptor\_  
 x87344mrna#26\_769-945,dma,\_dmb,\_hla-  
 z1,\_ipp2,\_lmp2,\_tap1,\_lmp7,\_tap2,\_dob,\_dqb2\_and\_ring8,\_9,andgene  
 all\_z14093\_1190-1743,mrna\_for\_branched\_chain\_decarboxylase\_alpha\_subunit\_

Metagene 452

m38180mrna\_1319-1623,3-beta-hydroxysteroid\_dehydrogenase/delta-5-delta-4-  
 isomerase\_(3-beta-hsd)\_gene

Metagene 395

hg881-ht881\_at\_hg881-ht881\_mucin\_6,\_gastric  
 l00190mrna\_912-1384,antithrombin\_iii\_(ataiii)\_gene,\_exonand\_complete\_cds  
 m16973mrna\_1406-1910,complement\_protein\_c8\_beta\_subunit\_mrna,\_complete\_cds\_  
 all\_m21642\_180-  
 301,(dysfunctional)\_antithrombin\_iii\_(atiii)\_utah\_gene,(dysfunctional)\_antithro  
 mbin\_i  
 m26682\_721-1171,t-cell\_translocation\_gene(ttg-1)\_mrna,\_complete\_cds\_  
 m54992\_924-1494,b\_cell\_differentiation\_antigen\_mrna,\_complete\_cds\_  
 m81883mrna\_3226-3538,glutamate\_decarboxylase\_(gad67)\_mrna,\_complete\_cds\_  
 m83712\_1078-1646,nicotinic\_receptor\_alphasubunit\_mrna,\_complete\_cds.  
 s75174\_1316-1511,\_e2f-  
 4=transcription\_factor\_[human,\_naln6\_and\_hela\_cells,\_mrna,\_1539\_nt]\_  
 u16129\_2108-2684,glutamate\_receptor\_(glur4)\_mrna,\_complete\_cds.  
 u50360\_81-385,calcium,\_calmodulin-  
 dependent\_protein\_kinase\_ii\_gamma\_mrna,\_partial\_cds/gb=u50360\_/nty  
 u79248\_1157-1553,clone\_23826\_mrna\_sequence\_  
 x51698cds\_39-343:in\_reversesequence,\_387-465,spasmolytic\_polypeptide\_(sp)\_mrna

all\_x72925\_3671-4008,mrna\_for\_desmocollin\_type\_1\_  
 x90828exon#2\_233-752,mrna\_for\_transcription\_factor,\_lhx1\_  
 y11180mrna\_31-247,mrna\_for\_twist\_protein,\_partial/gb=y11180\_/ntype=rna\_

Metagene 84

d28589mrna\_281-743,mrna\_(kiaa00167),\_partial\_sequence/gb=d28589\_/ntype=rna\_  
 d79991\_5181-5613,mrna\_for\_kiaa0169\_gene,\_partial\_cds\_  
 l11573\_1101-1665,surfactant\_protein\_b\_mrna,\_complete\_cds/gb=l11573\_/ntype=rna\_  
 u79528\_1038-1577,sr31747\_binding\_proteinmrna,\_complete\_cds

Metagene 5

m20030\_68-612,small\_proline\_rich\_protein\_(sprii)\_mrna,\_clone\_930\_

Metagene 164

af009674\_2870-3308,axin\_(axin)\_mrna,\_partial\_cds  
 d13748\_812-1352,mrna\_for\_eukaryotic\_initiation\_factor\_4ai  
 d16562\_514-1042,mrna\_for\_atp\_synthase\_gamma-subunit\_(l-type),\_complete\_cds\_  
 d28473\_3882-4418,t-lymphocyte\_mrna\_for\_ileucyl-trna\_synthetase,\_complete\_cds\_  
 d29643\_1079-1469,mrna\_for\_kiaa0115\_gene,\_complete\_cds\_  
 d32050\_2761-3307,mrna\_for\_alanyl-trna\_synthetase,\_complete\_cds\_  
 d42073\_1551-2049,mrna\_for\_reticulocalbin,\_complete\_cds\_  
 d50063\_1139-1553,mrna\_for\_proteasome\_subunit\_p40/\_mov34\_protein,\_complete\_cds\_  
 d63478\_2816-3308,mrna\_for\_kiaa0144\_gene,\_complete\_cds\_  
 d80000\_5250-5754,mrna\_for\_kiaa0178\_gene,\_partial\_cds\_  
 d86970\_5998-6400,mrna\_for\_kiaa0216\_gene,\_complete\_cds\_  
 d87071\_5779-6223,mrna\_for\_kiaa0233\_gene,\_complete\_cds\_  
 d87437\_4613-5039,mrna\_for\_kiaa0250\_gene,\_complete\_cds\_  
 d89052\_428-938,mrna\_for\_proton-atpase-like\_protein,\_complete\_cds\_  
 hg1153-ht1153\_at\_hg1153-ht1153\_nucleoside\_diphosphate\_kinase\_nm23-h2s  
 hg2279-ht2375\_at\_hg2279-ht2375\_triosephosphate\_isomerase\_  
 j03191mrna\_192-684,profilin\_mrna,\_complete\_cds\_  
 j04031\_2529-3057,methylenetetrahydrofolate\_dehydrogenase-  
 \_methenyltetrahydrofolate\_cyclohydrolase-fo  
 j04988cds\_1925-2147:in\_reversesequence,\_7591-  
 7831,90\_kd\_heat\_shock\_protein\_gene,\_complete\_cds\_  
 l10678\_1128-1650,profilin\_ii\_mrna,\_complete\_cds\_  
 l11669\_1355-1715,tetracycline\_transporter-like\_protein\_mrna,\_complete\_cds\_  
 l14076\_1469-2051,pre-mrna\_splicing\_factor\_srp75\_mrna,\_complete\_cds\_  
 l16842\_1402-1792,ubiquinol\_cytochrome-  
 c\_reductase\_core\_i\_protein\_mrna,\_complete\_cds\_  
 l20010\_7717-8185,hcfl1\_gene\_related\_mrna\_sequence\_  
 l33243mrna\_13655-  
 14051,polycystic\_kidney\_diseaseprotein\_(pkd1)\_mrna,\_complete\_cds\_  
 l38696\_961-1375,autoantigen\_p542\_mrna,\_3'\_end\_of\_cds\_  
 m11433\_115-403,cellular\_retinol-binding\_protein\_mrna,\_complete\_cds\_  
 m31606mrna\_1102-1528,phosphorylase\_kinase\_(psk-c3)\_mrna,\_complete\_cds\_  
 all\_m34677\_1486-1913,nested\_gene\_protein\_gene,\_complete\_cds\_  
 m57567\_491-953,adp-ribosylation\_factor\_(harf5)\_mrna,\_complete\_cds

m61832\_1472-2002,s-adenosylhomocysteine\_hydrolase\_(ahcy)\_mrna,\_complete\_cds  
 m81601\_2039-2483,transcription\_elongation\_factor\_(sii)\_mrna,\_complete\_cds  
 m86400\_2239-2743,phospholipase\_a2\_mrna,\_complete\_cds\_  
 m88458\_585-1095,elp-1\_mrna\_sequence  
 m94362\_3717-4179,lamin\_b2\_(lamb2)\_mrna,\_partial\_cds  
 m97856\_2016-2430,histone-binding\_protein\_mrna,\_complete\_cds\_  
 s75463\_1145-  
 1565,\_p43=mitochondrial\_elongation\_factor\_homolog\_[human,\_liver,\_mrna,\_1644\_nt]  
 \_  
 all\_u02493\_2130-2485,54\_kda\_protein\_mrna,\_complete\_cds\_  
 u02619\_6437-6965,tfiic\_box\_b-binding\_subunit\_mrna,\_complete\_cds\_  
 u18321\_1065-  
 1569,ionizing\_radiation\_resistance\_conferring\_protein\_mrna,\_complete\_cds\_  
 u20285\_1283-1811,gps1\_(gps1)\_mrna,\_complete\_cds  
 u25988\_680-720,pregnancy-specific\_glycoprotein(psg13'\_)\_mrna,\_complete\_cds\_  
 u28386\_1405-  
 1933,nuclear\_localization\_sequence\_receptor\_hsrplalpha\_mrna,\_complete\_cds  
 u31556\_1445-1679,transcription\_factor\_e2f-5\_mrna,\_complete\_cds\_  
 u33053\_2381-2879,lipid-activated\_protein\_kinase\_prk1\_mrna,\_complete\_cds  
 u36764\_721-997,tgf-beta\_receptor\_interacting\_protein\_mrna,\_complete\_cds  
 u39400\_1407-1887,nof1\_mrna,\_complete\_cds\_  
 u47077\_13025-13463,dna-dependent\_protein\_kinase\_catalytic\_subunit\_(dna-  
 pkcs)\_mrna,\_complete\_cds  
 u51586\_1262-1676,siah\_binding\_protein(siahbp1)\_mrna,\_partial\_cds  
 u62136\_660-  
 1050,putative\_enterocyte\_differentiation\_promoting\_factor\_mrna,\_partial\_cds\_  
 u66711mrna\_556-1102,ly-6-related\_protein\_-9804\_gene,\_complete\_cds\_  
 u73379\_193-661,cyclin-selective\_ubiquitin\_carrier\_protein\_mrna,\_complete\_cds\_  
 u81375\_1669-  
 2119,placental\_equilibrative\_nucleoside\_transporter(hent1)\_mrna,\_complete\_cds\_  
 v00599mrna\_903-1380,mrna\_fragment\_encoding\_beta-tubulin(from\_clone\_d-beta-1)\_  
 all\_x02152\_1090-1625,mrna\_for\_lactate\_dehydrogenase-a\_(ldh-a,\_ec\_1.1.1.27)\_  
 all\_x04366\_2448-  
 2986,mrna\_for\_calcium\_activated\_neutral\_protease\_large\_subunit\_(mucanp,\_calpain  
 ,\_ec\_  
 all\_x05130\_1362-1876,mrna\_for\_prolyl\_4-  
 hydroxylase\_beta\_subunit\_(ec\_1.14.11.2)\_(procollagen-1-proline  
 all\_x14850\_1122-1555,h2a.x\_mrna\_encoding\_histone\_h2a.x\_  
 all\_x52142\_2163-2734,mrna\_for\_ctp\_synthetase\_(ec\_6.3.4.2)  
 x58079mrna\_43-565,mrna\_for\_s100\_alpha\_protein  
 x67951cds\_312-576:in\_reversesequence,\_642-888,mrna\_for\_proliferation-  
 associated\_gene\_(pag)\_  
 all\_x75208\_3276-3781,hek2\_mrna\_for\_protein\_tyrosine\_kinase\_receptor  
 all\_x97335\_3247-3704,mrna\_for\_kinase\_a\_anchor\_protein  
 y10807\_650-1227,mrna\_for\_arginine\_methyltransferase,\_splice\_variant,\_1262\_bp\_  
 z27113cds\_73-325:in\_reversesequence,\_439-  
 463,gene\_for\_rna\_polymerase\_ii\_subunit\_14.4\_kd\_  
 z48501cds\_957-  
 1429,mrna\_for\_polyadenylate\_binding\_protein\_ii/gb=z48501/\_ntype=rna  
 z48950exon#4\_794-1100,hh3.3b\_gene\_for\_histone\_h3.3\_

Metagene 136

ac000064cds#2\_102-372:in\_fullsequence,\_6375-  
 6621,\_wugsc:h\_rg083m05.2\_gene\_extracted\_frombac\_clone\_rg

ac000064cds#1\_1287-1581:in\_reversesequence,\_16950-17160,\_wugsc:h\_rg083m05.2\_gene\_extracted\_frombac\_c  
af000177\_293-851,sm-like\_protein\_casm\_(casm)\_mrna,\_complete\_cds/gb=af000177\_/ntype=rna  
af000231\_1768-2308,rab11a\_gtpase\_mrna,\_complete\_cds.  
af015950\_3501-3909,telomerase\_reverse\_transcriptase\_(htrt)\_mrna,\_complete\_cds.  
d10656\_988-1528,mrna\_for\_crk-ii,\_complete\_cds  
d63391\_341-773,mrna\_for\_platelet\_activating\_factor\_acetylhydrolase\_ib\_gamma-subunit,\_complete\_cds  
d86959\_5435-5867,mrna\_for\_kiaa0204\_gene,\_complete\_cds  
hg3104-ht3280\_at\_hg3104-ht3280\_serine\_protease\_met1  
l34820\_566-938,nad+-dependent\_succinate-semialdehyde\_dehydrogenase\_(ssadh)\_mrna,\_3'\_end  
m37400mrna\_1352-1886,cytosolic\_aspartate\_aminotransferase\_mrna,\_complete\_cds\_  
m63483\_757-1255,major\_nuclear\_matrix\_protein\_mrna  
m68891\_2398-2686,gata-binding\_protein\_(gata2)\_mrna,\_complete\_cds\_  
s72370\_3422-3962,\_pyruvate\_carboxylase\_[human,kidney,\_mrna,\_4017\_nt]  
u01160\_1056-1635,transmembranesuperfamily\_protein\_(sas)\_mrna,\_complete\_cds  
u39412\_675-1209:not\_in\_gb\_record,platelet\_alpha\_snap\_mrna,\_complete\_cds\_  
u44755\_965-1487,pse-binding\_factor\_ptf\_delta\_subunit\_mrna,\_complete\_cds\_  
u44839\_2566-3088,putative\_ubiquitin\_c-terminal\_hydrolase\_(uhx1)\_mrna,\_complete\_cds\_  
u66469\_819-1209,cell\_growth\_regulator\_cgr19\_mrna,\_complete\_cds\_  
u87972\_91-373,nad+-isocitrate\_dehydrogenase\_mrna,\_partial\_cds/gb=u87972\_/ntype=rna\_  
all\_x12433\_1247-1734,phs1-2\_mrna\_with\_orf\_homologous\_to\_membrane\_receptor\_proteins\_  
all\_x17025\_1254-1807,homolog\_of\_yeast\_ipp\_isomerase

## Metagene 262

d90070\_1329-1828,atl-derived\_pma-responsive\_(apr)\_peptide\_mrna\_  
m69181\_6995-7523,nonmuscle\_myosin\_heavy\_chain-b\_(myh10)\_mrna,\_partial\_cds  
u02680\_2435-2837,protein\_tyrosine\_kinase\_mrna,\_complete\_cds

## Metagene 391

l76627mrna\_5831-6329,metabotropic\_glutamate\_receptoralpha\_(mglur1alpha)\_mrna,\_complete\_cds\_  
m55422\_2463-2733,krueppel-related\_zinc\_finger\_protein\_(h-plk)\_mrna,\_complete\_cds\_  
all\_m61855\_1535-1714,cytochrome\_p4502c9\_(cyp2c9)\_mrna,\_clone\_25  
all\_x14968\_1221-1636,testis\_mrna\_for\_the\_rii-alpha\_subunit\_of\_camp\_dependent\_protein\_kinase  
x61079mrna\_10-211,mrna\_for\_t\_cell\_receptor,\_clone\_igra24.  
z16411cds\_2917-3110:in\_reversesequence,\_3137-3441,mrna\_encoding\_phospholipase\_c

## Metagene 276

hg1067-ht1067\_r\_at\_hg1067-ht1067\_mucin\_  
u43292\_706-1252,mds1b\_(mds1)\_mrna,\_complete\_cds

all\_x83492\_418-500,mrna\_for\_fas/apo-1\_(clone\_pcrtm11-  
fasdelta(4,7))/gb=x83492\_/ntype=rna,mrna\_for\_fa  
x95826cds\_203-773,art4\_gene/gb=x95826\_/ntype=dna\_/annot=cds  
x99894\_936-1482,mrna\_coding\_for\_insulin\_promoter\_factor\_1

Metagene 76

d50310\_731-1127,mrna\_for\_cyclin\_i,\_complete\_cds  
d87735\_127-643,mrna\_for\_ribosomal\_protein\_l14,\_complete\_cds  
hg1515-ht1515\_f\_at\_hg1515-ht1515\_transcription\_factor\_btf3b  
hg3117-ht3293\_at\_hg3117-ht3293\_mps1  
hg384-ht384\_at\_hg384-ht384\_ribosomal\_protein\_l26\_  
hg429-ht429\_at\_hg429-ht429\_b-cell\_growth\_factor\_  
hg613-ht613\_at\_hg613-ht613\_ribosomal\_protein\_s12\_  
hg688-ht688\_f\_at\_hg688-ht688\_major\_histocompatibility\_complex,\_ii,\_dr\_beta\_2\_  
j03459mrna\_1459-1855,leukotriene\_a-4\_hydrolase\_mrna,\_complete\_cds  
l08666\_953-1421,porin\_(por)\_mrna,\_complete\_cds\_and\_truncated\_cds  
l36870mrna\_3077-3533,map\_kinase\_kinase(mkk4)\_mrna,\_complete\_cds  
m13934cds#2\_41-407:in\_reversesequence,\_5551-  
5557,\_rps14\_gene\_(unknown\_protein)\_extracted\_fromribosom  
m14199\_2-381,laminin\_receptor\_(2h5\_epitope)\_mrna,\_5'\_end\_  
m17885mrna\_532-946,acidic\_ribosomal\_phosphoprotein\_p0\_mrna,\_complete\_cds\_  
m26730cds\_3-273:in\_reversesequence,\_99-204,mitochondrial\_ubiquinone-  
binding\_protein\_gene,\_5'\_flank\_w  
m75126\_3159-3537,hexokinase(hk1)\_mrna,\_complete\_cds\_  
m84711\_345-831,v-fos\_transformation\_effector\_protein\_(fte-1),\_mrna\_complete\_cds  
u12404\_111-651,csa-19\_mrna,\_complete\_cds\_  
u14970\_122-656,ribosomal\_protein\_s5\_mrna,\_complete\_cds\_  
u14972\_103-499,ribosomal\_protein\_s10\_mrna,\_complete\_cds  
u21049cds\_61-319:in\_reversesequence,\_592-760,dd96\_mrna,\_complete\_cds  
u58682\_31-313,ribosomal\_protein\_s28\_mrna,\_complete\_cds\_  
u65092\_324-774,melanocyte-specific\_gene(msg1)\_mrna,\_complete\_cds  
u70323\_3897-4401,ataxin-2\_(sca2)\_mrna,\_complete\_cds  
u70439\_956-1407,silver-stainable\_protein\_ssp29\_mrna,\_complete\_cds  
v01516cds\_713-1044:in\_reversesequence,\_1070-  
1293,messenger\_fragment\_encoding\_cytoskeletal\_keratin\_(t  
all\_x04347\_618-917,liver\_mrna\_fragment\_dna\_binding\_protein\_upi\_homologue\_(c-  
terminus)  
x12671mrna\_1450-  
1726,\_hnrrnp\_a1\_protein\_gene\_extracted\_fromgene\_for\_heterogeneous\_nuclear\_ribonu  
cleop  
x15940cds\_66-348:in\_reversesequence,\_379-385,mrna\_for\_ribosomal\_protein\_l31\_  
x16560cds\_1-163:in\_reversesequence,\_13-  
295,cox\_viic\_gene\_for\_subunit\_viic\_of\_cytochrome\_c\_oxidase\_(e  
x53777cds\_81-435,l23\_mrna\_for\_putative\_ribosomal\_protein\_  
x55733cds\_1611-1773:in\_reversesequence,\_1840-2056,initiation\_factor\_4b\_cdna  
x55954cds\_19-385:in\_reversesequence,\_427-  
433,mrna\_for\_hl23\_ribosomal\_protein\_homologue  
x62691cds\_13-343,mrna\_for\_ribosomal\_protein\_(homologuous\_to\_yeast\_s24)\_  
x73460cds\_725-1133:in\_reversesequence,\_1211,mrna\_for\_ribosomal\_protein\_l3\_  
x76013cds\_1933-2257:in\_reversesequence,\_2328-2394,qgrshs\_mrna\_for\_glutaminy1-  
trna\_synthetase\_  
x80822cds\_13-331:in\_reversesequence,\_56-578,mrna\_for\_orf  
x80909cds\_297-591:in\_reversesequence,\_694-754,alpha\_nac\_mrna  
all\_y00339\_913-1465,mrna\_for\_carbonic\_anhydrase\_ii\_(ec\_4.2.1.1)

y08915\_749-1235,mrna\_for\_alphaprotein\_

Metagene 130

ab002315\_4819-5347,mrna\_for\_kiaa0317\_gene,\_complete\_cds/gb=ab002315\_/ntype=rna  
 ab002382\_4858-5320,mrna\_for\_kiaa0384\_gene,\_complete\_cds/gb=ab002382\_/ntype=rna  
 ac002115mrna#2\_3349-  
 7559:not\_in\_gb\_record,\_cox6b\_gene\_(coxg)\_extracted\_fromdna\_from\_overlapping\_chr  
 o  
 af002020\_4090-4600,niemann-  
 pick\_c\_disease\_protein\_(npc1)\_mrna,\_complete\_cds/gb=af002020\_/ntype=rna  
 d14657\_355-775,mrna\_for\_kiaa0101\_gene,\_complete\_cds  
 d25248\_4510-5050,randomly\_sequenced\_mrna\_  
 d25304\_4431-4701,mrna\_for\_kiaa0006\_gene,\_partial\_cds\_  
 d25547\_779-864,mrna\_for\_pimt\_isozyme\_i,\_complete\_cds\_  
 d28476\_5899-6385,mrna\_for\_kiaa0045\_gene,\_complete\_cds  
 d55716\_1952-2378,mrna\_for\_plcdc47,\_complete\_cds  
 d63876\_3171-3717,mrna\_for\_kiaa0154\_gene,\_partial\_cds\_  
 d79998\_3100-3562,mrna\_for\_kiaa0176\_gene,\_partial\_cds\_  
 d83004\_644-1148,epidermoid\_carcinoma\_mrna\_for\_ubiquitin-  
 conjugating\_enzyme\_e2\_similar\_to\_drosophila\_  
 d83785\_5214-5634,mrna\_for\_kiaa0200\_gene,\_complete\_cds  
 d85181\_1502-2018,mrna\_for\_fungal\_sterol-c5-desaturase\_homolog,\_complete\_cds  
 d86550\_5888-6338,mrna\_for\_serine/threonine\_protein\_kinase,\_complete\_cds  
 d87451\_2622-3162,mrna\_for\_kiaa0262\_gene,\_complete\_cds  
 d87969\_1206-1686,mrna\_for\_cmp-sialic\_acid\_transporter,\_complete\_cds  
 hg2492-ht2588\_at\_hg2492-ht2588\_glutamate\_receptor\_subunit  
 hg4557-ht4962\_at\_hg4557-ht4962\_small\_nuclear\_ribonucleoprotein\_u1,\_1snrp\_  
 l07758\_1288-1762,iif\_ssp\_9502\_mrna,\_complete\_cds\_  
 l13738mrna\_4076-4490,activated\_p21cdc42hs\_kinase\_(ack)\_mrna,\_complete\_cds  
 all\_l19314\_3362-3789,hry\_gene,\_complete\_cds  
 l20859\_2655-3159,leukemia\_virus\_receptor(glvrl)\_mrna,\_complete\_cds  
 l21936\_1796-  
 2222,succinate\_dehydrogenase\_flavoprotein\_subunit\_(sdh)\_mrna,\_complete\_cds\_  
 l27706\_1445-1985,chaperonin\_protein\_(tcp20)\_gene\_complete\_cds  
 l34600\_1958-2426,nuclear-  
 encoded\_mitochondrial\_initiation\_factormrna,\_complete\_cds  
 all\_m22877\_1917-2434,somatic\_cytochrome\_c\_(hcs)\_gene,\_complete\_cds\_  
 m29960mrna\_1721-2141,steroid\_receptor\_(tr2-11)\_mrna,\_complete\_cds  
 m31932mrna\_1771-  
 2341,igg\_low\_affinity\_fc\_fragment\_receptor\_(fcrlia)\_mrna,\_complete\_cds\_  
 m32011mrna\_1623-2157,neutrophil\_oxidase\_factor\_(p67-phox)\_mrna,\_complete\_cds\_  
 m33336\_2441-3005,camp-dependent\_protein\_kinase\_type\_i-  
 alpha\_subunit\_(prkarla)\_mrna,\_complete\_cds\_  
 m75715\_1635-2185,tb3-1\_mrna,\_complete\_cds  
 u07559\_1832-2366,isl-1\_(islet-1)\_mrna,\_complete\_cds  
 u11872\_36-72,interleukin-  
 8\_receptor\_type\_b\_(il8rb)\_mrna,\_splice\_variant\_il8rb1,\_partial\_cds/gb=u1187  
 u15642\_975-1472,transcription\_factor\_e2f-5\_mrna,\_complete\_cds  
 u47927\_2598-3132,isopectidase\_t\_(isot)\_mrna,\_complete\_cds  
 u48296\_1629-  
 2175,protein\_tyrosine\_phosphatase\_ptpcaax1\_(hptpcaax1)\_mrna,\_complete\_cds  
 u52154\_2352-2610,g\_protein-  
 coupled\_inwardly\_rectifying\_potassium\_channel\_kir3.4\_mrna,\_complete\_cds\_

u63541mrna\_431-977,mrna\_expressed\_in\_hc/hcc\_livers\_and\_molt-  
 4\_proliferating\_cells,\_partial\_sequence  
 u77456\_2006-2414,nucleosome\_assembly\_proteinmrna,\_complete\_cds  
 u84720\_1431-1611,mrna\_export\_protein\_rae1\_(rae1)\_mrna,\_complete\_cds  
 u89336exon#34-35\_35-  
 87:not\_in\_gb\_record,\_unknown\_gene\_extracted\_fromhla\_iii\_region\_containing\_notch  
 4  
 u94832\_2732-2958,kh\_type\_splicing\_regulatory\_protein\_ksrp\_mrna,\_complete\_cds.  
 u94836\_3450-3894,erprot\_213-21\_mrna,\_complete\_cds  
 all\_x06272\_2379-  
 2854,mrna\_for\_docking\_protein\_(signal\_recognition\_particle\_receptor)\_  
 all\_x17567\_432-1018,rna\_for\_snrnp\_protein\_b  
 all\_x63741\_3695-4230,pilot\_mrna  
 x66113cds\_2199-2633:in\_reversesequence,\_2682-  
 2729,mrna\_for\_pm/scl\_100kd\_nucleolar\_protein\_  
 all\_x67155\_2735-3228,mrna\_for\_mitotic\_kinesin-like\_protein-1\_  
 all\_x79888\_965-1500,auh\_mrna\_  
 x87613cds\_1996-2236:in\_reversesequence,\_2780-  
 2912,mrna\_for\_skeletal\_muscle\_abundant\_protein\_  
 all\_x95632\_1680-1784,mrna\_for\_arg\_protein\_tyrosine\_kinase-binding\_protein\_  
 y07707\_1136-1634,mrna\_for\_itba4\_gene/gb=y07707\_/ntype=rna  
 z84721cds#1\_81-390:in\_reversesequence,\_15248-  
 15488,dna\_sequence\_from\_cosmid\_gg1\_from\_a\_contig\_from\_t  
 reverse\_z86000\_20444-20634,dna\_sequence\_from\_pac\_151b14\_on\_chromosome\_22q12-  
 qter\_contains\_somatostat

Metagene 42

ab000462\_6801-7227,mrna\_for\_sh3\_binding\_protein,\_clone\_res4-23a,\_complete\_cds  
 m65062\_1233-1527,insulin-like\_growth\_factor\_binding\_protein(igfbp-  
 5)\_mrna,\_complete\_cds\_  
 m93221mrna\_4618-5110,macrophage\_mannose\_receptor\_(mrc1)\_gene\_  
 u25801\_225-675,tax1\_binding\_protein\_mrna,\_partial\_cds  
 all\_x16699\_2053-2130,mrna\_for\_cytochrome\_p-450hp\_  
 x72177mrna\_2964-3510,c6\_gene,\_exon\_1

Metagene 427

m60459\_1277-1745,erythropoietin\_receptor\_mrna,\_complete\_cds  
 u45880\_1969-2515,x-linked\_inhibitor\_of\_apoptosis\_protein\_xiap\_mrna,\_complete\_cds  
 u89326\_1533-1965,bone\_morphogenetic\_protein\_receptor\_type\_i\_alk-  
 6\_mrna,\_complete\_cds\_  
 all\_x66610\_1372-1697,mrna\_for\_enolase  
 all\_x78678\_1384-1871,khk\_mrna\_for\_ketohexokinase,\_clone\_phkhk3a

Metagene 230

all\_d29675\_1092-  
 1149,inducible\_nitric\_oxide\_synthase\_gene,\_promoter\_and\_exon/gb=d29675\_/ntype=d  
 na\_/a



d29675exon\_2-  
 136,inducible\_nitric\_oxide\_synthase\_gene,\_promoter\_and\_exon/gb=d29675\_/ntype=dna\_/annot  
 hg2730-ht2827\_s\_at\_hg2730-  
 ht2827\_fibrinogen,\_a\_alpha\_polypeptide,\_altsplice\_2,\_e  
 l17128\_1940-2480,(clone\_h4/h16)\_gamma-glutamic\_carboxylase\_mrna,\_complete\_cds\_  
 all\_m10943\_444-1929,metallothionein-if\_gene\_(hmt-if)  
 m18731\_at\_m18731\_m18731,not\_in\_gb\_record,galactose-1-  
 phosphate\_uridylyltransferase\_(galt)\_mrna,\_comple  
 m81933\_1920-2394,cdc25a\_mrna,\_complete\_cds\_  
 s79862\_1641-  
 2226,\_26\_s\_protease\_subunit\_5b=50\_kda\_subunit\_[human,\_hela\_cells,\_mrna\_partial,  
 \_2253\_nt]  
 u20734cds\_709-1014:in\_reversesequence,\_7020-  
 7258,transcription\_factor\_junb\_(junb)\_gene,\_5'\_region\_an  
 u43328\_1158-1698,link\_protein\_mrna,\_complete\_cds\_  
 u52155\_1646-2168,atp-  
 dependent\_inwardly\_rectifying\_potassium\_channel\_kir4.1\_mrna,\_complete\_cds\_  
 u77664\_417-891,رناسه پروتئين p38 (rpp38)\_mrna,\_complete\_cds.  
 all\_x79483\_1063-1556,erk6\_mrna\_for\_extracellular\_signal\_regulated\_kinase\_  
 y07829exon#2\_13-  
 364,\_exon\_fromgene\_encoding\_ring\_finger\_protein/gb=y07829\_/ntype=dna\_/annot=exon,  
 \_ex  
 all\_y08765\_1854-2207,mrna\_for\_splicing\_factor,\_sf1-hl1\_isoform\_

Metagene 201

reverse\_ac000063\_31010-31140,cosmid\_clone\_luca19\_from\_3p21.3\_  
 hg1761-ht1778\_s\_at\_hg1761-ht1778\_tyrosine\_kinase\_fer\_  
 hg2149-ht2219\_at\_hg2149-ht2219\_mucin\_  
 l10338\_953-1360,sodium\_channel\_beta-1\_subunit\_(scn1b)\_mrna,\_complete\_cds\_  
 l20860\_2219-2684,glycoprotein\_ib\_beta\_mrna,\_complete\_cds\_  
 m11186exon#3\_20-134:not\_in\_gb\_record,prepro-oxytocin-  
 neurophysin\_i\_(oxt)\_gene,\_complete\_cds\_  
 m29273\_1749-2307,myelin-associated\_glycoprotein\_(mag)\_mrna,\_complete\_cds\_  
 m55040mrna\_1689-2187,acetylcholinesterase\_(ache)\_mrna,\_complete\_cds\_  
 m64082\_1605-2055,flavin-containing\_monooxygenase\_(fmo1)\_mrna,\_complete\_cds\_  
 m73481mrna\_1227-  
 1641,gastrin\_releasing\_peptide\_receptor\_(grpr)\_mrna,\_complete\_cds\_  
 m76446\_1521-1977,alpha-a1-adrenergic\_receptor\_mrna,\_complete\_cds\_  
 m86546\_1284-1716,pbx1a\_and\_pbx1b\_mrna,\_complete\_cds\_  
 m88282mrna\_4784-5180,tactile\_protein\_mrna,\_complete\_cds\_  
 s75578\_755-1286,\_4-  
 aminobutyrate\_aminotransferase\_[human,\_neuroblastoma\_be\_cells,\_mrna\_partial,\_13  
 52  
 u18991\_2113-2638,retinal\_pigment\_epithelium-  
 specific\_61\_kda\_protein\_(rpe65)\_mrna,\_complete\_cds\_  
 u37251\_1908-  
 2328,krab\_zinc\_finger\_protein\_(znf177)\_mrna,\_splicing\_variant,\_complete\_cds\_  
 u38268cds\_61-  
 379,cytochrome\_b\_pseudogene,\_partial\_cds/gb=u38268\_/ntype=dna\_/annot=cds  
 u40990\_2251-2797,voltage\_gated\_potassium\_channel\_(kvlqt1)\_mrna,\_complete\_cds\_  
 u70663\_1532-1928,zinc\_finger\_transcription\_factor\_hezf\_(ezf)\_mrna,\_complete\_cds\_  
 u78190mrna\_159-  
 687,gtp\_cyclohydrolase\_i\_feedback\_regulatory\_protein\_gene,\_complete\_cds\_

all\_x00237\_613-824,f\_variable\_segment\_5' to\_antithrombin\_iii\_gene\_(at\_iii)\_  
 x07495cds\_389-764:in\_reversesequence,\_1383-  
 1449,mrna\_for\_cp19\_homeobox\_from\_hox-3\_locus.  
 all\_x51408\_1626-2017,mrna\_for\_n-chimaerin  
 all\_x75308\_2091-2608,mrna\_for\_collagenase\_3  
 x80062cds\_1187-1268:in\_reversesequence,\_1430-1463,sa\_mrna\_

Metagene 190

126584\_3368-3933,(cdc25)\_mrna,\_complete\_cds  
 s75168mrna\_1515-2079,\_matk=megakaryocyte-  
 associated\_tyrosine\_kinase\_[human,\_genomic,\_2617\_ntsegments  
 u02609\_1934-2450,transducin-like\_protein\_mrna,\_complete\_cds  
 u07882\_1382-1730,delta\_opioid\_receptor\_mrna,\_complete\_cds  
 u16307\_996-1458,glioma\_pathogenesis-related\_protein\_(glipr)\_mrna,\_complete\_cds\_  
 u59831mrna\_1876-2385,transcription\_factor,\_forkhead\_related\_activator(freac-  
 4)\_gene,\_complete\_cds  
 y10313\_1352-1730:not\_in\_gb\_record,mrna\_for\_nerve\_growth\_factor-  
 inducible\_pc4\_homologue  
 all\_z83741\_654-1183,hh2a/m\_gene

Metagene 69

d85759\_2398-2701,fetuses,\_20-  
 26\_weeks\_brain\_mrna\_for\_mnb\_protein\_kinase,\_complete\_cds  
 hg2479-ht2575\_s\_at\_hg2479-ht2575\_helix-loop-helix\_protein\_sef2-1d  
 l76528exon\_146-615,presenilin(ps1;\_s182)\_gene  
 m29551\_2520-3054,calcineurin\_a2\_mrna,\_complete\_cds\_  
 m83941\_2764-3124,receptor\_tyrosine\_kinase\_(hek)\_mrna,\_complete\_cds\_  
 s77154\_1862-2362,\_tinur=ngfi-b/nur77\_beta-  
 type\_transcription\_factor\_homolog\_[human,\_t\_lymphoid\_cell  
 u17989\_3352-3796,nuclear\_autoantigen\_gs2na\_mrna,\_complete\_cds  
 u56244\_at\_u56244\_u56244,not\_in\_gb\_record,hig-1\_mrna,\_complete\_cds\_  
 u58091\_427-883,hs-cul-4b\_mrna,\_partial\_cds\_  
 u69611\_2905-2985,tnf-alpha\_converting\_enzyme\_mrna,\_complete\_cds  
 u72648cds\_1037-1354:in\_reversesequence,\_4177-4210,alpha2-c4-  
 adrenergic\_receptor\_gene,\_complete\_cds  
 u80456\_3416-3788,transcription\_factor\_sim2\_long\_form\_mrna,\_complete\_cds  
 u86755\_2390-2735,tnf-alpha\_converting\_enzyme\_mrna,\_complete\_cds  
 all\_x79204\_10002-10585,sca1\_mrna\_for\_ataxin  
 x83573\_1377-1803,arse\_mrna\_  
 x84194cds\_61-271:in\_reversesequence,\_501-  
 555,mrna\_for\_acylphosphatase,\_erythrocyte\_(ct)\_isoenzyme\_  
 x91196mrna#2\_3588-4161,mrna\_for\_e14\_and\_a-t\_proteins/gb=x91196\_/ntype=rna

Metagene 178

ab000895\_25-385,mrna\_for\_cadherin\_fib1,\_partial\_cds/gb=ab000895\_/ntype=rna  
 all\_d00408\_1838-1946,fetal\_liver\_cytochrome\_p-450\_(p-  
 450\_hfla),\_complete\_cds,fetal\_liver\_cytochrome\_  
 d26018\_2865-3381,mrna\_for\_kiaa0039\_gene,\_partial\_cds\_

d83646\_1984-2452,mrna\_for\_metalloproteinase,\_complete\_cds  
 d83767\_917-1319,clone\_n9\_rep-8\_mrna,\_complete\_cds  
 d84307\_1321-  
 1813,cdna\_for\_phosphoethanolamine\_cytidylyltransferase,\_complete\_cds\_  
 hg2714-ht2810\_at\_hg2714-ht2810\_tyrosine\_kinase\_  
 hg3893-ht4163\_at\_hg3893-ht4163\_phosphoglucomutase\_1,\_altsplice\_  
 l12701cds\_103-283:in\_reversesequence,\_325-  
 463,engrailed\_protein\_(en2)\_gene,\_5'\_end\_  
 l37882\_1340-1814,frizzled\_gene\_product\_mrna,\_complete\_cds  
 l41919mrna\_1877-2450,hic-1\_gene\_fragment\_  
 l76937mrna\_4642-  
 5098,\_unnamed\_protein\_product\_gene\_extracted\_fromwerner\_syndrome\_gene,\_complete\_cds  
 all\_m32053\_2900-3489,h19\_rna\_gene,\_complete\_cds\_(spliced\_in\_silico)  
 all\_m58569\_4044-4260,fibrinogen\_alpha-subunit\_bipartite\_transcript,\_complete\_cds\_of\_extended\_(alpha-m64710cds\_64-353:in\_reversesequence,\_1226-1353,c-type\_natriuretic\_peptide\_gene,\_complete\_cds  
 m77829\_737-1269,channel-like\_integral\_membrane\_protein\_(chip28)\_mrna,\_complete\_cds\_  
 m81830cds\_716-1040:in\_reversesequence,\_1170-1326,somatostatin\_receptor\_isoform(ssstr2)\_gene,\_complete  
 u03399\_1649-2147,t-complex\_protein\_10a\_(tcp10a)\_mrna,\_complete\_cds\_  
 u11287\_5386-5932,n-methyl-d-aspartate\_receptor\_subunit\_nr3\_(hnr3)\_mrna,\_complete\_cds\_  
 u12622\_4-  
 358,beaded\_intermediate\_filament\_protein\_cp115\_mrna,\_partial\_cds/gb=u12622\_/ntype=rna\_  
 u22314\_2753-3311,rest\_protein\_mrna,\_complete\_cds\_  
 u48436\_5739-  
 6290,fragile\_x\_mental\_retardation\_protein\_fmr2p\_(fmr2)\_mrna,\_complete\_cds  
 u50315\_2179-2551,enhancer\_of\_zeste\_homolog(ezh1)\_mrna,\_complete\_cds\_  
 all\_u58658\_522-1093,unknown\_protein\_mrna\_within\_the\_p53\_intron\_1,\_complete\_cds\_  
 u62431\_2093-  
 2633,nicotinic\_acetylcholine\_receptor\_alpha2\_subunit\_precursor,\_mrna,\_complete\_cds\_  
 u87460\_3537-4113,putative\_endothelin\_receptor\_type\_b-like\_protein\_mrna,\_complete\_cds\_  
 u89335exon#30\_375-  
 909,\_notch4\_gene\_(notch4)\_extracted\_fromhla\_iii\_region\_containing\_notch4\_(notch4)\_  
 x62429cds\_438-784:in\_reversesequence,\_877-  
 994,mrna\_for\_transcription\_factor\_pit-1\_  
 all\_x75315\_849-1348,seb4b\_mrna\_  
 x83703mrna\_1284-1854,mrna\_for\_cytokine\_inducible\_nuclear\_protein\_  
 all\_z35102\_2543-3018,mrna\_for\_ndr\_protein\_kinase\_  
 z48512exon#4\_87-303,xg\_mrna\_(clone\_pep6)/gb=z48512\_/ntype=rna  
 all\_z83742\_507-757,hh2a/c\_gene.

Metagene 162

hg3242-ht4231\_s\_at\_hg3242-ht4231\_calcium\_channel,\_voltage-gated,\_alpha\_1e\_subunit,\_altsplice\_3\_  
 hg4258-ht4528\_at\_hg4258-ht4528\_kinase\_inhibitor\_p27kip1,\_cyclin-dependent  
 hg4411-ht4681\_at\_hg4411-ht4681\_mucin,\_gastric

hg4677-ht5102\_s\_at\_hg4677-ht5102\_oncogene\_ret/ptc2, \_fusion\_activated\_  
 k01900mrna\_655-1213, lymphocyte\_interferon\_alpha\_type\_201\_mrna, \_complete\_cds  
 l32961\_1584-1679, 4-aminobutyrate\_aminotransferase\_(gabat)\_mrna, \_complete\_cds\_  
 l78267mrna\_2573-3113, par-5\_mrna, \_probable\_5'\_end  
 m10612cds\_17-275:in\_reversesequence, \_2926-  
 3822: not\_in\_gb\_record, apolipoprotein\_c-ii\_gene, \_complete\_c  
 m13686\_388-897, pulmonary\_surfactant-  
 associated\_protein\_mrna, \_complete\_cds, \_clone\_mpsap-6a  
 m16591mrna\_1446-1933, hemopoietic\_cell\_protein-  
 tyrosine\_kinase\_(hck)\_gene, \_complete\_cds, \_clone\_lambda  
 m81829cds\_915-1137:in\_reversesequence, \_1260-  
 1476, somatostatin\_receptor\_isoformgene, \_complete\_cds\_  
 s38953cds\_611-820:in\_reversesequence, \_4446-4527, \_xa\_[human, \_genomic, \_6873\_nt]  
 s79281\_25-  
 463, pancreatic\_ribonuclease\_[human, \_mrna\_recombinant\_partial, \_491\_nt]/gb=s7928  
 1\_/ntype=rn  
 u25826cds\_795-1017:in\_reversesequence, \_4190-  
 4436, transcription\_factor\_(sc1)\_gene, \_complete\_cds\_  
 u29725\_2517-2937, bmkl\_alpha\_kinase\_mrna, \_complete\_cds\_  
 u31986\_877-1381, cartilage-specific\_homeodomain\_protein\_cart-  
 1\_mrna, \_complete\_cds\_  
 u36798\_4071-4551, platelet\_cgi-pde\_mrna, \_complete\_cds\_  
 u48936\_15-139, amiloride-  
 sensitive\_epithelial\_sodium\_channel\_gamma\_subunit\_mrna, \_5'\_end, \_partial\_cds/  
 u49248\_4807-  
 5251, canalicular\_multispecific\_organic\_anion\_transporter\_(cmoat), \_gene, \_complet  
 e\_cds\_  
 u49837\_684-1218, lim\_protein\_mlp\_mrna, \_complete\_cds\_  
 u53174\_1639-2059, cell\_cycle\_checkpoint\_control\_protein\_mrna, \_complete\_cds\_  
 u56814\_495-957, dnase\_i\_homologous\_protein\_(dhp2)\_mrna, \_complete\_cds\_  
 u60062\_1060-1550, fezl-t\_mrna, \_alternatively\_spliced\_form, \_complete\_cds\_  
 u63090\_1303-1813, gal\_beta-1,3\_galnac\_alpha-  
 2,3\_sialyltransferase\_(st3gal\_ii)\_mrna, \_complete\_cds\_  
 u79295\_817-1345, clone\_23961\_mrna\_sequence  
 all\_x65857\_1542-2053, hgmp07e\_gene\_for\_olfactory\_receptor\_  
 x70070cds\_954-1194:in\_reversesequence, \_1608-1800, mrna\_for\_neurotensin\_receptor\_  
 x77307cds\_1244-1382:in\_reversesequence, \_1491-1701, mrna\_for\_5-  
 ht2b\_serotonin\_receptor  
 all\_x87160\_2768-3339, mrna\_for\_gamma\_subunit\_of\_epithelial\_amiloride-  
 sensitive\_sodium\_channel\_  
 all\_x95095\_487-1058, mrna\_for\_pdgfralpha\_protein/gb=x95095\_/ntype=rna\_  
 z26653cds\_8896-9286:in\_reversesequence, \_9383-  
 9509, mrna\_for\_laminin\_m\_chain\_(merosin)  
 all\_z37976\_6411-6916, mrna\_for\_latent\_transforming\_growth\_factor-  
 beta\_binding\_protein\_(ltbp-2)  
 all\_z38133\_5578-5993, mrna\_for\_myosin\_  
 all\_z49825\_1747-2253, mrna\_for\_hepatocyte\_nuclear\_factoralpha  
 z70276cds\_2-294, mrna\_for\_fibroblast\_growth\_factor(partial).  
 z83805\_199-463, mrna\_for\_axonemal\_dynein\_heavy\_chain\_(partial, \_id\_hdhc8)

Metagene 148

d13644\_4013-4523, mrna\_for\_kiaa0019\_gene, \_complete\_cds  
 l35545mrna\_689-  
 1223, endothelial\_cell\_protein\_c/apc\_receptor\_(epcr)\_mrna, \_complete\_cds\_

m33882\_2348-2762, p78\_protein\_mrna, \_complete\_cds  
 m60750cds\_3-  
 348, histone\_h2b.1\_(h2b)\_gene, \_complete\_cds/gb=m60750/\_ntype=dna/\_annot=cds\_  
 u78798\_1699-2203, tnfr\_receptor\_associated\_factor(traf6)\_mrna, \_complete\_cds.  
 all\_y08319\_1743-2272, mrna\_for\_kinesin-2  
 y12556\_427-877, mrna\_for\_AMP-activated\_protein\_kinase\_beta-  
 1/gb=y12556/\_ntype=rna\_

Metagene 165

af000959\_759-1269, transmembrane\_protein\_mrna, \_complete\_cds  
 d28364\_4-  
 118, mrna\_for\_annexin\_ii, \_5'\_utr\_(sequence\_from\_the\_5'\_cap\_to\_the\_start\_codon)/g  
 b=d28364/\_nt  
 hg2239-ht2324\_at\_hg2239-ht2324\_potassium\_channel\_protein\_  
 hg3075-ht3236\_s\_at\_hg3075-ht3236\_focal\_adhesion\_kinase\_  
 m28214\_255-723, gtp-binding\_protein\_(rab3b)\_mrna, \_complete\_cds\_  
 m91368\_2656-3189, na+/ca+\_exchanger\_(cnc)\_mrna, \_complete\_cds  
 u79734\_4119-4683, huntingtin\_interacting\_protein\_(hip1)\_mrna, \_complete\_cds  
 x71345mrna\_222-798, mrna\_for\_trypsinogen\_iv\_b-form  
 all\_x83535\_1791-2208, mrna\_for\_membrane-type\_matrix\_metalloproteinase\_

Metagene 120

121998\_15275-15677, intestinal\_mucin\_(muc2)\_mrna, \_complete\_cds  
 126234mrna\_298-  
 796, apolipoprotein\_b\_mrna\_editing\_enzyme, \_catalytic\_polypeptide(apobec1)\_mrna, \_  
 comple  
 m55905\_1340-  
 1820, mitochondrial\_nad(p)+\_dependent\_malic\_enzyme\_mrna, \_complete\_cds\_  
 m96956\_2590-2639, (clone\_cr-3)\_teratocarcinoma-  
 derived\_growth\_factor(tdgf3)\_mrna, \_complete\_cds\_  
 u00952\_488-998, clone\_a9a2brb7\_(cac)n/(gtg)n\_repeat-containing\_mrna\_  
 u01062mrna\_8334-8778, typeinositol\_1,4,5-  
 trisphosphate\_receptor\_(itpr3)\_mrna, \_complete\_cds\_  
 u17418\_1591-2071, parathyroid\_hormone/parathyroid\_hormone-  
 related\_peptide\_receptor\_mrna, \_complete\_cds  
 u31099\_13-469, dp\_prostanoid\_receptor\_(ptgdr)\_mrna, \_partial\_cds.  
 u33838\_2-188, nf-kappa-  
 b\_p65delta3\_mrna, \_spliced\_transcript\_lacking\_exonsand\_7, \_partial\_cds/gb=u33838  
 u40622\_999-1449, xrcc4\_mrna, \_complete\_cds\_  
 u40705\_2127-2625, telomeric\_repeat\_binding\_factor\_(trf1)\_mrna, \_complete\_cds  
 u66561\_2158-2614, kruppel-related\_zinc\_finger\_protein\_(znf184)\_mrna, \_partial\_cds  
 u90313\_212-758, glutathione-s-transferase\_homolog\_mrna, \_complete\_cds  
 u94333\_2877-3429, clq/mb1/spa\_receptor\_clqr(p)\_mrna, \_complete\_cds.  
 x89576\_1772-2255, mrna\_for\_putative\_mt4-mmp\_protein\_  
 z19002cds\_1508-1994:in\_reversesequence, \_2075-  
 2081, of\_plzf\_gene\_encoding\_kruppel-like\_zinc\_finger\_pro

Metagene 32

d85376exon\_2003-2453,dna\_for\_thyrotropin-releasing\_hormon\_receptor\_  
 hg1034-ht1034\_f\_at\_hg1034-ht1034\_atpase\_na+/k+\_transporting,\_alphapolypeptide  
 hg1471-ht3923\_s\_at\_hg1471-ht3923\_transcription\_factor\_oct-  
 1a/1b,\_altsplice\_2,\_oct-1b\_  
 hg2147-ht2217\_r\_at\_hg2147-ht2217\_mucin\_3,\_intestinal\_  
 hg3565-ht3768\_at\_hg3565-ht3768\_zinc\_finger\_protein\_  
 all\_k03431\_5910-6163:not\_in\_gb\_record,\_hpr\_gene\_(haptoglobin-  
 related\_protein)\_extracted\_fromhaptoglo  
 103840\_2419-2970,fibroblast\_growth\_factor\_receptor(fgfr4)\_mrna,\_complete\_cds  
 107590\_4754-  
 5138,protein\_phosphatase\_2a\_130\_kda\_regulatory\_subunit\_mrna,\_complete\_cds  
 111708\_761-1205,\_humanbeta\_hydroxysteroid\_dehydrogenase\_typemrna,\_complete\_cds\_  
 113197\_1853-2099,(clone\_d21s418e)\_pregnancy-associated\_plasma\_protein\_a\_(papp-  
 a)\_gene,\_5'\_utr  
 127943mrna\_291-867,cytidine\_deaminase\_(cda)\_mrna,\_complete\_cds  
 128821\_4394-4838,alpha\_mannosidase\_ii\_isozyme\_mrna,\_complete\_cds  
 140992mrna\_906-1368,(clone\_pebp2aa1)\_core-  
 binding\_factor,\_runt\_domain,\_alpha\_subunit(cbfa1)\_mrna,\_3'  
 149169mrna\_3270-3612,g0s3\_mrna,\_complete\_cds\_  
 ml14016mrna\_644-947,uroporphyrinogen\_decarboxylase\_mrna,\_complete\_cds\_  
 ml14660exon\_1123-1363:in\_reversesequence,\_1460-1646,isg-  
 54k\_gene\_(interferon\_stimulated\_gene)\_encodin  
 m23892mrna\_2101-2549,15-lipoxygenase\_mrna,\_complete\_cds  
 m27288exon\_225-555:in\_reversesequence,\_567-768,oncostatin\_m\_gene  
 m27783\_2-433,neutrophil\_elastase\_mrna,\_3'\_end  
 m28213\_94-627,gtp-binding\_protein\_(rab2)\_mrna,\_complete\_cds\_  
 m31525mrna\_517-1081,mhc\_ii\_lymphocyte\_antigen\_(hla-dna)\_gene,\_complete\_cds\_  
 m55131mrna\_5636-  
 6134,cystic\_fibrosis\_transmembrane\_conductance\_regulator\_(cftr)\_gene\_  
 m55172\_6712-  
 7102,large\_aggregating\_cartilage\_proteoglycan\_core\_protein\_mrna,\_complete\_cds  
 m63896cds\_927-1197:in\_reversesequence,\_1866-  
 2022,transcriptional\_enhancer\_factor\_(tef1)\_dna,\_complet  
 m63967exon#2\_1319-  
 1625,mitochondrial\_aldehyde\_dehydrogenase\_x\_gene,\_complete\_cds\_  
 m80478exon#3\_119-  
 635,platelet\_glycoprotein\_ix\_precursor\_(gpix)\_gene,\_complete\_cds  
 m96995\_497-1025,epidermal\_growth\_factor\_receptor-binding\_protein\_grb2\_(egfrbp-  
 grb2)\_mrna\_sequence\_  
 s50017cds\_904-1241:in\_reversesequence,\_444-505,\_2'\_,\_3'\_-cyclic\_nucleotide\_3'\_-  
 phosphodiesterase\_[hum  
 u07563\_cds1\_at\_u07563\_u07563,not\_in\_gb\_record,abl\_gene,\_exon\_1b\_and\_intron\_1b,\_  
 and\_putative\_m8604\_me  
 u11861\_511-949,g10\_homolog\_(edg-2)\_mrna,\_complete\_cds  
 u33841\_8844-9294,ataxia\_telangiectasia\_(atm)\_mrna,\_complete\_cds  
 u34605\_3365-3851,retinoic\_acid-\_and\_interferon-  
 inducible\_58k\_protein\_ri58\_mrna,\_complete\_cds\_  
 u35246\_1518-1962,vacuolar\_protein\_sorting\_homolog\_h-vps45\_mrna,\_complete\_cds\_  
 u38980\_841-972,pms2\_related\_(hpmsr6)\_mrna,\_complete\_cds  
 u43586\_1531-2101,kinase\_suppressor\_of\_ras-1\_(ksr1)\_mrna,\_partial\_cds\_  
 u43747\_993-1425,frataxin\_(frda)\_mrna,\_complete\_cds\_  
 u50839\_1969-2413:not\_in\_gb\_record,g16\_protein\_(g16)\_mrna,\_partial\_cds.  
 u52513\_1318-1642,rig-g\_mrna,\_complete\_cds  
 u65533\_3076-  
 3620,regulator\_of\_nonsense\_transcript\_stability\_(rent1)\_mrna,\_complete\_cds\_  
 u66828\_2341-2500,carnitine\_palmitoyltransferase\_i\_(cpti)\_mrna,\_complete\_cds  
 u70867\_3444-3936,prostaglandin\_transporter\_hpgt\_mrna,\_complete\_cds\_

u75362\_2155-2557, isopeptidase\_t-3\_(isot-3)\_mrna, \_complete\_cds  
u92971\_1235-1805, protease-activated\_receptor(par3)\_mrna, \_complete\_cds.  
u93049\_1841-2375, slp-76\_associated\_protein\_mrna, \_complete\_cds  
x01038mrna\_285-824, fetal\_gene\_for\_apolipoprotein\_ai\_precursor\_  
x14445exon#3\_240-702, int-2\_proto-oncogene  
all\_x14789\_1204-1793, alpha-a\_crystallin\_gene\_exon\_1,2\_and\_pseudoexon\_  
x15357cds\_2853-3135:in\_reversesequence, \_3262-  
3454, mrna\_for\_natriuretic\_peptide\_receptor\_(anp-a\_recep  
x71874cds#1\_268-739:in\_reversesequence, \_4531-4534, \_proteasome-  
like\_subunit\_mecl-1\_gene\_extracted\_fro  
x84746cds\_544-1012, histo-blood\_group\_ab0\_gene, \_exon\_1  
all\_x85137\_3131-3726, mrna\_for\_kinesin-related\_protein  
x98833mrna\_3475-3937, mrna\_for\_zinc\_finger\_protein, \_hsall  
all\_y10260\_1483-2048, eyal\_gene\_  
z30643cds\_1860-1921, mrna\_for\_chloride\_channel\_(putative)\_2139bp  
z46967cds\_1216-1714, mrna\_for\_calicin\_(partial)\_

Metagene 384

x92689cds\_1457-1853, mrna\_for\_udp-galnac:polypeptide\_n-  
acetyl galactosaminy1\_transferase/gb=x92689\_/nt

Metagene 392

d49728\_2002-2330, nak1\_mrna\_for\_dna\_binding\_protein, \_complete\_cds\_  
l10717\_6303-6332, t\_cell-specific\_tyrosine\_kinase\_mrna, \_complete\_cds\_  
l25119\_1561-2119, mu\_opiate\_receptor\_(mor1)\_mrna, \_complete\_cds  
m32304\_423-983, metalloproteinase\_inhibitor\_mrna, \_complete\_cds  
m84526\_470-890, adipsin/complement\_factor\_d\_mrna, \_complete\_cds  
u44103\_339-559, small\_gtp\_binding\_protein\_rab9\_mrna, \_complete\_cds.  
u60319\_2133-2643, hereditary\_haemochromatosis\_protein\_hla-h\_mrna, \_complete\_cds  
u63825\_269-  
737, hepatitis\_delta\_antigen\_interacting\_protein\_a\_(dipa)\_mrna, \_complete\_cds\_  
u77735\_1516-2026, pim-2\_protooncogene\_homolog\_pim-2h\_mrna, \_complete\_cds\_  
u90544\_1665-2145, sodium\_phosphate\_transporter\_(npt3)\_mrna, \_complete\_cds  
all\_x76092\_1925-2460, hrfx3\_mrna  
z22780cds\_1528-1774:in\_reversesequence, \_1780-1870, cylicin\_mrna\_

Metagene 73

ab000466\_2465-2963, \_clone\_res4-24c, \_exon\_1, \_2, \_3  
aj001487\_25-265, mrna\_for\_transformation-  
sensitive\_protein, \_3'\_utr/gb=aj001487\_/ntype=rna  
hg4755-ht5203\_s\_at\_hg4755-ht5203\_spinal\_muscular\_atrophy  
j03260mrna\_2076-2576, transducin\_alpha-subunit\_(gnaz)\_mrna, \_complete\_cds  
all\_m20530\_85-212, pancreatic\_secretory\_trypsin\_inhibitor\_(psti)\_gene\_  
m59911\_4048-4612, integrin\_alpha-3\_chain\_mrna, \_complete\_cds\_  
m62400\_1400-1928, gamma-aminobutyric\_acid\_receptor\_type\_a\_rho-1\_subunit\_(gaba-  
a\_rho-1)\_mrna, \_complete  
m74826\_1928-2396, glutamate\_decarboxylase\_(gad-2)\_mrna, \_complete\_cds

all\_u01317\_19502-63478,\_epsilon-  
 globin\_gene\_extracted\_frombeta\_globin\_region\_on\_chromosome\_11,\_epsil  
 u13220\_1586-2066,forkhead\_protein\_freac-2\_mrna,\_partial\_cds  
 u54999\_1795-2287,lgn\_protein\_mrna,\_complete\_cds  
 all\_x00734\_8016-8239,beta-tubulin\_gene\_(5-beta)\_with\_ten\_alu\_family\_members  
 x65293cds\_1670-2180,mrna\_for\_protein\_kinase\_c-epsilon  
 all\_x71348\_2835-3436,vhnf1-c\_mrna  
 all\_x76057\_1206-1765,pmil\_mrna\_for\_phosphomannose\_isomerase  
 all\_x98311\_1901-2274,mrna\_for\_carcinoembryonic\_antigen,\_cgm2\_  
 z49205mrna\_2454-2976,mrna\_for\_purinergic\_receptor

Metagene 428

hg3344-ht3521\_at\_hg3344-ht3521\_ubiquitin-conjugating\_enzyme\_ubch5  
 all\_m35999\_3904-4463,platelet\_glycoprotein\_iiia\_(gp11a)\_mrna,\_complete\_cds  
 all\_u19906\_5284-5711,arginine\_vasopressin\_receptor(avpr1)\_gene,\_complete\_cds  
 u54617\_1233-1737,pyruvate\_dehydrogenase\_kinase\_isoformmrna,\_complete\_cds  
 x94703cds\_244-628:in\_reversesequence,\_640-748,rab28\_mrna

Metagene 224

hg3859-ht4129\_at\_hg3859-ht4129\_mage-4a\_antigen\_  
 u61741\_25-137,clone(hl-  
 18),\_dynein\_heavy\_chain\_(dnahc14)\_mrna,\_partial\_cds/gb=u61741/\_ntype=rna  
 u67784\_1106-1640,orphan\_g\_protein-coupled\_receptor\_(rdc1)\_mrna,\_partial\_cds

Metagene 437

all\_m73548\_9853-10274,polyposis\_locus\_(dp2.5\_gene)\_mrna,\_complete\_cds  
 u30245exon\_3-  
 56,myelomonocytic\_specific\_protein\_(mnda)\_gene,\_5'\_flanking\_sequence\_and\_comple  
 te\_exon/  
 u36448\_1252-1792,ca2+-  
 dependent\_activator\_protein\_for\_secretion\_mrna,\_complete\_cds\_  
 u41737\_103-  
 523,pancreatic\_beta\_cell\_growth\_factor\_(ingap)\_mrna,\_complete\_cds/gb=u41737/\_nt  
 ype=rna  
 u48697\_1787-2276,mariner-like\_element-containing\_mrna,\_clone\_pchmt2  
 x89986cds\_271-387:in\_reversesequence,\_794-  
 1043,mrna\_for\_nbk\_apoptotic\_inducer\_protein\_

Metagene 216

l01087\_2189-2693,protein\_kinase\_c-theta\_(prkct)\_mrna,\_complete\_cds\_  
 m16652mrna\_324-  
 858,pancreatic\_elastase\_iiia\_mrna,\_complete\_cds,pancreatic\_elastase\_iiia\_mrna,\_co  
 mplete  
 m27691\_1901-2417,transactivator\_protein\_(creb)\_mrna,\_complete\_cds  
 m94893\_989-1499,testis-specific\_protein\_(tspy)\_mrna,\_3'\_end,\_clone\_pja923



u30610\_239-749,cd94\_protein\_mrna,\_complete\_cds\_  
 all\_x17094\_3675-4180,fur\_mrna\_for\_furin  
 x55019cds\_1128-1521:in\_reversesequence,\_1538-  
 1701,mrna\_for\_acetylcholine\_receptor\_delta\_subunit.

Metagene 449

d79988\_6383-6899,mrna\_for\_kiaa0166\_gene,\_complete\_cds  
 d80001\_4465-4939,mrna\_for\_kiaa0179\_gene,\_partial\_cds\_  
 d87450\_5572-6034,mrna\_for\_kiaa0261\_gene,\_partial\_cds\_  
 hg2573-ht2669\_at\_hg2573-ht2669\_zinc\_finger\_protein\_kup\_  
 m22638exon#4\_154-682,lyl-1\_protein\_gene,\_complete\_cds  
 m62402\_453-927,insulin-  
 like\_growth\_factor\_binding\_protein(igfbp6)\_mrna,\_complete\_cds  
 m85164\_1354-1852,srf\_accessory\_protein\_1b\_(sap-1)\_mrna,\_complete\_cds  
 s79873\_3394-3969,\_h-lamp-2=lysosome-associated\_membrane\_protein-  
 2\_{alternatively\_spliced}\_[human,\_li  
 u15174\_224-746,nip3\_(nip3)\_mrna,\_complete\_cds  
 u24186cds\_465-747:in\_reversesequence,\_1223-  
 1391,replication\_protein\_a\_complex\_subunit\_homolog\_rpa4\_g  
 u34976\_1059-1575,gamma-sarcoglycan\_mrna,\_complete\_cds  
 u47677mrna\_2495-2636,transcription\_factor\_e2f1\_(e2f1)\_gene,\_promoter\_and\_  
 u59914\_802-1240,chromosomemad\_homolog\_smad6\_mrna,\_complete\_cds\_  
 u80628\_2216-  
 2588,thymidine\_kinaseisoform\_b\_(tk2)\_mrna,\_alternatively\_spliced,\_partial\_cds\_  
 all\_x16323\_5339-5814,mrna\_for\_hepatocyte\_growth\_factor\_(hgf)\_  
 x52009cds\_813-1315:in\_reversesequence,\_1629,alpha-  
 1\_strychnine\_binding\_subunit\_of\_inhibitory\_glycine

Metagene 491

hg3510-ht3704\_at\_hg3510-ht3704\_v-erba\_related\_ear-3\_protein  
 hg880-ht880\_s\_at\_hg880-ht880\_mucin\_6,\_gastric  
 u37519\_2304-2784,aldehyde\_dehydrogenase\_(aldh8)\_mrna,\_complete\_cds\_  
 all\_x98263\_520-1019,mrna\_for\_m-phase\_phosphoprotein,\_mpp6

Metagene 429

d13628\_2506-2998,mrna\_for\_kiaa0003\_gene,\_complete\_cds  
 hg2171-ht2241\_r\_at\_hg2171-ht2241\_12-lipoxygenase\_  
 l47726\_2090-2552,phenylalanine\_hydroxylase\_(pah)\_mutant\_q20stop\_mrna  
 all\_m11591\_5495-6174:in\_m11591cds\_567-598,mhc\_ii\_hla-sx-alpha\_gene  
 u55764\_784-1072,estrogen\_sulfotransferase\_mrna,\_partial\_cds  
 all\_x51362\_2101-2583,mrna\_for\_dopamine\_d2\_receptor\_  
 x60708mrna\_2812-3364,pchdp7\_mrna\_for\_liver\_dipeptidyl\_peptidase\_iv\_

Metagene 210

j04111exon#1\_2735-3251,c-jun\_proto\_oncogene\_(jun),\_complete\_cds,\_clone\_hcj-1\_

m19154mrna\_2143-2503,transforming\_growth\_factor-beta-2\_mrna,\_complete\_cds  
 m55210mrna#1\_7322-7844,laminin\_b2\_chain\_(lamb2)\_gene\_  
 m93426\_7455-7845,protein\_tyrosine\_phosphatase\_zeta-  
 polypeptide\_(ptprz)\_mrna,\_complete\_cds  
 u04636mrna\_3882-4386,cyclooxygenase-2\_(hcox-2)\_gene,\_complete\_cds\_  
 u32114\_756-1278,caveolin-2\_mrna,\_complete\_cds  
 u60805\_3576-4146,oncostatin-  
 m\_specific\_receptor\_beta\_subunit\_(osmrp)\_mrna,\_complete\_cds

## Metagene 208

d14686mrna\_1554-2046,gene\_for\_glycine\_cleavage\_system\_t-protein  
 d14695\_1259-1817,mrna\_for\_kiaa0025\_gene,\_complete\_cds  
 d23673\_1204-  
 1666,\_clone\_hh109\_(screened\_by\_the\_monoclonal\_antibody\_of\_insulin\_receptor\_subs-  
 trate-1\_(  
 d86965\_6166-6490,mrna\_for\_kiaa0210\_gene,\_complete\_cds  
 d89667\_440-1004,mrna\_for\_c-myc\_binding\_protein,\_complete\_cds\_  
 hg2379-ht3996\_s\_at\_hg2379-  
 ht3996\_serine\_hydroxymethyltransferase,\_cytosolic,\_altsplise\_2\_  
 hg270-ht270\_at\_hg270-ht270\_lymphocyte\_chemoattractant\_factor\_  
 hg2868-ht3012\_s\_at\_hg2868-ht3012\_xe7,\_pseudoautosomal\_gene,\_altsplise\_2  
 hg371-ht1063\_s\_at\_hg371-ht1063\_mucin\_1,\_epithelial,\_altsplise\_6  
 hg3936-ht4206\_at\_hg3936-ht4206\_interleukinreceptor  
 j00287exon#1\_8-248:not\_in\_gb\_record,pepsinogen\_gene\_  
 l02867\_2179-2689,62\_kda\_paraneoplastic\_antigen\_mrna,\_3'\_end\_  
 l13744\_2775-3345,af-9\_mrna,\_complete\_cds\_  
 l14927exon#7\_1-159:in\_reversesequence,\_5382-  
 5676,tear\_prealbumin\_(tp)\_gene,\_complete\_cds\_and\_promote  
 l38935mrna\_564-1026,gt212\_mrna  
 m14218mrna\_1044-1440,argininosuccinate\_lyase\_mrna,\_complete\_cds  
 m38449\_40-599,transforming\_growth\_factor-beta\_mrna,\_complete\_cds,\_clone\_ptgf-  
 beta-trp114\_  
 m57763\_731-1151,adp-ribosylation\_factor\_(harf6)\_mrna,\_complete\_cds\_  
 m60278\_1771-2221,heparin-binding\_egf-like\_growth\_factor\_mrna,\_complete\_cds\_  
 m79462\_3853-4333,pml-1\_mrna,\_complete\_cds  
 m91196\_938-1513,dna-binding\_protein\_mrna,\_complete\_cds\_  
 m96326mrna\_370-886,azurocidin\_gene,\_complete\_cds  
 m96739\_1964-2510,nscl-1\_mrna\_sequence  
 s72043mrna\_5-68,\_gif=growth\_inhibitory\_factor\_[human,\_brain,\_genomic,\_2015\_nt]\_  
 s82362\_1119-1690,\_hrar-\_beta\_2=retinoic-acid-  
 receptor\_beta/suspected\_tumor\_suppressor\_{5'\_region,\_tr  
 u03494\_2213-2393,transcription\_factor\_lsf\_mrna,\_complete\_cds\_  
 u05875\_1655-2105,clone\_psk1\_interferon\_gamma\_receptor\_accessory\_factor-1\_(af-  
 1)\_mrna,\_complete\_cds\_  
 u40714\_692-1142,tyrosyl-trna\_synthetase\_mrna,\_complete\_cds/gb=u40714\_/ntype=rna  
 u41068cds\_2-268:in\_reversesequence,\_944-  
 l155,retinoid\_x\_receptor\_beta\_(rxrbeta)\_gene,\_partial\_3'\_tra  
 u47101\_428-758,nifu-like\_protein\_(hnifu)\_mrna,\_partial\_cds\_  
 u52112mrna#1\_3929-  
 4463,xq28\_genomic\_dna\_in\_the\_region\_of\_the\_llcam\_locus\_containing\_the\_genes\_for  
 \_ne  
 u54644\_1437-1806,tub\_homolog\_mrna,\_complete\_cds  
 u58087\_2096-2462,hs-cul-1\_mrna,\_complete\_cds\_  
 u62531\_3465-4029,ae2\_anion\_exchanger\_(slc4a2)\_mrna,\_complete\_cds\_

u65785\_4028-4442,150\_kda\_oxygen-regulated\_protein\_orp150\_mrna,\_complete\_cds  
 u72515\_1279-1811,c3f\_mrna,\_complete\_cds  
 u79255\_760-1180,x11\_protein\_mrna,\_partial\_cds  
 all\_x13451\_84-268,mrna\_for\_lymphocyte\_lineage-restricted\_mb-  
 1\_membrane\_glycoprotein\_c-term(m-mb-1\_ho  
 x13973cds\_996-1356:in\_reversesequence,\_1770-  
 1896,mrna\_for\_ribonuclease/angiogenin\_inhibitor\_(rai)\_  
 all\_x16135\_1552-  
 2003,mrna\_for\_novel\_heterogeneous\_nuclear\_rnp\_protein,\_l\_protein\_  
 x66362cds\_743-1097:in\_reversesequence,\_1121-1217,mrna\_pctaire-  
 3\_for\_serine/threonine\_protein\_kinase\_  
 all\_x80818\_3601-3860,mrna\_for\_metabotropic\_glutamate\_receptor\_type\_4\_  
 x85106\_2196-2712,mrna\_for\_ribosomal\_s6\_kinase

## Metagene 160

d14811\_644-1124,mrna\_for\_kiaa0110\_gene,\_complete\_cds\_  
 d14889\_760-1240,mrna\_for\_small\_gtp-binding\_protein,\_s10,\_complete\_cds  
 d21878\_816-1386,mrna\_for\_bst-1,\_complete\_cds\_  
 hg3288-ht3465\_at\_hg3288-ht3465\_xanthine\_dehydrogenase  
 j04102\_1830-2184,erythroblastosis\_virus\_oncogene\_homolog(ets-  
 2)\_mrna,\_complete\_cds  
 l25798\_1061-1589,3-hydroxy-3-  
 methylglutaryl\_coenzyme\_a\_synthase\_mrna,\_complete\_cds  
 l41349mrna\_3238-3646,phospholipase\_c\_beta(plcb4)\_mrna,\_complete\_cds  
 m17219\_758-1286,brain\_guanine\_nucleotide-binding\_protein\_alpha-  
 i\_subunit\_mrna,\_5'\_end  
 u55054\_3199-3697,k-cl\_cotransporter\_(hkcc1)\_mrna,\_complete\_cds\_  
 u57094\_502-1018,small\_gtp-binding\_protein\_mrna,\_complete\_cds\_  
 u93091\_4410-4806,toll\_protein\_homolog\_mrna,\_complete\_cds\_and\_line-  
 1\_reverse\_transcriptase\_homolog,\_p

## Metagene 156

hg2887-ht3031\_r\_at\_hg2887-ht3031\_sry-related\_hmg-boxprotein  
 hg4099-ht4369\_s\_at\_hg4099-ht4369\_adrenergic\_receptor,\_alpha\_1b\_  
 l04947\_3659-  
 4199,(clones\_bt3.081.8,\_bt3.129.5\_and\_bt4.169)\_receptor\_tyrosine\_kinase\_(kdr)\_m  
 rna,\_3'\_e  
 m74088\_8374-8717,apc\_gene\_mrna,\_complete\_cds\_  
 m96738cds\_719-1221,somatostatin\_receptor\_subtype(ssstr3)\_gene,\_complete\_cds  
 m99435\_2069-2325,transducin-like\_enhancer\_protein\_(tle1)\_mrna,\_complete\_cds  
 s72487\_1134-1582,\_orf1\_5'\_to\_pd-ecgf/tp...orf2\_5'\_to\_pd-  
 ecgf/tp\_[human,\_epidermoid\_carcinoma\_cell\_li  
 u28043\_1989-  
 2499,plasma\_membrane\_na+/h+\_exchanger\_isoform(nhe3)\_mrna,\_complete\_cds  
 u28049\_1684-2221,tbx2\_(txb2)\_mrna,\_complete\_cds  
 u51003\_2591-3169,dlx-2\_(dlx2)\_mrna,\_complete\_cds\_  
 u62739\_986-1430,branched-  
 chain\_amino\_acid\_aminotransferase\_(eca40)\_mrna,\_complete\_cds  
 u72509mrna\_2-  
 255,alternatively\_spliced\_b8\_(b7)\_mrna,\_partial\_sequence/gb=u72509\_/ntype=rna\_  
 u79300\_930-1404,clone\_23629\_mrna\_sequence

all\_x69654\_4-422,mrna\_for\_ribosomal\_protein\_s26  
 x79439cds\_16-277,notchdna\_sequence/gb=x79439\_/ntype=dna\_/annot=cds  
 x82850cds\_722-1090:in\_reversesequence,\_1108-  
 1238,mrna\_for\_thyroid\_transcript\_factor\_1\_  
 y00414cds\_1266-1537:in\_reversesequence,\_1573-  
 1785,mrna\_for\_tyrosine\_hydroxylase\_type\_3  
 all\_y08265\_1306-1834,mrna\_for\_dan26\_protein,\_partial\_  
 z49254cds\_75-435:in\_reversesequence,\_549-651,123-related\_mrna\_

Metagene 149

d00097exon#2\_152-  
 710,serum\_amyloid\_p\_component\_(sap)\_gene\_with\_upstream\_promoter\_  
 d14533\_812-1322,mrna\_for\_xpac\_protein  
 d16815\_1642-2086,mrna\_for\_ear-1r,\_complete\_cds\_  
 d87683\_6419-6941,mrna\_for\_kiaa0243\_gene,\_partial\_cds\_  
 hg2510-ht2606\_at\_hg2510-ht2606\_ras-specific\_guanine\_nucleotide-releasing\_factor  
 j00314mrna#1\_4079-4173,beta-tubulin\_gene,\_clone\_m40  
 j05200mrna\_14740-15238,ryanodine\_receptor\_mrna,\_complete\_cds  
 l11329\_1162-1630,protein\_tyrosine\_phosphatase\_(pac-1)\_mrna,\_complete\_cds  
 l12760exon#9\_396-  
 721,phosphoenolpyruvate\_carboxykinase\_(pck1)\_gene,\_complete\_cds\_with\_repeats  
 all\_l35263\_3222-3721,csaids\_binding\_protein\_(csbp1)\_mrna,\_complete\_cds\_  
 m22976mrna\_21-303:in\_reversesequence,\_668-728,cytochrome\_b5\_mrna,\_3'\_end  
 m62397\_3586-4126,colorectal\_mutant\_cancer\_protein\_mrna,\_complete\_cds\_  
 all\_m83554\_3167-3576,lymphocyte\_activation\_antigen\_cd30\_mrna,\_complete\_cds\_  
 m84424exon\_1073-1217,cathepsin\_e\_(ctse)\_gene\_  
 all\_m93311\_1950-2085,metallothionein-iii\_gene,\_complete\_cds  
 s83549\_19-571,\_na+/h+\_exchanger\_isoform\_nhe-  
 2\_[human,\_various\_tissues,\_mrna\_partial,\_595\_nt]/gb=s835  
 u02082\_1643-  
 2201,guanine\_nucleotide\_regulatory\_protein\_(tim1)\_mrna,\_complete\_cds\_  
 u14528\_2357-2807,sulfate\_transporter\_(dtd)\_mrna,\_complete\_cds  
 u18009\_1900-2338,chromosome\_17q21\_mrna\_clone\_lf113\_  
 u19517\_1692-2010,(apoargc)\_long\_mrna,\_complete\_cds\_  
 u22680\_6048-6558,x2\_box\_repressor\_mrna,\_complete\_cds\_  
 u36601\_2620-3166,heparan\_n-deacetylase/n-sulfotransferase-2\_mrna,\_complete\_cds\_  
 u49436\_1303-1783,translation\_initiation\_factor(eif5)\_mrna,\_complete\_cds\_  
 u53003\_1093-1609,gt335\_mrna,\_complete\_cds  
 u73338\_6615-7113,methionine\_synthase\_mrna,\_complete\_cds  
 u73682\_2255-2651,meningioma-expressed\_antigen(meal1)\_mrna,\_partial\_cds\_  
 u78876\_1789-2317,mek\_kinase\_mrna,\_complete\_cds\_  
 u80811\_1092-1536,lysophosphatidic\_acid\_receptor\_homolog\_mrna,\_complete\_cds\_  
 x02176cds\_1397-1656:in\_reversesequence,\_1681-  
 1859,mrna\_fragment\_for\_complement\_component\_c9  
 x05997cds#1\_726-1158:in\_reversesequence,\_1280-1316,mrna\_for\_gastric\_lipase  
 x51956mrna\_1881-2397,eno2\_gene\_for\_neuron\_specific\_(gamma)\_enolase  
 all\_x60483\_975-1171,h4/d\_gene\_for\_h4\_histone\_  
 x67325cds\_31-337:in\_reversesequence,\_43-541,p27\_mrna  
 x67683cds\_34-319:in\_reversesequence,\_13,mrna\_for\_keratin/gb=x67683\_/ntype=rna  
 x68149exon#2\_2249-2687,blr1\_gene\_for\_burkitt\_lymphoma\_receptor\_1\_  
 x85133mrna\_2399-2897,rbq-1\_mrna  
 x85372cds\_18-210:in\_reversesequence,\_19-115,mrna\_for\_sm\_protein\_f\_  
 all\_x87342\_2921-3456,mrna\_for\_giant\_larvae\_homolog\_  
 x90908cds\_11-353,mrna\_for\_i-15p\_(i-babp)\_protein\_

all\_y00978\_2012-2535,mrna\_for\_dihydrolipoamide\_acetyltransferase\_(pdc-e2)\_(ec\_2.3.1.12)  
 y12393\_346-819,mrna\_for\_srp1-like\_protein,\_partial\_  
 z24459exon#1\_13-  
 199,\_exon2a\_frommtcp1\_gene,\_exons\_2a\_to(and\_joined\_mrna)/gb=z24459\_/ntype=dna\_/annot

Metagene 125

d14827\_1564-1966,mrna\_for\_tax\_helper\_protein\_1,\_complete\_cds\_  
 all\_d26561\_2433-  
 3022,\_orf\_for\_l1\_protein\_gene\_extracted\_frompapillomavirus\_5b\_genome\_integrated\_into  
 l34060\_2124-2502,cadherin-8\_mrna,\_complete\_cds  
 m94167\_1894-2326,heregulin-beta2\_gene,\_complete\_cds  
 s83390\_2318-2865,\_t3\_receptor-associating\_cofactor-1\_[human,\_fetal\_liver,\_mrna,\_2930\_nt]  
 u03398\_1069-1576,receptor\_4-lbb\_ligand\_mrna,\_complete\_cds  
 u52152\_2642-  
 3020,inwardly\_rectifying\_potassium\_channel\_kir3.3\_mrna,\_complete\_cds\_  
 u64871cds\_870-1212:in\_reversesequence,\_1665-1773,putative\_g\_protein-coupled\_receptor\_(gpr19)\_gene,\_c  
 u95626mrna#2\_1641-  
 2133,\_ccr2\_gene\_(ccr2a)\_extracted\_fromccr2b\_(ccr2),\_ccr2a\_(ccr2),\_ccr5\_(ccr5)\_and\_  
 x77094cds\_634-994:in\_reversesequence,\_1136-1214,mrna\_for\_p40phox

Metagene 71

ab000220\_4588-5134,mrna\_for\_semaphorin\_e,\_complete\_cds\_  
 l09749\_1019-1463,(clone\_f4)\_transmembrane\_protein\_mrna\_sequence\_  
 m87313\_793-1335,myotonin\_protein\_kinase\_(dm)\_mrna\_  
 u04520mrna\_6221-6641,type\_iv\_collagen\_a5\_chain\_(col4a5)\_gene\_  
 all\_x87904\_4159-4670,mrna\_for\_sep\_protein  
 z78285\_3-137,mrna\_(clone\_la7)

Metagene 374

ab000896\_49-391,mrna\_for\_cadherin\_fib2,\_partial\_cds/gb=ab000896\_/ntype=rna  
 ac002115mrna#1\_932-  
 1448,\_cox6b\_gene\_(coxg)\_extracted\_fromdna\_from\_overlapping\_chromosomecosmids\_r3  
 13  
 d29641\_2800-3292,mrna\_for\_kiaa0052\_gene,\_partial\_cds\_  
 d83699\_623-  
 1001,brain\_3'\_utr\_of\_mrna\_for\_neuronal\_death\_protein,\_partial\_sequence  
 d86960\_5652-6168,mrna\_for\_kiaa0205\_gene,\_complete\_cds  
 hg2152-ht2222\_at\_hg2152-ht2222\_zinc\_finger\_protein\_92  
 hg3707-ht3922\_f\_at\_hg3707-ht3922\_guanine\_nucleotide-binding\_protein,\_alpha\_inhibiting\_activity\_polyp  
 l13994\_2830-3196,prec\_gene,\_complete\_cds;\_orf\_x,\_complete\_cds\_  
 l22343\_1136-1517,nuclear\_phosphoprotein\_mrna,\_complete\_cds\_

l41607mrna\_1772-2330,beta-1,6-n-acetylglucosaminyltransferase\_(ignt)\_gene  
 all\_m11437\_1562-2440:in\_m11437cds#1\_1198-  
 1226,\_kng\_gene\_(kininogen)\_extracted\_fromkininogen\_gene,\_kn  
 m27533\_883-1451,ig\_rearranged\_b7\_protein\_mrna\_vc1-region,\_complete\_cds.  
 m61764mrna\_1015-1495,gamma-tubulin\_mrna,\_complete\_cds  
 m65085\_1792-2302,follicle\_stimulating\_hormone\_receptor\_mrna,\_complete\_cds  
 m81778\_2123-2689,serotonin\_5-ht1c\_receptor\_mrna,\_complete\_cds  
 s66541cds\_375-687:in\_reversesequence,\_99-314,\_b-  
 50=neural\_phosphoprotein\_[human,\_genomic,\_1845\_ntseg  
 u03911\_2485-3013,mutator\_gene\_(hms2)\_mrna,\_complete\_cds\_  
 u22816\_3784-4288,lar-interacting\_protein\_1b\_mrna,\_complete\_cds\_  
 u51095\_1230-1656,homeobox\_protein\_cdx1\_mrna,\_complete\_cds  
 u59748\_28-187,desert\_hedgehog\_(hdhh)\_mrna,\_partial\_cds/gb=u59748\_/ntype=rna  
 u61538\_199-751,calcium-binding\_protein\_chp\_mrna,\_complete\_cds  
 u74324\_1797-2349,guanine\_nucleotide\_exchange\_factor\_mss4\_mrna,\_complete\_cds  
 u81787\_1686-2238,wnt10b\_mrna,\_complete\_cds.  
 u90437\_43-259,rp1\_homolog\_mrna,\_3'\_utr\_region/gb=u90437\_/ntype=rna\_  
 all\_x04391\_1779-2320,mrna\_for\_lymphocyte\_glycoprotein\_t1/leu-1\_  
 x15673mrna\_623-1121,ptr2\_mrna\_for\_repetitive\_sequence/gb=x15673\_/ntype=rna\_  
 all\_x15949\_1543-2144,mrna\_for\_interferon\_regulatory\_factor-2\_(irf-2)\_  
 x56667mrna\_915-1341,mrna\_for\_calretinin  
 x78924cds\_55-466:in\_reversesequence,\_622-631,hzf1\_mrna\_for\_zinc\_finger\_protein  
 x97630\_2420-2897,mrna\_for\_serine/threonine\_protein\_kinase\_emk  
 all\_x99657\_783-1318,mrna\_for\_protein\_containing\_sh3\_domain,\_sh3gl2\_

## Metagene 168

d00761\_252-750,mrna\_for\_proteasome\_subunit\_hc5\_  
 d00762\_237-777,mrna\_for\_proteasome\_subunit\_hc8\_  
 d13435\_526-832,mrna\_for\_pig-f\_(phosphatidyl-inositol-glycan\_f),\_complete\_cds\_  
 d13969\_1638-2148,mrna\_for\_mel-18\_protein,\_complete\_cds\_  
 d29677\_5709-6231,mrna\_for\_kiaa0054\_gene,\_complete\_cds  
 d31762\_6385-6775,mrna\_for\_kiaa0057\_gene,\_complete\_cds  
 d31766\_2024-2552,mrna\_for\_kiaa0060\_gene,\_complete\_cds  
 d38449\_2311-2791,mrna\_for\_g\_protein-coupled\_receptor,\_complete\_cds\_  
 d38535\_2583-2973,mrna\_for\_pk-120\_  
 d43950\_1355-1739,mrna\_for\_kiaa0098\_gene,\_partial\_cds\_  
 d50487\_3756-4098,mrna\_for\_rna\_helicase\_(hrh1),\_complete\_cds  
 d50863\_1908-2370,mrna\_for\_tesk1,\_complete\_cds  
 d50922\_1972-2452,mrna\_for\_kiaa0132\_gene,\_complete\_cds  
 d50923\_5018-5528,mrna\_for\_kiaa0133\_gene,\_complete\_cds  
 d78586\_6497-6923,cad\_mrna\_for\_multifunctional\_protein\_cad,\_complete\_cds  
 d79993\_2741-3167,mrna\_for\_kiaa0171\_gene,\_complete\_cds  
 d79997\_1881-2415,mrna\_for\_kiaa0175\_gene,\_complete\_cds  
 d80010\_4778-5198,mrna\_for\_kiaa0188\_gene,\_partial\_cds\_  
 d83776\_4596-5166,mrna\_for\_kiaa0191\_gene,\_partial\_cds\_  
 d83782\_3411-3915,mrna\_for\_kiaa0199\_gene,\_partial\_cds\_  
 d84557\_2412-2874,mrna\_for\_hsmcm6,\_complete\_cds\_  
 d86968\_4437-4899,mrna\_for\_kiaa0213\_gene,\_partial\_cds\_  
 d86971\_4851-5325,mrna\_for\_kiaa0217\_gene,\_partial\_cds\_  
 d86976\_3592-4060,mrna\_for\_kiaa0223\_gene,\_partial\_cds\_  
 hg1019-ht1019\_at\_hg1019-ht1019\_serine\_kinase\_psk-h1  
 hg1879-ht1919\_at\_hg1879-ht1919\_ras-like\_protein\_tc10\_  
 hg2190-ht2260\_at\_hg2190-ht2260\_crystallin,\_beta\_b3\_

hg2379-ht3997\_s\_at\_hg2379-  
 ht3997\_serine\_hydroxymethyltransferase, cytosolic, altsplice\_3\_  
 hg2649-ht2745\_s\_at\_hg2649-ht2745\_serine/threonine\_protein\_kinase\_cdk3  
 hg3033-ht3194\_r\_at\_hg3033-ht3194\_spliceosomal\_protein\_sap\_62\_  
 hg3327-ht3504\_s\_at\_hg3327-ht3504\_dna-binding\_protein\_hrfx2\_  
 hg3945-ht4215\_at\_hg3945-ht4215\_phospholipid\_transfer\_protein\_  
 hg4094-ht4364\_s\_at\_hg4094-ht4364\_transcription\_factor\_lsf-id\_  
 hg4433-ht4703\_at\_hg4433-ht4703\_cyclin\_d1\_promoter  
 hg511-ht511\_at\_hg511-ht511\_ras\_inhibitor\_inf\_  
 all\_j03764\_14604-15049, human, plasminogen\_activator\_inhibitor-  
 1\_gene, exonsto\_9\_  
 l04953\_2585-3065, x11\_protein\_(x11)\_mrna, 3'\_end  
 l09260\_781-1171, (chromosome\_3p25)\_membrane\_protein\_mrna  
 l11284\_1672-2122, homosapiens\_erk\_activator\_kinase\_(mek1)\_mrna  
 l12711\_1468-2000, transketolase\_(tk)\_mrna, complete\_cds  
 l16991\_679-1132, thymidylate\_kinase\_(cdc8)\_mrna, complete\_cds\_  
 l25286\_4549-5081, alpha-1\_type\_xv\_collagen\_mrna, complete\_cds  
 l32976\_2969-3533, protein\_kinase\_(mlk-3)\_mrna, complete\_cds\_  
 l36529mrna\_1491-2043, (clone\_n5-4)\_protein\_p84\_mrna, complete\_cds\_  
 l36983mrna\_3012-3546, dynamin\_(dnm)\_mrna, complete\_cds\_  
 l37347\_1301-1835, integral\_membrane\_protein\_(nramp2)\_mrna, partial  
 all\_m13241\_5990-6537, n-myc\_gene, exonsand\_3\_  
 all\_m15205\_12942-  
 l3411, thymidine\_kinase\_gene, complete\_cds, with\_clustered\_alu\_repeats\_in\_the\_in  
 tron  
 m16707mrna\_6-  
 357, histone\_h4\_gene, complete\_cds, clone\_fo108, histone\_h4\_gene, complete\_cds, c  
 lone\_fo1  
 m20747\_1519-2034, insulin-  
 responsive\_glucose\_transporter\_(glut4)\_mrna, complete\_cds\_  
 m21121\_958-1129, t\_cell-specific\_protein\_(rantes)\_mrna, complete\_cds  
 m21154mrna\_1234-1756, s-adenosylmethionine\_decarboxylase\_mrna, complete\_cds\_  
 m23668exon\_743-1271, adrenodoxin\_gene  
 m24470mrna\_911-1355, glucose-6-phosphate\_dehydrogenase, complete\_cds  
 m25280\_1753-2299, lymph\_node\_homing\_receptor\_mrna, complete\_cds\_  
 m28249\_4850-5306, very\_late\_antigen-2\_(vla-2)/collagen\_receptor\_alpha-  
 2\_subunit\_mrna, complete\_cds  
 m29536\_1025-1361, translational\_initiation\_factorbeta\_subunit\_(elf-2-  
 beta)\_mrna, complete\_cds  
 m34539\_1051-1477, fk506-binding\_protein\_(fkbp)\_mrna, complete\_cds\_  
 m38591\_120-600, cellular\_ligand\_of\_annexin\_ii\_(p11)\_mrna, complete\_cds\_  
 m54915\_2208-2236, h-pim-1\_protein\_(h-pim-1)\_mrna, complete\_cds  
 m60091\_1118-1248, galactose-1-phosphate\_uridyl\_transferase\_mrna, complete\_cds\_  
 m60450\_1932-2404, voltage-gated\_potassium\_channel\_(hk1)\_mrna, complete\_cds  
 m60527mrna\_1877-2369, deoxycytidine\_kinase\_mrna, complete\_cds\_  
 m63180\_2055-2505, threonyl-trna\_synthetase\_mrna, complete\_cds\_  
 m69013\_1053-1515, guanine\_nucleotide-binding\_regulatory\_protein\_(g-y-  
 alpha)\_mrna, complete\_cds  
 m69039\_625-1171, pre-mrna\_splicing\_factor\_sf2p32, complete\_sequence\_  
 m86852\_1041-1557, peroxisome\_assembly\_factor-1\_mrna, complete\_cds\_  
 m87339\_875-1361, replication\_factor\_37-kda\_subunit\_mrna, complete\_cds  
 m87434\_2316-2862, 71\_kda\_2'\_5'\_oligoadenylate\_synthetase\_(p69\_2-  
 5a\_synthetase)\_mrna, complete\_cds\_  
 s77356\_3-  
 41, transcript\_ch21=oligomycin\_sensitivity\_conferral\_protein\_oscp\_homolog\_[huma  
 n, rf1, rf48\_  
 s78187\_2548-3064, \_cdc25hu2=cdc25+\_homolog\_[human, \_mrna, \_3118\_nt]

u04810\_2050-2536,tastin\_mrna,\_complete\_cds\_  
 u05681exon#7\_111-544,proto-oncogene\_bcl3\_gene  
 u10362\_848-1352,gp36b\_glycoprotein\_mrna,\_complete\_cds  
 u14391\_4095-4623,myosin-ic\_mrna,\_complete\_cds  
 u15131\_3802-4252,p126\_(st5)\_mrna,\_complete\_cds\_  
 u20428\_2450-2840,snc19\_mrna\_sequence\_  
 u24704\_790-1264,antisecretory\_factor-1\_mrna,\_complete\_cds  
 u29607\_1974-2148,methionine\_aminopeptidase\_mrna,\_complete\_cds  
 u34683\_1261-1735,glutathione\_synthetase\_mrna,\_complete\_cds\_  
 u41668\_520-976,deoxyguanosine\_kinase\_mrna,\_complete\_cds  
 u52828\_1418-1882,cri-du-chat\_region\_mrna,\_clone\_niba2  
 u53347\_2278-2812,neutral\_amino\_acid\_transporter\_b\_mrna,\_complete\_cds\_  
 u56402\_2969-  
 3471,chromatin\_structural\_protein\_homolog\_(supt5h)\_mrna,\_complete\_cds  
 u58766\_741-1299,fx\_protein\_mrna,\_complete\_cds  
 u59752\_524-938,sec7p-like\_protein\_mrna,\_partial\_cds  
 u59919\_2047-2575,smg\_gds-associated\_protein\_smap\_mrna,\_complete\_cds  
 u60325\_3700-  
 4252,dna\_polymerase\_gamma\_mrna,\_nuclear\_gene\_encoding\_mitochondrial\_protein,\_co  
 mplete\_cd  
 u62293mrna\_2576-3152,\_limk1\_gene\_(lim-kinase1)\_extracted\_fromlim-  
 kinase1\_and\_alternatively\_spliced\_1  
 u69127\_2758-3106,fuse\_binding\_protein(fbp3)\_mrna,\_partial\_cds\_  
 u71374\_617-1157,hspex13p\_mrna,\_complete\_cds/gb=u71374/\_ntype=rna\_  
 all\_u73167\_4971-  
 35099,\_h\_luca14.2a\_gene\_extracted\_fromcosmid\_luca14,\_h\_luca14.2a\_gene\_extracted  
 \_from  
 u83463\_1406-1862,scaffold\_protein\_pbp1\_mrna,\_complete\_cds  
 u86070\_629-1205,phosphomannomutase\_mrna,\_complete\_cds  
 u87269\_1976-2468,p120e4f\_transcription\_factor\_mrna,\_complete\_cds.  
 u91985\_1014-1320,dna\_fragmentation\_factor-45\_mrna,\_complete\_cds  
 u94319\_2044-2404,autoantigen\_dfs70\_mrna,\_partial\_cds.  
 all\_x03794\_570-1150,embryonic\_mrna\_3'\_end\_with\_homoeo\_box\_(clone\_hhoc10)\_  
 all\_x05299\_2010-2572,mrna\_(~95%)\_for\_major\_centromere\_autoantigen\_cenp-b\_  
 all\_x06389\_1582-2087,mrna\_for\_synaptophysin\_(p38)  
 all\_x07695\_1175-1722,mrna\_for\_cytokeratinc-terminal\_region  
 all\_x15331\_813-1194,mrna\_for\_phosphoribosylpyrophosphate\_synthetase\_subunit\_one  
 x15722cds\_931-1411:in\_reversesequence,\_1569-  
 1575,mrna\_for\_glutathione\_reductase\_(ec\_1.6.4.2)  
 x15822cds\_18-222:in\_reversesequence,\_13-379,cox\_viia-1\_mrna\_for\_liver-  
 specific\_cytochrome\_c\_oxidase\_  
 x17620mrna\_257-  
 677,mrna\_for\_nm23\_protein,\_involved\_in\_developmental\_regulation\_(homologto\_dros  
 ophila  
 x54637cds\_3359-3539:in\_reversesequence,\_3857-4133,tyk2\_mrna\_for\_non-  
 receptor\_protein\_tyrosine\_kinase  
 all\_x59727\_3618-4201,63\_kda\_protein\_kinase\_related\_to\_rat\_erk3\_  
 x63417cds\_170-524:in\_reversesequence,\_560,irlb\_mrna\_  
 all\_x63522\_1800-1997,mrna\_daudi6\_for\_retinoic\_acid\_x\_receptor\_b  
 x63657mrna\_1683-2169,fvt1\_mrna\_  
 x63679cds\_587-1073,mrna\_for\_tramp\_protein  
 all\_x69115\_718-998,znf37a\_mrna\_for\_zinc\_finger\_protein\_  
 x71129cds\_213-705,mrna\_for\_electron\_transfer\_flavoprotein\_beta\_subunit\_  
 x74330cds\_788-1154:in\_reversesequence,\_1281-  
 1335,mrna\_for\_dna\_primase\_(subunit\_p48)\_  
 x74801cds\_1282-1552:in\_reversesequence,\_1636-1837,cctg\_mrna\_for\_chaperonin



x74874mrna\_5857-  
 6262,\_rna\_polymerase\_ii\_largest\_subunit\_gene\_extracted\_fromgene\_for\_rna\_pol\_ii\_  
 large  
 x78992cds\_1349-1373,erf-2\_mrna\_  
 all\_x80910\_3085-3566,ppplcb\_mrna\_  
 x81788\_397-799,ds-1\_mrna\_  
 x92720cds\_1540-1888:in\_reversesequence,\_1978-  
 2086,mrna\_for\_phosphoenolpyruvate\_carboxykinase  
 x93510cds\_548-956:in\_reversesequence,\_1021-  
 1069,mrna\_for\_37\_kda\_lim\_domain\_protein  
 x97544cds\_291-453:in\_reversesequence,\_508-  
 724,mrna\_for\_tim17\_preprotein\_translocase\_  
 x98248mrna\_3140-3698,mrna\_for\_sortilin  
 x98534exon#10\_287-798,vasp\_gene,\_exonsto\_13\_  
 x99947\_2580-2922:in\_reversesequence,\_2994-3084,mrna\_dynein-related\_protein  
 y00636cds\_586-688:in\_reversesequence,\_739-  
 985,mrna\_for\_lymphocyte\_function\_associated\_antigen-3\_(lfa  
 all\_y11681\_529-  
 1040,mrna\_for\_mitochondrial\_ribosomal\_protein\_sl2/gb=y11681/\_ntype=rna\_  
 z23064\_1461-1755,mrna\_gene\_for\_hnrnp\_g\_protein\_  
 all\_z48042\_2679-3232,mrna\_encoding\_gpi-anchored\_protein\_p137\_  
 all\_z70219\_4-188,mrna\_for\_5'utr\_for\_unknown\_protein\_(clone\_icrfp507c0696)  
 z84497cds\_1915-2230:in\_fullsequence,\_18383-  
 18624,dna\_sequence\_from\_cosmid\_o14\_on\_chromosomecontains\_

## Metagene 388

d38128exon\_604-1126,ip\_gene\_for\_prostacyclin\_receptor  
 d43638\_2961-3393,mrna\_for\_mtga8a\_protein,\_complete\_cds  
 hg2167-ht2237\_at\_hg2167-ht2237\_protein\_kinase\_ht31,\_camp-dependent\_  
 hg2715-ht2811\_at\_hg2715-ht2811\_tyrosine\_kinase\_  
 hg3492-ht3686\_at\_hg3492-ht3686\_uncoupling\_protein\_ucp  
 l11373\_4183-4609,protocadherin\_43\_mrna,\_complete\_cds\_for\_abbreviated\_pc43  
 l34409\_624-990,(clone\_b3b3e13)\_chromosome\_4p16.3\_dna\_fragment\_  
 l36645mrna\_2716-3034,receptor\_protein-  
 tyrosine\_kinase\_(hek8)\_mrna,\_complete\_cds\_  
 m16801mrna\_5250-5724,mineralocorticoid\_receptor\_mrna\_(hmr),\_complete\_cds\_  
 m60556mrna#1\_503-839,\_tgfb3\_gene\_(transforming\_growth\_factor-  
 beta\_3)\_extracted\_fromtransforming\_grow  
 m74096\_1694-2096,long\_chain\_acyl-coa\_dehydrogenase\_(acadl)\_mrna,\_complete\_cds  
 m97676\_1406-1646,(region\_7)\_homeobox\_protein\_(hox7)\_mrna,\_complete\_cds  
 s73840\_408-  
 784,\_type\_ix\_myosin\_heavy\_chain\_{3'\_region}\_[human,\_skeletal\_muscle,\_mrna\_part  
 ial,\_827\_n  
 s81661\_588-1164,\_keratinocyte\_growth\_factor\_[human,\_mrna,\_1200\_nt]  
 u02683\_2758-3318,alpha\_palindromic\_binding\_protein\_mrna,\_complete\_cds  
 u08096exon\_31-481,peripheral\_myelin\_protein-22\_(pmp22)\_gene,\_non-  
 coding\_exon\_1b/gb=u08096/\_ntype=dna  
 u37122\_1877-2387,adducin\_gamma\_subunit\_mrna,\_complete\_cds  
 u44754\_809-1253,pse-binding\_factor\_ptf\_gamma\_subunit\_mrna,\_complete\_cds  
 u69546\_1903-2299,rna\_binding\_protein\_etr-3\_mrna,\_complete\_cds  
 u79251\_1285-1747,clone\_23878\_mrna\_sequence\_  
 all\_x04325\_1113-1558,liver\_mrna\_for\_gap\_junction\_protein\_  
 all\_x59350\_2679-3220,mrna\_for\_b\_cell\_membrane\_protein\_cd22\_  
 x67697cds\_1-145:in\_reversesequence,\_63-603,he2\_mrna\_

## Metagene 378

d87011cds\_1308-1590:in\_fullsequence,\_24060-  
 24222,(lamuda)\_dna\_for\_immunoglobulin\_light\_chain\_  
 j04156mrna\_1030-1510,interleukin(il-7)\_mrna,\_complete\_cds\_  
 s95936\_1806-2268,\_transferrin\_[human,\_liver,\_mrna,\_2347\_nt]\_  
 u24153\_1796-1994,p21-activated\_protein\_kinase\_(pak2)\_gene,\_complete\_cds

## Metagene 359

d86975\_5570-5978,mrna\_for\_kiaa0222\_gene,\_complete\_cds  
 l05514cds\_20-116:in\_reversesequence,\_1789-  
 1815:not\_in\_gb\_record,histatin(his2)\_gene\_  
 all\_x83857\_1431-1809,mrna\_for\_prostaglandin\_e\_receptor\_(ep3a1)\_

## Metagene 261

hg274-ht274\_s\_at\_hg274-ht274\_gamma-glutamyltransferase  
 u49379\_2051-2537,diacylglycerol\_kinase\_epsilon\_dgk\_mrna,\_complete\_cds  
 u81607\_6007-6535,gravin\_mrna,\_complete\_cds\_  
 all\_x81479\_2655-3118,mrna\_for\_emr1\_hormone\_receptor  
 x86816mrna\_4-193,estrogen\_receptor\_cdna,\_5'\_splice\_variant/gb=x86816\_/ntype=rna

## Metagene 234

u50822mrna\_909-1375,neurogenic\_helix-loop-  
 helix\_protein\_neurod\_(neurod)\_gene,\_complete\_cds  
 u68030\_2365-2665,g\_protein-coupled\_receptor\_(strl22)\_mrna,\_complete\_cds  
 all\_u77827\_1053-1630,orphan\_g\_protein-  
 coupled\_receptor\_(cepr)\_gene,\_complete\_cds.  
 all\_x77366\_4160-4689,hbz17\_mrna

## Metagene 227

aj001047cds\_485-791:in\_reversesequence,\_959-1013,mrna\_for\_matrilin-  
 3/gb=aj001047\_/ntype=rna  
 d25216\_4968-5256,mrna\_for\_kiaa0014\_gene,\_complete\_cds  
 d29012\_230-752,mrna\_for\_proteasome\_subunit\_y,\_complete\_cds\_  
 d29954\_4458-4920,mrna\_for\_kiaa0056\_gene,\_partial\_cds\_  
 d45906\_3097-3613,mrna\_for\_limk-2,\_complete\_cds\_  
 d50810\_3494-3992,mrna\_for\_placental\_leucine\_aminopeptidase,\_complete\_cds\_  
 d50913\_1494-2052,mrna\_for\_kiaa0123\_gene,\_partial\_cds\_  
 d63160exon\_6-306:in\_reversesequence,\_9:not\_in\_gb\_record,dna\_for\_lectin\_p35\_  
 d83703\_2605-3169,mrna\_for\_peroxisome\_assembly\_factor-2,\_complete\_cds\_  
 d90042\_675-1215,liver\_arylamine\_n-acetyltransferase\_(ec\_2.3.1.5)\_gene

hg2036-ht2090\_at\_hg2036-ht2090\_stimulatory\_gdp/gtp\_exchange\_protein\_for\_c-ki-  
 ras\_p21\_and\_smg\_p21\_  
 hg2566-ht4867\_at\_hg2566-ht4867\_microtubule-  
 associated\_protein\_tau,\_altsplice\_5,\_exon\_4a  
 hg2706-ht2802\_at\_hg2706-ht2802\_serine/threonine\_kinase\_  
 hg3976-ht4246\_at\_hg3976-ht4246\_pou-domain\_dna\_binding\_factor\_pit1,\_pituitary-  
 specific  
 hg870-ht870\_at\_hg870-ht870\_golgin,\_165\_kda\_polypeptide\_  
 hg909-ht909\_at\_hg909-ht909\_mg81  
 j02876mrna\_616-1180,placental\_folate\_binding\_protein\_mrna,\_complete\_cds  
 l05147\_266-812,dual\_specificity\_phosphatase\_tyrosine/serine\_mrna,\_complete\_cds\_  
 l10405\_1364-  
 1910,dna\_binding\_protein\_for\_surfactant\_protein\_b\_mrna,\_complete\_cds/gb=110405\_  
 /ntype=rn  
 l14754\_3369-3813,dna-binding\_protein\_(smbp2)\_mrna,\_complete\_cds  
 l19058\_2599-3163,glutamate\_receptor\_(glur5)\_mrna,\_complete\_cds\_  
 l26494\_1598-2084,(oct-6)\_mrna,\_complete\_cds\_  
 l29433exon\_53-587,factor\_x\_(blood\_coagulation\_factor)\_gene\_  
 l36861exon#4\_247-757,guanylate\_cyclase\_activating\_protein\_(gcap)\_gene\_exons\_1-  
 4,\_complete\_cds\_  
 all\_l36922\_938-1125,met-ase\_gene,\_exon\_1  
 l40377mrna\_766-1276,cytoplasmic\_antiproteinase(cap2)\_mrna,\_complete\_cds  
 l47738\_2286-2856,inducible\_protein\_mrna,\_complete\_cds\_  
 all\_m16652\_714-  
 760,pancreatic\_elastase\_iaa\_mrna,\_complete\_cds,pancreatic\_elastase\_iaa\_mrna,\_co  
 mplete  
 m31651cds\_900-1146:in\_reversesequence,\_5912-6098,human\_sex\_hormone-  
 binding\_globulin\_(shbg)\_gene,\_com  
 all\_m34041\_1414-2015,alpha-2-adrenergic\_receptor\_(alpha-  
 2\_c2)\_gene,\_complete\_cds\_  
 m35878exon#4\_1993-2443,insulin-like\_growth\_factor-binding\_protein-  
 3\_gene,\_complete\_cds,\_clone\_hl1006  
 all\_m58378\_75-406:in\_m58378cds#1\_1893-  
 1930:in\_m58378cds#2\_2002,\_syn1\_gene\_(synapsin\_i)\_extracted\_fro  
 m64595mrna\_216-648,small\_g\_protein\_(gx)\_mrna,\_3'\_end\_  
 m76180\_1461-1887,aromatic\_amino\_acid\_decarboxylase\_(ddc)\_mrna,\_complete\_cds  
 m86757\_2-372,psoriasin\_mrna,\_complete\_cds  
 m91438cds\_55-181:in\_reversesequence,\_300-540,kazal-  
 type\_serine\_proteinase\_(husi-ii)\_gene,\_complete\_c  
 m93718\_3536-4034,nitric\_oxide\_synthase\_mrna,\_complete\_cds  
 m94077exon#2\_657-1125,loricrin\_gene\_exonsand\_2,\_complete\_cds  
 m94547mrna\_55-565,\_hummlc2at;\_homo\_sapiens;\_;\_593\_base-pairs  
 m95712\_2005-2407,b-raf\_mrna,\_complete\_cds  
 m98045\_1593-2097,folylpolyglutamate\_synthetase\_mrna,\_complete\_cds\_  
 all\_s57887\_739-  
 980,(t1)=elastin\_translocation\_allele\_{exon\_28,\_translocation}\_[human,\_genomic  
 \_mutan  
 s67070\_55-  
 421,\_heat\_shock\_protein\_hsp72\_homolog\_[human,\_thyroid\_associated\_opthalmopathy  
 \_patient,\_m  
 s82198\_323-827,\_caldecrin=serum\_calcium-  
 decreasing\_factor\_[human,\_pancreas,\_mrna\_partial,\_894\_ntl\_  
 u06088exon\_220-730,n-acetylgalactosamine\_6-sulphatase\_(galns)\_gene\_  
 u08191\_4687-5220,r\_kappa\_b\_mrna,\_complete\_cds  
 u09850\_3337-3769,zinc\_finger\_protein\_(znfl43)\_mrna,\_complete\_cds\_  
 u13045\_2126-2690,nuclear\_respiratory\_factor-2\_subunit\_betamrna,\_complete\_cds  
 all\_u15177\_2291-2724,cosmid\_cri-jc2015\_at\_d10s289\_in\_10sp13

u22526\_2677-3157,2,3-oxidosqualene-lanosterol\_cyclase\_mrna,\_complete\_cds\_  
 u35234\_6175-6290,protein\_tyrosine\_phosphatase\_sigma\_mrna,\_complete\_cds\_  
 u41763\_4933-5485,muscle\_specific\_clathrin\_heavy\_chain\_(cltd)\_mrna,\_complete\_cds\_  
 u42412\_977-1535,5'\_\_-amp-activated\_protein\_kinase,\_gamma-  
 1\_subunit\_mrna,\_complete\_cds\_  
 u48408\_752-1322,kidney\_water\_channel\_(hkid)\_mrna,\_complete\_cds\_  
 u49260\_1284-  
 1761,mevalonate\_pyrophosphate\_decarboxylase\_(mpd)\_mrna,\_complete\_cds\_  
 u49395\_1361-1907,ionotropic\_atp\_receptor\_p2x5a\_mrna,\_complete\_cds\_  
 u52112mrna#5\_896-  
 1340,xq28\_genomic\_dna\_in\_the\_region\_of\_the\_llcam\_locus\_containing\_the\_genes\_for  
 \_neu  
 u55258cds\_3452-3872:in\_reversesequence,\_4031-4091,hbravo/nr-  
 cam\_precursor\_(hbravo/nr-cam)\_gene,\_comp  
 all\_u57341\_2-  
 129,neurofilament\_triplet\_1\_protein\_mrna,\_partial\_cds/gb=u57341\_/ntype=rna,neur  
 ofilamen  
 u60666\_1923-  
 2415,testis\_specific\_leucine\_rich\_repeat\_protein\_(tslrp),\_complete\_cds\_  
 u65402cds\_651-915:in\_reversesequence,\_1437-1647,seven\_transmembrane\_g-  
 coupled\_receptor\_(gpr31)\_gene,  
 u68485\_1356-1788:not\_in\_gb\_record,box-dependent\_myc-interacting\_protein-  
 1\_(bin1)\_mrna,\_complete\_cds\_  
 u70064\_6458-7030,lysosomal\_trafficking\_regulator\_(lyst)\_mrna,\_partial\_cds  
 u72209\_432-990,yy1-associated\_factor(yaf2)\_mrna,\_complete\_cds\_  
 u87964\_1515-2094,putative\_g-protein\_(gp-1)\_mrna,\_complete\_cds  
 x00090cds\_6-356,histone\_h3\_gene  
 all\_x00695\_6073-6372,interleukin-2\_(il-2)\_gene\_and\_5'\_\_-flanking\_region\_  
 x01715cds\_1338-  
 1537:not\_in\_gb\_record,gene\_fragment\_for\_the\_acetylcholine\_receptor\_gamma\_subuni  
 t\_prec  
 x05360cds\_353-785,cdc2\_gene\_involved\_in\_cell\_cycle\_control\_  
 all\_x13810\_1940-1986,otf-2\_mrna\_for\_lymphoid-specific\_transcription\_factor\_  
 x51952mrna\_355-  
 517,\_ucp\_fromucp\_gene\_for\_uncoupling\_protein\_exonsand/gb=x51952\_/ntype=dna/\_ann  
 ot=exo  
 all\_x63717\_1962-2473,mrna\_for\_apo-1\_cell\_surface\_antigen\_  
 x66839cds\_909-1335:in\_reversesequence,\_1407-  
 1491,matu\_mn\_mrna\_for\_p54/58n\_protein\_  
 x69950exon#1\_1485-2039,dna\_sequence\_for\_wilms'\_tumor\_gene  
 all\_x70297\_1563-2020,mrna\_for\_neuronal\_nicotinic\_acetylcholine\_receptor\_alpha-  
 7\_subunit  
 x77777\_2210-2771,intestinal\_vip\_receptor\_related\_protein\_mrna  
 all\_x96969\_1470-1759,mrna\_for\_urea\_transporter\_  
 x99656cds\_798-1068:in\_reversesequence,\_1251-  
 1329,mrna\_for\_protein\_containing\_sh3\_domain,\_sh3gll\_  
 reverse\_y10871\_4016-4220,twist\_gene  
 z25884cds\_2453-2897:in\_reversesequence,\_3062-3068,mrna\_for\_clc-  
 1\_muscle\_chloride\_channel\_protein  
 z48475cds\_1531-1795:in\_reversesequence,\_1918-  
 2128,gckr\_mrna\_for\_glucokinase\_regulator\_  
 all\_z69720\_14484-  
 15067,dna\_sequence\_from\_cosmid\_ra36\_from\_a\_contig\_from\_the\_tip\_of\_the\_short\_arm  
 \_of\_  
 all\_z70220\_31-266,mrna\_for\_5'utr\_for\_unknown\_protein\_(clone\_icrfp507o0882).  
 reverse\_z95624\_34190-  
 34542,dna\_sequence\_from\_cosmid\_u237h1\_contains\_ras\_like\_gtpase\_and\_ests.

## Metagene 217

d17793\_633-1161,mrna\_for\_kiaa0119\_gene,\_complete\_cds\_  
hg64-ht64\_at\_hg64-ht64\_nf-kappa\_b-binding\_protein\_kbp-1  
k03474exon#5\_562-829:in\_reversesequence,\_2817-  
2919,mullerian\_inhibiting\_substance\_gene,\_complete\_cds  
l00022cds\_1249-1679:in\_reversesequence,\_1750-1816,ig\_active\_epsilon1\_5'\_ut,\_v-  
d-j\_region\_subgroup\_vh  
m31774\_1858-2392,thyrotropin\_receptor\_(tsh)\_mrna,\_complete\_cds\_  
u58033\_24-  
366,myotubularin\_related\_protein(mtmr2)\_gene,\_partial\_cds/gb=u58033\_/ntype=rna  
x06290cds\_13307-13442:in\_reversesequence,\_13709-  
13913,mrna\_for\_apolipoprotein(a)\_  
x87843cds\_690-894:in\_reversesequence,\_1045-  
1201,mrna\_for\_cyclin\_h\_assembly\_factor\_  
x99350mrna\_1863-2424,\_hfh4\_cds\_gene\_extracted\_fromhfh4\_gene,\_exonand\_joined\_cds

## Metagene 66

d49824\_945-1110,hla-b\_null\_allele\_mrna,hla-b\_null\_allele\_mrna\_  
hg862-ht862\_s\_at\_hg862-ht862\_transition\_protein\_  
j04040mrna\_563-1016,glucagon\_mrna,\_complete\_cds  
m15881\_1752-2310,uromodulin\_(tamm-horsfall\_glycoprotein)\_mrna,\_complete\_cds  
u77970\_2339-2855,neuronal\_pas2\_(npas2)\_mrna,\_complete\_cds  
x67318cds\_851-1229:in\_reversesequence,\_1260,mrna\_for\_procarboxypeptidase\_a1\_

## Metagene 60

u31382\_69-621,g\_protein\_gamma-4\_subunit\_mrna,\_complete\_cds\_  
x07820cds\_1252-1378:in\_reversesequence,\_1430-  
1694,mrna\_for\_metalloproteinase\_stromelysin-2  
x14329cds\_1050-1350:in\_reversesequence,\_1569-  
1641,mrna\_for\_carboxypeptidase\_n\_small\_subunit\_(ec\_3.4.  
z47043cds\_540-  
1080,partial\_cdna\_sequence,\_clone\_x529,\_unknown\_open\_reading\_frame;/gb=z47043\_/ntype=d

## Metagene 48

d26561cds#2\_153-435:in\_reversesequence,\_3711-  
3717,\_orf\_for\_l1\_protein\_gene\_extracted\_frompapillomavi  
hg3703-ht3915\_s\_at\_hg3703-ht3915\_udp-  
glucuronosyltransferasefamily,\_polypeptide\_1,\_altsplice\_1  
all\_l37868\_3521-4088,pou-domain\_transcription\_factor\_(n-oct-3),\_complete\_cds  
x74819cds\_509-809:in\_reversesequence,\_913-1015,mrna\_for\_cardiac\_troponin\_t

## Metagene 21

af012270\_815-1325,peropsin\_(rrh)\_mrna,\_complete\_cds/gb=af012270\_/ntype=rna  
 l40411mrna\_43-511,thyroid\_receptor\_interactor\_(trip8)\_mrna,\_3'\_end\_of\_cds\_  
 all\_x64877\_494-529,mrna\_for\_serum\_protein,mrna\_for\_serum\_protein

Metagene 17

d50931\_2527-2971,mrna\_for\_kiaa0141\_gene,\_complete\_cds  
 m97016\_1231-1803,osteogenic\_protein-2\_(op-2)\_mrna,\_complete\_cds.  
 s58544\_1884-2382,\_75\_kda\_infertility-  
 related\_sperm\_protein\_[human,testis,\_mrna\_partial,\_2427\_nt]\_  
 s81737\_1159-1681,\_alphasyntrophin\_[human,\_mrna\_partial,\_1771\_nt]\_  
 u06233\_2545-3055,pou\_domain\_protein\_(brn-3b)\_mrna,\_complete\_cds  
 u07681\_2075-2585,nad(h)-  
 specific\_isocitrate\_dehydrogenase\_alpha\_subunit\_precursor\_mrna,\_complete\_cds  
 u68385\_1259-1643,meis1-related\_protein(mrg2),\_mrna,\_partial\_cds.  
 u69108\_2155-2632,tnf\_receptor\_associated\_factor\_mrna,\_partial\_cds\_  
 all\_x79066\_390-973,\_hsapiens\_erf-1\_mrna\_5'\_end  
 x91653exon\_5-125,dna\_for\_exon\_encoding\_for\_n-  
 acetylglucosaminyltransferase\_v\_(340\_bp)/gb=x91653\_/nty  
 y00083cds\_902-1201:in\_reversesequence,\_1416-1641,mrna\_for\_glioblastoma-  
 derived\_t-cell\_suppressor\_fac

Metagene 478

k02402exon#8\_1383-1875,coagulation\_factor\_ix\_gene,\_complete\_cds  
 l41162\_1879-2419,collagen\_alphatype\_ix\_(col9a3)\_mrna,\_complete\_cds\_  
 all\_m21388\_2-95,unproductively\_rearranged\_ig\_mu-chain\_mrna\_v-  
 region\_(vd),\_5'\_end,\_clone\_mu-3ala.,unp  
 all\_m29610\_446-  
 476,glycophorin\_e\_mrna,\_complete\_cds,glycophorin\_e\_mrna,\_complete\_cds  
 u79286\_934-1294,arginine\_methyltransferase\_mrna,\_complete\_cds

Metagene 313

ac002045mrna#1\_643-838,\_a-589h1.1\_fromchromosomebac\_clone\_cit987-ska-  
 589h1\_~complete\_genomic\_sequenc  
 aj000099\_1243-1750,mrna\_for\_lyosomal\_hyaluronidase/gb=aj000099\_/ntype=rna  
 d83260\_604-1150,hxc-26\_mrna,\_complete\_cds  
 j04823mrna\_61-391,cytochrome\_c\_oxidase\_subunit\_viii\_(cox8)\_mrna,\_complete\_cds\_  
 l11066\_2272-2770,mrna\_sequence\_  
 l13939\_3297-3791,beta\_adaptin\_protein\_mrna,\_complete\_cds\_  
 l25878\_1092-1657,p33/heh\_epoxide\_hydrolase\_(ephx)\_mrna,\_complete\_cds  
 m34668\_3044-3590,protein\_tyrosine\_phosphatase\_(ptpase-alpha)\_mrna  
 m64929\_1572-2100,protein\_phosphatase\_2a\_alpha\_subunit\_mrna,\_complete\_cds\_  
 m74491\_3066-3552,adp-ribosylation\_factor\_mrna,\_complete\_cds  
 m88279\_1591-2131,immunophilin\_(fkbp52)\_mrna,\_complete\_cds  
 m94046\_1788-2346,zinc\_finger\_protein\_(maz)\_mrna  
 s82470\_1398-1836,\_bb1=malignant\_cell\_expression-  
 enhanced\_gene/tumor\_progression-enhanced\_gene\_[human

u04241\_979-  
 1264,homolog\_of\_drosophila\_enhancer\_of\_split\_m9/m10\_mrna,\_complete\_cds  
 u13991\_335-713,tata-  
 binding\_protein\_associated\_factor\_30\_kda\_subunit\_(tafii30)\_mrna,\_complete\_cds  
 u18937\_1840-2344,histidyl-trna\_synthetase\_homolog\_(ho3)\_mrna,\_complete\_cds\_  
 u32986\_3609-4126,xeroderma\_pigmentosum\_group\_e\_uv-  
 damaged\_dna\_binding\_factor\_mrna,\_complete\_cds  
 u37146\_5411-  
 5927,silencing\_mediator\_of\_retinoid\_and\_thyroid\_hormone\_action\_(smrt)\_mrna,\_com  
 plete\_cds  
 u41635\_2207-2651,os-9\_precursosor\_mrna,\_complete\_cds  
 u60644\_1537-1957,hu-k4\_mrna,\_complete\_cds  
 u65579\_138-648,mitochondrial\_nadh\_dehydrogenase-ubiquinone\_fe-  
 s\_protein\_8,\_23\_kda\_subunit\_precursor\_  
 u67171\_229-697,selenoprotein\_w\_(selw)\_mrna,\_complete\_cds/gb=u67171\_/ntype=rna  
 u78735\_5872-6424,abc3\_mrna,\_complete\_cds.  
 u79287\_813-1305,clone\_23867\_mrna\_sequence  
 u82108\_987-1464,sip-1\_mrna,\_complete\_cds\_  
 u83246\_1364-1904,copine\_i\_mrna,\_complete\_cds\_  
 u95040\_2366-2876,transcriptional\_corepressor\_hkap1/tif1b\_mrna,\_complete\_cds  
 all\_x04106\_907-1478,mrna\_for\_calcium\_dependent\_protease\_(small\_subunit)  
 x57346cds\_308-674:in\_reversesequence,\_1118-1154,mrna\_for\_hs1\_protein  
 x70649\_2231-2663,cl.1042\_mrna\_of\_dead\_box\_protein\_family\_  
 all\_x72964\_606-1027,mrna\_for\_caltractin  
 all\_x73358\_355-815,haes-1\_mrna\_  
 x92896exon#2-3\_39-222:in\_reversesequence,\_295-301,mrna\_for\_itba2\_protein  
 x98801cds\_3489-3729:in\_reversesequence,\_3771-4017,mrna\_for\_dynactin\_  
 x99728exon\_13-247,ndufv3\_gene,\_exon/gb=x99728\_/ntype=dna\_/annot=exon  
 y07604cds\_291-483:in\_reversesequence,\_572-776,mrna\_for\_nucleoside-  
 diphosphate\_kinase\_  
 z14244cds\_31-169:in\_reversesequence,\_43-  
 409,coxviib\_mrna\_for\_cytochrome\_c\_oxidase\_subunit\_viib  
 z56281cds\_772-1222:in\_reversesequence,\_1334-  
 1382,mrna\_for\_interferon\_regulatory\_factor\_3  
 all\_z69881\_3952-4535,mrna\_for\_adenosine\_triphosphatase,\_calcium

Metagene 207

hg2160-ht2230\_at\_hg2160-ht2230\_glutamate\_decarboxylase  
 u68723\_2126-2576,checkpoint\_suppressormrna,\_complete\_cds  
 x76059cds\_1208-1424:in\_reversesequence,\_1709-1807,mrna\_for\_yrrm1

Metagene 206

m90354cds\_29-301:in\_reversesequence,\_1165-  
 1197,btf3\_protein\_homologue\_gene,\_complete\_cds  
 u57452\_43-103,snf1-like\_protein\_kinase\_mrna,\_partial\_cds/gb=u57452\_/ntype=rna  
 u62432\_1759-  
 1881,nicotinic\_acetylcholine\_receptor\_alpha3\_subunit\_precursor,\_mrna,\_complete\_  
 cds\_  
 x87852cds\_5374-5560:in\_reversesequence,\_5780-5966,mrna\_for\_sex\_gene\_  
 all\_z29678\_1247-1740,mitf\_mrna\_

## Metagene 62

u07132\_1415-1961,steroid\_hormone\_receptor\_ner-i\_mrna,\_complete\_cds\_  
x99374cds\_1846-2174:in\_reversesequence,\_2211-2318,mrna\_for\_fertilin\_beta

## Metagene 387

ab002409\_293-791,mrna\_for\_slc,\_complete\_cds/gb=ab002409\_/ntype=rna  
af009368\_901-1345,luman\_mrna,\_complete\_cds/gb=af009368\_/ntype=rna\_  
d11327\_2099-2638,mrna\_for\_protein-tyrosine\_phosphatase,\_complete\_cds\_  
d16827cds\_767-1064:in\_reversesequence,\_1124-  
1132,gene\_for\_fifth\_somatostatin\_receptor\_subtype\_  
d17461exon#1-3\_13-102:not\_in\_gb\_record,gulo\_gene\_for\_l-gulono-gamma-  
lactone\_oxidase,\_exon\_9,10\_and/g  
d21089\_2957-3515,mrna\_for\_xp-  
c\_repair\_complementing\_protein\_(p125),\_complete\_cds\_  
d31891\_3786-4275,mrna\_for\_kiaa0067\_gene,\_complete\_cds\_  
d32002\_2454-3001,mrna\_for\_nuclear\_cap\_binding\_protein,\_complete\_cds\_  
d42053\_3755-4277,mrna\_for\_kiaa0091\_gene,\_complete\_cds\_  
d50312\_1206-1668,mrna\_for\_ukatp-1,\_complete\_cds\_  
d63485\_2710-3196,mrna\_for\_kiaa0151\_gene,\_complete\_cds\_  
d85939\_746-1037,mrna\_for\_p97\_homologous\_protein,\_complete\_cds\_  
d87012cds\_1986-2226:in\_fullsequence,\_34522-  
34687,(lambda)\_dna\_for\_immunoglobulin\_light\_chain  
d87432\_5731-6253,mrna\_for\_kiaa0245\_gene,\_complete\_cds\_  
d90279\_5154-5590,mrna\_for\_collagen\_alpha\_1(v)\_chain,\_complete\_cds\_  
hg2442-ht2538\_at\_hg2442-  
ht2538\_tropomyosin,\_alpha,\_muscle,\_altsplice\_2,\_skeletal\_muscle\_(fibroblast)  
hg2686-ht2782\_at\_hg2686-ht2782\_ryanodine\_receptor\_  
hg2992-ht5186\_at\_hg2992-ht5186\_beta-  
hexosaminidase,\_alpha\_polypeptide,\_abnormal\_splice\_mutation  
hg3175-ht3352\_at\_hg3175-ht3352\_carcinoembryonic\_antigen  
hg3254-ht3431\_at\_hg3254-ht3431\_phosphatidylinositol\_3-kinase\_p110,\_beta\_isoform  
j00220\_cds4\_at\_j00220\_j00220,not\_in\_gb\_record,ig\_germline\_h-chain\_g-e-  
a\_region\_a:\_gamma-3\_5'\_flank,i  
j02854\_531-1089,20-kda\_myosin\_light\_chain\_(mlc-2)\_mrna,\_complete\_cds\_  
j03810\_2627-3113,liver\_glucose\_transporter-like\_protein\_(glut2),\_complete\_cds\_  
all\_k03430\_414-853,complement\_c1q\_b-chain\_gene\_  
104751\_1994-2510,cytochrome\_p-450\_4a\_(cyp4a)\_mrna,\_complete\_cds\_  
110378\_1130-1640,(clone\_ctg-b43a)\_mrna\_sequence  
110955cds#1\_184-560:in\_reversesequence,\_394-  
467,\_carbonic\_anhydrase\_iv\_gene\_extracted\_fromcarbonic\_a  
111369\_756-  
1296,protocadherin\_42\_mrna,\_3'\_end\_of\_cds\_for\_alternative\_splicing\_pc42-8\_  
all\_111672\_3552-  
3579,kruppel\_related\_zinc\_finger\_protein\_(htf10)\_mrna,\_complete\_cds,kruppel\_rel  
ated\_  
113329exon\_434-938,iduronate-2-sulfatase\_(ids)\_gene\_  
114565exon#9\_5-359,peripherin\_(prph)\_gene\_exons\_1-9,\_complete\_cds\_  
115409\_1227-1719,(clone\_g7)\_von\_hippel-  
lindau\_disease\_tumor\_suppressor\_mrna\_sequence  
120815\_2031-2445,s\_protein\_mrna,\_complete\_cds\_  
129376\_616-1126,(clone\_3.8-1)\_mhc\_i\_mrna\_fragment\_



133930\_1504-2054,cd24\_signal\_transducer\_mrna,\_complete\_cds\_and\_3'\_region  
 142324cds\_530-944,(clone\_gpcr\_w)\_g\_protein-  
 linked\_receptor\_gene\_(gpcr)\_gene,\_5'\_end\_of\_cds/gb=142324  
 142450mrna\_1022-  
 1448,pyruvate\_dehydrogenase\_kinase\_isoenzyme(pdk1)\_mrna,\_complete\_cds  
 147125mrna\_1504-2055,(chromosome\_x)\_glypican\_(gpc3)\_mrna,\_complete\_cds  
 148211cds\_31-151:in\_reversesequence,\_1691-  
 1775,angiotensin\_ii\_receptor\_gene,\_complete\_cds  
 149173cds\_13-116,ocp2\_gene,\_partial\_cds/gb=149173/\_ntype=dna/\_annot=cds  
 m14539\_3238-3730,factor\_xiii\_subunit\_a\_mrna,\_3'\_end  
 m19507mrna#4\_2620-3184,myeloperoxidase\_mrna,\_complete\_cds  
 m20778\_401-974,\_homo\_sapien,\_alpha-3\_(vi)\_collagen  
 m20786exon\_630-1146,alpha-2-plasmin\_inhibitor\_gene\_  
 all\_m21494\_152-645:in\_m21494cds\_888-  
 967,muscle\_creatine\_kinase\_gene\_(ckmm),\_5'\_flank  
 all\_m22919\_3226-3665,\_mlc\_gene\_(non-  
 muscle\_myosin\_light\_chain)\_extracted\_fromnonmuscle/smooth\_muscle  
 m37755exon\_15-256:in\_reversesequence,\_280-453:not\_in\_gb\_record,pregnancy-  
 specific\_beta-1-glycoprotei  
 m58583\_989-1487,precerebellin\_and\_cerebellin\_mrna,\_complete\_cds  
 m64347\_3336-3720,novel\_growth\_factor\_receptor\_mrna,\_3'\_cds\_  
 m74297\_1161-1551,homeobox\_1.4\_protein\_mrna,\_complete\_cds\_  
 m75106\_1138-1618,prepro-plasma\_carboxypeptidase\_b\_mrna,\_complete\_cds\_  
 m77810\_2324-2585,transcription\_factor\_gata-2\_(gata-2)\_mrna,\_complete\_cds\_  
 m82827mrna\_2078-2228,fusion\_protein\_mrna,\_complete\_cds.  
 m91467\_1375-1861,serotonin\_receptor\_(5ht1e)\_mrna,\_complete\_cds\_  
 m95929\_1015-1399,homeobox\_protein\_(phox1)\_mrna,\_3'\_end\_  
 s76638\_2553-3003,\_p50-nf-  
 kappa\_b\_homolog\_[human,\_peripheral\_blood\_t\_cells,\_mrna,\_3113\_ntl]  
 s82240\_274-  
 802,\_rhoe=26\_kda\_gtpase\_homolog\_[human,\_hela\_cell\_line,\_mrna,\_833\_ntl]  
 u03090\_457-955,ca2+-dependent\_phospholipase\_a2\_mrna,\_complete\_cds  
 all\_u04325\_3581-3780,\_psg11\_gene\_(pregnancy-specific\_beta-1-glycoproteinc-  
 a\_domain)\_extracted\_frompr  
 u07969\_2956-3259,intestinal\_peptide-associated\_transporter\_hpt-  
 1\_mrna,\_complete\_cds  
 u08438exon#15\_1106-1571,beta-adrenergic\_receptor\_kinase\_(adrbk1)\_gene  
 u17034\_4182-4584,soluble\_pla2\_receptor\_mrna,\_complete\_cds  
 u18550exon\_1402-1954,gpr3\_g\_protein-coupled\_receptor\_gene,\_complete\_cds  
 u22961\_2627-3194,mrna\_clone\_with\_similarity\_to\_l-glycerol-3-  
 phosphate:nad\_oxidoreductase\_and\_albumin  
 u24685cds\_123-336:in\_reversesequence,\_420-447,anti-  
 b\_cell\_autoantibody\_igm\_heavy\_chain\_variable\_v-d-  
 u40152\_2541-3103,origin\_recognition\_complex(hsorc1)\_mrna,\_complete\_cds  
 u55766\_535-1081,rev\_interacting\_protein\_rip-1\_mrna,\_complete\_cds\_  
 u64805\_1668-2218,brca1-delta11b\_(brca1)\_mrna,\_complete\_cds/gb=u64805/\_ntype=rna  
 u65011\_1625-  
 2039,preferentially\_expressed\_antigen\_of\_melanoma\_(prame)\_mrna,\_complete\_cds.  
 u69961\_1565-1997,solurshin\_(rgs)\_mrna,\_complete\_cds  
 u70136\_4546-4957,megakaryocyte\_stimulating\_factor\_mrna,\_complete\_cds\_  
 u71598\_444-792,zinc\_finger\_protein\_zfp2\_(zf2)\_mrna,\_partial\_cds  
 u88726\_55-433,symplekin\_mrna,\_partial\_cds/gb=u88726/\_ntype=rna\_  
 u90919\_1637-2129,clones\_23667\_and\_23775\_zinc\_finger\_protein\_mrna,\_complete\_cds\_  
 all\_x05276\_1466-2031,mrna\_for\_fibroblast\_tropomyosin\_tm30\_(pl)  
 all\_x05309\_4846-5240,mrna\_for\_c3b/c4b\_receptor\_(cr1)\_f\_allotype  
 x14046cds\_479-809:in\_reversesequence,\_944-1082,mrna\_for\_leukocyte\_antigen\_cd37  
 all\_x14362\_1961-2370,cr1\_mrna\_for\_c3b/c4b\_receptor\_secreted\_form

x14675cds\_31-163,bcr-abl\_mrna\_5'\_fragment\_(clone\_3c)/gb=x14675\_/ntype=rna  
 x55448exon#22\_131-683,\_g6pd\_gene\_(glucose-6-phosphate\_dehydrogenase)\_extracted\_fromg6pd\_gene\_for\_glu  
 x61373mrna#1\_3441-3693:not\_in\_gb\_record,microtubule-associated\_protein\_tau\_(tau)\_gene,\_alternatively  
 all\_x62078\_1997-2400,mrna\_for\_gm2\_activator\_protein  
 x68264mrna\_3300-3552,\_muc18\_gene\_(melanoma\_associated\_glycoprotein)\_extracted\_frommgf\_gene\_exons\_1&2  
 x77567cds\_853-1215:in\_reversesequence,\_1354-1518,mrna\_for\_insp3\_5-phosphatase\_all\_x77753\_2390-2787,trop-2\_gene  
 all\_x83492\_418-500,mrna\_for\_fas/apo-1\_(clone\_pcrtm11-fasdelta(4,7))/gb=x83492\_/ntype=rna,mrna\_for\_fa  
 x85740mrna\_1112-1604,mrna\_for\_c-c\_chemokine\_receptor-4\_x87211cds\_486-1041,mrna\_for\_anion\_exchange\_protein/gb=x87211\_/ntype=rna  
 all\_x90846\_2935-3407,mrna\_for\_mixed\_lineage\_kinase\_2,mrna\_for\_mixed\_lineage\_kinase\_2  
 x97303mrna\_11-93,mrna\_for\_ptg-12\_protein/gb=x97303\_/ntype=rna  
 x98260cds\_1280-1706,mrna\_for\_m-phase\_phosphoprotein,\_mpp11\_y08134cds\_1026-1362:in\_reversesequence,\_1531-1573,mrna\_for\_asm-like\_phosphodiesterase\_3b  
 all\_y08223\_2471-2952,mfh-1\_gene  
 z11518mrna\_1546-2066,mrna\_for\_histidyl-trna\_synthetase\_z26256exon\_64-364,isoformgene\_for\_l-type\_calcium\_channel,\_exon/gb=z26256\_/ntype=dna\_/annot=exon

## Metagene 482

107515\_253-790,heterochromatin\_protein\_homologue\_(hp1)\_mrna,\_complete\_cds  
 136051exon#6\_678-1086,thrombopoietin\_gene,\_complete\_cds  
 u04811\_1931-2375,trophinin\_mrna,\_complete\_cds  
 u09646exon\_358-874,carnitine\_palmitoyltransferase\_ii\_precursor\_(cpt1)\_gene\_u11701\_1316-1862,lim-homeobox\_domain\_protein\_(hlh-2)\_mrna,\_complete\_cds  
 u23946\_1986-2496,putative\_tumor\_suppressor\_(luca15)\_mrna,\_complete\_cds\_u42359mrna\_1197-1217,n33\_protein\_form(n33)\_gene,\_exonand\_complete\_cds/gb=u42359\_/ntype=dna\_/annot=exon  
 u49973cds#2\_37-367,\_orf1;\_mer37;\_putative\_transposase\_similar\_to\_pogo\_element\_fromtigger1\_transposab  
 u79263\_995-1535,clone\_23760\_mrna,\_partial\_cds  
 u86529\_584-1130,glutathione\_transferase\_zeta(gstz1)\_mrna,\_complete\_cds/gb=u86529\_/ntype=rna  
 all\_x52943\_2163-2728,mrna\_for\_atf-a\_transcription\_factor\_x98266cds#2\_1028-1340:in\_reversesequence,\_2103-2223,\_ligase-like\_protein\_gene\_extracted\_frommrna\_for  
 z83802\_133-511,mrna\_for\_axonemal\_dynein\_heavy\_chain\_(partial,\_id\_hdhc3)

## Metagene 358

hg2841-ht2970\_at\_hg2841-ht2970\_albumin,\_altsplice\_5

u12259cds\_492-808:in\_reversesequence,\_16275-  
16368,paired\_box\_homeotic\_protein\_(pax3)\_gene  
all\_y07701\_3290-3651,mrna\_for\_aminopeptidase\_

Metagene 305

d17357exon\_25-295,activin\_beta-  
a\_gene\_regulatory\_sequence\_of\_5'\_upstream\_region/gb=d17357\_/ntype=dn  
d28124\_1346-1886,mrna\_for\_unknown\_product,\_complete\_cds  
d86425\_4224-4776,osteoblast\_mrna\_for\_osteonidogen,\_complete\_cds  
l12350mrna\_5247-5721,thrombospondin(thbs2)\_mrna,\_complete\_cds\_  
l13923\_9109-9601,fibrillin\_mrna,\_complete\_cds\_  
m12125mrna\_671-1013,fibroblast\_muscle-type\_tropomyosin\_mrna,\_complete\_cds  
m83186\_103-  
316,cytochrome\_c\_oxidase\_subunit\_viia\_(cox7a)\_muscle\_isoform\_mrna,\_complete\_cds  
-  
m92934mrna\_1492-2026,connective\_tissue\_growth\_factor,\_complete\_cds\_  
u09278\_2285-2735,fibroblast\_activation\_protein\_mrna,\_complete\_cds  
u19718\_479-947,microfibril-associated\_glycoprotein\_(mfap2)\_mrna,\_complete\_cds  
u30521\_1621-1951,p311\_hum\_-3.1\_mrna,\_complete\_cds  
u89942\_2867-3383,lysyl\_oxidase-related\_protein\_(ws9-14)\_mrna,\_complete\_cds\_  
x02419mrna\_1754-2210,upa\_gene\_  
x57579exon\_545-840:in\_reversesequence,\_1392-1555,activin\_beta-  
a\_subunit\_(exon\_2)  
all\_x63759\_1241-1752,htnp2\_gene\_for\_transition\_protein\_2\_

Metagene 197

ab000114\_1818-2208,mrna\_for\_osteomodulin,\_complete\_cds\_  
ab000905\_1045-1253,dna\_for\_h4\_histone,\_complete\_cds  
af005043\_3474-3990,poly(adp-  
ribose)\_glycohydrolase\_(hparg)\_mrna,\_complete\_cds/gb=af005043\_/ntype=rna  
d42108\_4054-4414,mrna\_for\_phospholipase\_complete\_cds  
d50927\_3955-4411,mrna\_for\_kiaa0137\_gene,\_complete\_cds  
all\_d87023\_19383-  
19642,\_j1\_gene\_extracted\_from(lambda)\_dna\_for\_immunoglobulin\_light\_chain\_  
hg3231-ht3408\_at\_hg3231-ht3408\_protease\_receptor-1,\_effector\_cell  
l40384mrna\_22-  
487,thyroid\_receptor\_interactor\_(trip13)\_mrna,\_partial\_cds/gb=l40384\_/ntype=rna  
-  
m60052\_2004-2280,histidine-  
rich\_calcium\_binding\_protein\_(hrc)\_mrna,\_complete\_cds\_  
m60315\_2334-2838,transforming\_growth\_factor-beta\_(tgf-beta)\_mrna,\_complete\_cds\_  
u09368\_1908-2298,zinc\_finger\_protein\_znf140  
u36621exon\_17-536,y-chromosome\_rna\_recognition\_motif\_protein\_(yrrm)\_gene  
u47414\_1449-1959,cyclin\_g2\_mrna,\_complete\_cds  
u64198\_3571-3955,il-12\_receptor\_beta2\_mrna,\_complete\_cds\_  
y09443\_1545-1935,mrna\_for\_alkyl-dihydroxyacetonephosphate\_synthase\_precursor\_  
all\_z17240\_956-1014,for\_mrna\_encoding\_hmg2b\_

Metagene 386

ab000584\_618-1032,mrna\_for\_tgf-beta\_superfamily\_protein,\_complete\_cds  
 ab002366\_5112-5616,mrna\_for\_kiaa0368\_gene,\_partial\_cds/gb=ab002366\_/ntype=rna  
 ab004884\_2491-2995,mrna\_for\_pku-alpha,\_partial\_cds/gb=ab004884\_/ntype=rna  
 d10995cds\_828-1128:in\_reversesequence,\_1245-  
 1401,gene\_for\_serotonin\_1b\_receptor,\_complete\_cds\_  
 d28588\_2747-3263,mrna\_for\_kiaa0048\_gene,\_complete\_cds\_  
 d63813\_1154-1676,mrna\_for\_rod\_photoreceptor\_protein,\_complete\_cds\_  
 hg2730-ht2828\_s\_at\_hg2730-  
 ht2828\_fibrinogen,\_a\_alpha\_polypeptide,\_altsplce\_3,\_e\_  
 j05428\_1624-1800,3,4-catechol\_estrogen\_udp-  
 glucuronosyltransferase\_mrna,\_complete\_cds\_  
 l27080cds\_538-946:in\_reversesequence,\_1159-  
 1207,melanocortinreceptor\_(mc5r)\_gene,\_complete\_cds\_  
 m34192mrna\_1406-1826,isovaleryl-coa\_dehydrogenase\_(ivd)\_mrna,\_complete\_cds\_  
 m37075\_at\_m37075\_m37075,not\_in\_gb\_record,embryonic/atrial\_myosin\_light\_chain\_(m  
 lc-1-emb/a\_isoform)\_g  
 m58285\_3356-3788,membrane-associated\_protein\_(hem-1)\_mrna,\_complete\_cds\_  
 m93143\_461-499,plasminogen-like\_protein\_(plgl)\_mrna,\_complete\_cds\_  
 m93415\_1865-2303,activin\_type\_ii\_receptor\_mrna,\_complete\_cds\_  
 m97496\_25-409,guanylin\_mrna,\_complete\_cds\_  
 u03858\_806-1040,flt3\_ligand\_mrna,\_complete\_cds\_  
 u09579\_1537-2041,melanoma\_differentiation\_associated\_(mda-6)\_mrna,\_complete\_cds\_  
 u10690exon#3\_934-1499,mage-5b\_antigen\_(mage5b)\_gene,\_complete\_cds\_  
 u11863\_1914-1974,clone\_hp-  
 dao2\_diamine\_oxidase,\_copper/topa\_quinone\_containing\_mrna,\_complete\_cds\_  
 u15197\_74-363,histo-blood\_group\_abo\_protein\_mrna,\_partial\_3'\_utr\_sequence  
 u17838\_7401-7899,zinc\_finger\_protein\_riz\_mrna,\_complete\_cds\_  
 u55853\_1917-2433,130\_kd\_golgi-  
 localized\_phosphoprotein\_(gpp130)\_mrna,\_complete\_cds\_  
 all\_x83127\_1494-1624,mrna\_for\_voltage\_gated\_potassium\_channels,\_beta\_subunit\_  
 x95654cds\_2682-2862:in\_reversesequence,\_3022-3202,mrna\_for\_scpl1\_protein\_  
 all\_x98253\_1221-1334,znf183\_gene/gb=x98253\_/ntype=rna

## Metagene 294

a28102cds\_986-1442:in\_reversesequence,\_1546-1582,gabaa\_receptor\_alpha-  
 3\_subunit.  
 m17446mrna\_648-  
 1186,kaposi\_sarcoma\_oncogene\_fibroblast\_growth\_factor\_mrna,\_complete\_cds\_  
 m98528utr#1\_543-1101,neuron-specific\_protein\_gene,\_last\_exon,\_clone\_d4s234  
 u20816mrna#1\_258-795,nuclear\_factor\_kappa-b2\_(nf-  
 kb2)\_gene,\_partial\_cds/gb=u20816\_/ntype=dna\_/annot=  
 all\_u31799\_528-683:in\_u31799cds\_1746-1777,melanocyte\_protein\_pm1gene\_  
 all\_x87870\_2045-2289,mrna\_for\_hepatocyte\_nuclear\_factor\_4a\_

## Metagene 238

m15856mrna#1\_2984-3488,lipoprotein\_lipase\_mrna,\_complete\_cds\_  
 m23575\_1395-1933,pregnancy-specific\_beta-1\_glycoprotein\_mrna,\_complete\_cds\_  
 m60503cds\_2942-3212:in\_reversesequence,\_1915-  
 2047,profilaggrin\_gene,\_partial\_cds

s81294\_4-  
 160,\_dcc=deleted\_in\_colorectal\_cancer\_{alternatively\_spliced,\_exon\_1a}\_[human,\_  
 brain\_tumor,  
 all\_s85963\_4324-4544,\_hirs-1=rat\_insulin\_receptor\_substrate-  
 1\_homolog\_[human,\_cell\_line\_focus,\_genom

Metagene 200

m24351exon\_248-404,\_pthlh\_gene\_(parathyroid\_hormone-  
 like\_protein\_a)\_extracted\_fromparathyroid\_hormon  
 m31210\_2258-2708,endothelial\_differentiation\_protein\_(edg-  
 1)\_gene\_mrna,\_complete\_cds\_  
 m55024\_2-  
 331,cell\_surface\_glycoprotein\_p3.58\_mrna,\_partial\_cds/gb=m55024\_/ntype=rna  
 m58459\_295-829,ribosomal\_protein\_(rps4y)\_isoform\_mrna,\_complete\_cds  
 m60626mrna\_1283-1577,n-formylpeptide\_receptor\_(fm1p-r98)\_mrna,\_complete\_cds  
 m60724\_1847-2321,p70\_ribosomal\_s6\_kinase\_alpha-i\_mrna,\_complete\_cds  
 s72024cds\_13-437,\_eif-  
 5a=eukaryotic\_initiation\_factor\_5a\_{clone\_cos\_9.1}\_[human,\_placenta,\_genomic,\_  
 u13695cds\_2418-2754:in\_reversesequence,\_2858-  
 2954,homolog\_of\_yeast\_mutl\_(hpms1)\_gene,\_complete\_cds  
 u38896\_1411-1921,zinc\_finger\_protein\_c2h2-171\_mrna,\_complete\_cds\_  
 x59434mrna\_631-1129,rohu\_mrna\_for\_rhodanese  
 all\_x71661\_2263-2768,ergic-53\_mrna\_  
 all\_x96586\_2898-3343,mrna\_for\_fan\_protein

Metagene 364

l31573\_1849-2347,sulfite\_oxidase\_mrna,\_complete\_cds  
 m11973\_cds1\_at\_m11973\_m11973,not\_in\_gb\_record,gamma-b-crystallin\_gene\_(gamma\_1-  
 2)\_  
 m29474mrna\_5986-6490,recombination\_activating\_protein\_(rag-  
 1)\_gene,\_complete\_cds\_  
 u08471\_492-780,folate\_receptormrna,\_complete\_cds  
 u57352\_2094-2646,sodium\_channel(hbnac1)\_mrna,\_complete\_cds  
 u76388\_1630-1842,steroidogenic\_factor\_mrna,\_complete\_cds\_  
 all\_z22536\_1732-2333,alk-4\_mrna,\_complete\_cds\_

Metagene 343

d25217\_2864-3410,mrna\_for\_kiaa0027\_gene,\_partial\_cds\_  
 d45371mrna\_4040-4464,apml\_mrna\_for\_gs3109\_(novel\_adipose\_specific\_collagen-  
 like\_factor),\_complete\_cd  
 d85815cds\_282-564:in\_reversesequence,\_753-879,dna\_for\_rhoHP1,\_complete\_cds  
 hg1205-ht1205\_at\_hg1205-ht1205\_collagen,\_type\_iv,\_alpha\_2,\_n-terminus  
 hg4157-ht4427\_at\_hg4157-ht4427\_glycinamide\_ribonucleotide\_synthetase\_  
 hg732-ht732\_at\_hg732-ht732\_serum\_amyloid\_a1  
 j03600\_2058-2364,lipoxygenase\_mrna,\_complete\_cds\_  
 k01911mrna\_85-481,neuropeptide\_y\_(npY)\_mrna,\_complete\_cds  
 l05148\_1890-2388,protein\_tyrosine\_kinase\_related\_mrna\_sequence\_  
 l05779\_1535-2069,cytosolic\_epoxide\_hydrolase\_mrna,\_complete\_cds

l10123\_3572-4100,surfactant\_protein\_a\_mrna,\_complete\_cds  
 l19297\_602-1034,nuclear-  
 encoded\_mitochondrial\_carbonic\_anhydrase\_(ca5)\_mrna,\_complete\_cds  
 l29277\_2204-2762,dna-binding\_protein\_(aprf)\_mrna,\_complete\_cds  
 l38707mrna\_2405-2951,diacylglycerol\_kinase\_(dagk)\_mrna,\_complete\_cds.  
 l41668\_887-1433,udp-galactoseepimerase\_(gale)\_gene,\_complete\_cds  
 l48516\_473-1013,paraoxonase\_(pon3)\_mrna,\_3'\_end\_of\_cds  
 m13829\_603-1029,putative\_raf\_related\_protein\_(pks/a-raf)\_mrna,\_partial\_cds\_  
 m14565mrna\_1262-1712,cholesterol\_side-  
 chain\_cleavage\_enzyme\_p450scc\_mrna,\_complete\_cds\_  
 m20777\_434-956,\_homo\_sapiens,\_alpha-2\_(vi)\_collagen\_  
 m29696\_1063-1597,interleukin-7\_receptor\_(il-7)\_mrna,\_complete\_cds  
 m37271cds\_361-672:in\_reversesequence,\_2722-2909,cd7\_antigen\_gene,\_exons\_4-jan\_  
 m54951mrna\_438-852,atrial\_natriuretic\_factor\_gene  
 all\_m59829\_2774-3117,mhc\_iii\_hsp70-hom\_gene\_(hla),\_complete\_cds  
 m60298\_2117-  
 2615,erythrocyte\_membrane\_protein\_band\_4.2\_(epb42)\_mrna,\_complete\_cds  
 m68519mrna\_1542-1916,pulmonary\_surfactant-associated\_protein\_sp-  
 a\_(sftpl)\_gene,\_complete\_cds  
 m69197mrna#1\_611-1184,\_hpr\_fromhaptoglobin\_and\_haptoglobin-  
 related\_protein\_(hp\_and\_hpr)\_genes,\_compl  
 m74091\_925-1453,cyclin\_mrna  
 m80629\_1678-2170,cdc2-related\_protein\_kinase\_(ched)\_mrna,\_complete\_cds\_  
 m89957\_675-  
 1095,immunoglobulin\_superfamily\_member\_b\_cell\_receptor\_complex\_cell\_surface\_gly  
 coprotein\_  
 m93405\_888-1374,methylmalonate\_semialdehyde\_dehydrogenase\_gene,\_complete\_cds\_  
 m93650\_1119-1599,paired\_box\_gene\_(pax6)\_homologue,\_complete\_cds  
 m99701\_627-1137,(pp21)\_mrna,\_complete\_cds\_  
 s69265\_1402-1943,\_neuron-specific\_rna\_recognition\_motifs\_(rrms)-  
 containing\_protein\_[human,\_hippocamp  
 s75989\_1492-1948,\_gamma-  
 aminobutyric\_acid\_transporter\_type[human,\_fetal\_brain,\_mrna,\_1991\_nt]  
 s76475\_2144-2659,\_trkc\_[human,\_brain,\_mrna,\_2715\_nt]  
 u07358\_2794-3310,protein\_kinase\_(zpk)\_mrna,\_complete\_cds\_  
 u09877\_3381-3849,helicase-like\_protein\_(hlp)\_mrna,\_complete\_cds  
 u10991\_6267-6789,g2\_protein\_mrna,\_partial\_cds  
 u16031\_2451-2943,transcription\_factor\_il-4\_stat\_mrna,\_complete\_cds\_  
 u26398\_2628-3168,inositol\_polyphosphate\_4-phosphatase\_mrna,\_complete\_cds\_  
 u26403\_991-1495,receptor\_tyrosine\_kinase\_ligand\_lerk-  
 7\_precursor\_(eplg7)\_mrna,\_complete\_cds  
 u30930\_1877-2423,udp-  
 galactose\_ceramide\_galactosyl\_transferase\_(cgt)\_mrna,\_complete\_cds  
 u43431\_3166-3712,dna\_topoisomerase\_iii\_mrna,\_complete\_cds  
 u52840\_7503-7755,cri-du-chat\_region\_mrna,\_clone\_csa1\_  
 u64998cds\_61-  
 361,ribonuclease\_k6\_precursor\_gene,\_complete\_cds/gb=u64998\_/ntype=dna\_/annot=cd  
 s  
 u82535\_1485-2019,fatty\_acid\_amide\_hydrolase\_mrna,\_complete\_cds.  
 all\_v00565\_2218-  
 2422,gene\_for\_preproinsulin,\_from\_chromosomeincludes\_a\_highly\_polymorphic\_regio  
 n\_ups  
 x04445mrna\_521-1075,inha\_gene\_exon(and\_joined\_cds)\_  
 x06985mrna\_943-1393,mrna\_for\_heme\_oxygenase  
 x07732mrna#2\_991-1543,hepatoma\_mrna\_for\_serine\_protease\_hepsin\_  
 all\_x52773\_1343-1866,mrna\_for\_retinoic\_acid\_receptor-like\_protein  
 x60188mrna\_1360-1741,erk1\_mrna\_for\_protein\_serine/threonine\_kinase\_

x60957cds\_3066-3378:in\_reversesequence,\_3432-  
 3678,tie\_mrna\_for\_putative\_receptor\_tyrosine\_kinase\_  
 x86779cds\_1174-1606:in\_reversesequence,\_1741,mrna\_for\_fast\_kinase\_  
 x99961cds\_55-409,mrna\_for\_novel\_protein/gb=x99961\_/ntype=rna\_  
 z26317cds\_2904-3324:in\_reversesequence,\_3443-3491,mrna\_for\_desmoglein\_2\_

Metagene 174

d89289\_1431-1947,mrna\_for\_n-acetyl-beta-d-glucosaminide,\_complete\_cds  
 l05188cds\_2-194:in\_reversesequence,\_281-342,small\_proline-  
 rich\_protein(sprrr2b)\_gene,\_complete\_cds\_  
 m74509\_7730-8246,endogenous\_retrovirus\_type\_c\_oncovirus\_sequence.  
 s70004\_2347-2779,\_glycogen\_synthase\_[human,\_liver,\_mrna,\_2912\_nt]\_  
 u65416mrna\_1983-2316,mhc\_i\_molecule\_(micb)\_gene,\_complete\_cds\_  
 u79285\_892-1402,clone\_23828\_mrna\_sequence

Metagene 171

hg1111-ht1111\_at\_hg1111-ht1111\_ras-like\_protein\_tc21\_  
 k02100mrna\_983-  
 1421,ornithine\_transcarbamylase\_(otc)\_mrna,\_complete\_coding\_sequence  
 u08015mrna\_2388-2700,nf-atc\_mrna,\_complete\_cds\_  
 u09413\_1957-2389,zinc\_finger\_protein\_znf135\_mrna,\_complete\_cds\_  
 u70862\_1029-1248,nuclear\_factor\_i\_b3\_mrna,\_complete\_cds\_  
 all\_x01059\_941-  
 1512,placenta\_mrna\_for\_luteinizing\_hormone\_releasing\_hormone\_precursor\_(lhrh)\_  
 all\_x66436\_1427-1980,hsrl\_mrna\_(partial)\_  
 x80507cds\_1020-1314:in\_reversesequence,\_1624-1828,yap65\_mrna\_  
 all\_x99141\_1411-1715,mrna\_for\_hair\_keratin,\_hbb3\_

Metagene 51

d13988\_897-1353,rab\_gdi\_mrna,\_complete\_cds\_  
 d31763\_5458-5968,mrna\_for\_kiaa0065\_gene,\_partial\_cds\_  
 hg1747-ht1764\_s\_at\_hg1747-ht1764\_proto-oncogene\_met,\_altsplice\_form\_2  
 hg4074-ht4344\_at\_hg4074-ht4344\_rad2  
 j05614mrna\_4-  
 41,proliferating\_cell\_nuclear\_antigen\_(pcna)\_gene,\_promoter\_region/gb=j05614\_/n  
 type=dna  
 l23959\_971-1415,e2f-related\_transcription\_factor\_(dp-1)\_mrna,\_complete\_cds  
 l40386mrna\_657-1122,dp-2\_mrna,\_complete\_cds  
 l40403mrna\_1725-2277,(clone\_zap3)\_mrna,\_3'\_end\_of\_cds\_  
 m28209\_158-680,gtp-binding\_protein\_(rab1)\_mrna,\_complete\_cds  
 m37104\_13-  
 421,mitochondrial\_atpase\_coupling\_factorsubunit\_(atp5a)\_mrna,\_complete\_cds  
 m37583mrna\_368-824,histone\_(h2a.z)\_mrna,\_complete\_cds  
 m58525\_603-933,catechol-o-methyltransferase\_(comt)\_mrna,\_complete\_cds\_  
 m81118exon#2\_669-1149,alcohol\_dehydrogenase\_chi\_polypeptide\_(adh5)\_gene  
 m83738\_3328-3883,protein-tyrosine\_phosphatase\_(ptpase\_meg2)\_mrna,\_complete\_cds\_  
 m86737\_2236-2776,high\_mobility\_group\_box\_(ssrp1)\_mrna,\_complete\_cds\_  
 m92439\_4255-4633,leucine-rich\_protein\_mrna,\_complete\_cds\_

m94630\_832-1027,hnrnp-c\_like\_protein\_mrna,\_complete\_cds\_  
 s83364\_19-325,\_putative\_rab5-interacting\_protein\_{clone\_11-  
 57}\_[human,\_hela\_cells,\_mrna\_partial,\_366  
 s85655\_435-969,\_prohibitin\_[human,\_mrna,\_1043\_nt]\_  
 u25182\_350-860,antioxidant\_enzyme\_ace37-2\_mrna,\_complete\_cds\_  
 u41387\_2693-3263,gu\_protein\_mrna,\_partial\_cds  
 u56833\_940-1468,vhl\_binding\_protein-1\_(vbp-1)\_mrna,\_partial\_cds  
 u57627\_4598-  
 5078,fetal\_brain\_oculocerebrorenal\_syndrome\_(ocr11)\_mrna,\_complete\_cds\_  
 u65410\_961-1459,mad2\_(hsmad2)\_mrna,\_complete\_cds\_  
 u83843\_725-1145,hiv-1\_nef\_interacting\_protein\_(nip7-  
 1)\_mrna,\_partial\_cds/gb=u83843/\_ntype=rna  
 all\_x92396\_1999-2480,mrna\_for\_novel\_gene\_in\_xq28\_region  
 x94754cds\_2213-2645:in\_reversesequence,\_2712-2730,mrna\_for\_yeast\_methionyl-  
 trna\_synthetase\_homologue  
 all\_x99585\_193-608,mrna\_for\_smt3b\_protein

## Metagene 19

hg721-ht4827\_s\_at\_hg721-  
 ht4827\_placental\_protein\_14,\_endometrial\_alphaglobulin,\_altsplce\_2\_  
 l19593mrna\_2261-2747:in\_reversesequence,\_2765-  
 2771,interleukinreceptor\_beta\_(il8rb)\_mrna,\_complete\_c  
 s34389\_1166-1586,\_heme\_oxygenase-2\_[human,\_kidney,\_mrna,\_1627\_nt]\_  
 u19523\_2299-2851,gtp\_cyclohydrolase\_i\_mrna,\_complete\_cds\_  
 all\_x05232\_1530-1771,mrna\_for\_stromelysin  
 x12662mrna\_936-  
 1398,arginase\_gene\_exonand\_flanking\_regions\_(ec\_3.5.3.1)\_(and\_joined\_cds)\_  
 all\_x57809\_309-  
 474,rearranged\_immunoglobulin\_lambda\_light\_chain\_mrna,rearranged\_immunoglobulin  
 \_lambd  
 x72308\_419-842,mcp-3\_mrna\_for\_monocyte\_chemotactic\_protein-3\_  
 y00081cds\_293-588:in\_reversesequence,\_5486-5706,(bsf-  
 2/il6)\_gene\_for\_b\_cell\_stimulatory\_factor-2  
 y11306mrna\_1993-2395,\_htcf-4\_gene\_extracted\_frommrna\_for\_beta\_catenin/tcf-4\_

## Metagene 370

l20971\_3698-3992,phosphodiesterase\_mrna,\_complete\_cds  
 u03272\_9619-10081,fibrillin-2\_mrna,\_complete\_cds\_  
 u07802exon#2\_2748-3228,tis11d\_gene,\_complete\_cds\_  
 all\_x78565\_6971-7512,mrna\_for\_tenascin-c,\_7560bp\_

## Metagene 312

d31716\_4264-4831,mrna\_for\_gc\_box\_bindig\_protein,\_complete\_cds  
 l14430\_at\_l14430\_l14430,not\_in\_gb\_record,udp-  
 glucose\_pyrophosphorylase\_mrna,\_complete\_cds\_and\_flanki  
 u26591\_1640-  
 2108,clone\_is10\_diabetes\_mellitus\_type\_i\_autoantigen\_(icap69)\_mrna,\_complete\_cd  
 s\_



u33837\_13803-14343, glycoprotein\_receptor\_gp330\_precursor, \_mrna, \_complete\_cds\_  
u33880mrna\_189-  
240, betaintegrin\_isoform\_d\_(itgb1)\_gene, \_partial\_cds/gb=u33880/\_ntype=dna/\_anno  
t=exon  
u62434\_1665-  
1787, nicotinic\_acetylcholine\_receptor\_alpha5\_subunit\_precursor, \_mrna, \_complete\_  
cds\_  
all\_x56199\_1025-1614, xist, \_coding\_sequence\_a\_mrna\_(locus\_dxs399e)  
x60382mrna\_2717-3149, coll10a1\_gene\_for\_collagen\_(alpha-1\_type\_x)\_  
z48520exon#5\_1-98:in\_reversesequence, \_154-  
163, xg\_mrna\_(clone\_race6)/gb=z48520/\_ntype=rna

Metagene 114

hg3928-ht4198\_s\_at\_hg3928-ht4198\_surfacant\_protein\_sp-a1\_delta\_  
l05597cds\_729-1071:in\_reversesequence, \_1307-  
1499, serotonin\_receptor\_gene, \_complete\_cds  
u76189\_49-355, extl3\_mrna, \_partial\_cds/gb=u76189/\_ntype=rna\_

Metagene 110

d13705\_1151-1722, mrna\_for\_fatty\_acids\_omega-hydroxylase\_(cytochrome\_p-  
450hkv), \_complete\_cds  
d16105\_2703-2979, mrna\_for\_leukocyte\_tyrosine\_kinase, \_complete\_cds  
d83017\_2365-2810, mrna\_for\_nel-related\_protein, \_complete\_cds  
hg2255-ht2344\_f\_at\_hg2255-  
ht2344\_phosphoribosyl\_pyrophosphate\_synthetase, \_subunit\_iii  
hg2797-ht2906\_s\_at\_hg2797-ht2906\_clathrin, \_light\_polypeptide\_altsplice\_2  
k03192\_566-964, cytochrome\_p-450\_mrna, \_partial  
m13058exon#3\_1-372, acidic\_proline-rich\_protein\_(prh2)\_gene, \_complete\_cds\_  
m13149\_1540-2008, histidine-rich\_glycoprotein\_mrna, \_complete\_cds  
all\_m29335\_62-94, mhc\_ii\_do-alpha\_mrna, \_partial\_cds, mhc\_ii\_do-  
alpha\_mrna, \_partial\_cds  
all\_m32879\_690-1129, steroid\_11-beta-hydroxylase\_(cyp11b1)\_gene, steroid\_11-beta-  
hydroxylase\_(cyp11b1)  
m33772mrna\_69-631, fast\_skeletal\_muscle\_troponin\_c\_gene\_  
m55513mrna\_2274-2767, potassium\_channel\_(hpcn1)\_mrna, \_complete\_cds  
m62303\_726-872, retinoic\_acid\_receptor-  
beta\_associated\_open\_reading\_frame, \_complete\_sequence  
m64269cds\_389-718:in\_reversesequence, \_7859-  
7876, mast\_cell\_chymase\_gene, \_complete\_cds  
m74587mrna\_953-1425, insulin-  
like\_growth\_factor\_binding\_protein\_(higfbp1)\_gene, \_complete\_cds\_  
m83652\_932-1457, complement\_component\_properdin\_mrna, \_complete\_cds\_  
s77576\_3-  
60, \_erv9\_reverse\_transcriptase\_homolog\_{clone\_rt18}\_[human, \_multiple\_sclerosis,  
\_brain\_plaqua  
u05012\_2204-2720, receptor\_tyrosine\_kinase\_trkc\_(ntrk3)\_mrna, \_complete\_cds  
u11862\_1844-2402, clone\_hp-dao1\_diamine\_oxidase, \_copper/topa\_quinone-  
containing\_mrna, \_complete\_cds  
u12140\_3433-3673, tyrosine\_kinase\_receptor\_p145trk-b\_(trk-b)\_mrna, \_complete\_cds\_  
u23850\_8177-8697, inositol\_1,4,5\_trisphosphate\_receptor\_type\_mrna, \_partial\_cds  
u24488\_2519-3042, tenascin-x\_(xa)\_mrna, \_complete\_cds

u25771\_1383-1821,adp-ribosylation\_factor\_mrna,\_complete\_cds  
 u52373\_1810-2355,serine/threonine\_kinase\_mnb\_(mnb)\_mrna,\_complete\_cds  
 u57623exon#1-4\_51-  
 240:in\_reversesequence,\_6798,fatty\_acid\_binding\_protein\_fabp\_gene,\_complete\_cds  
 \_  
 u80034\_1785-  
 2283,mitochondrial\_intermediate\_peptidase\_precursor\_(mipep)\_mrna,\_mitochondrial\_gene\_enc  
 u81599\_751-1273,homeodomain\_protein\_hoxb13\_mrna,\_complete\_cds  
 u86214\_1736-2000,fas-associated\_death\_domain\_protein\_interleukin-1b-converting\_enzymemrna,\_complete\_  
 u88898\_561-757,endogenous\_retroviral\_h\_protease/integrase-derived\_orf1\_mrna,\_complete\_cds,\_and\_putat  
 all\_x07618\_880-1388,mrna\_for\_cytochrome\_p450\_db1\_variant\_a\_  
 all\_x07730\_1535-1680,mrna\_for\_prostate\_specific\_antigen  
 all\_x14253\_1410-2003,mrna\_for\_cripto\_protein\_  
 all\_x66867\_1864-2066:in\_x66867cds#2\_310,\_max\_gene\_extracted\_frommax\_gene\_  
 x94628mrna\_952-1510,mecp-2\_gene\_  
 x99688\_3790-4270,mrna\_from\_tyl\_gene  
 all\_y08613\_599-1164,alternative\_3'\_utr\_of\_nup88\_mrna/gb=y08613\_/ntype=rna  
 z35227cds\_385-547:in\_reversesequence,\_1162-1318,ttf\_mrna\_for\_small\_g\_protein  
  
 Metagene 98

ab002559\_1302-1746,mrna\_for\_hunc18b2,\_complete\_cds\_  
 af006087\_237-777,arp2/3\_protein\_complex\_subunit\_p20-arc\_(arc20)\_mrna,\_complete\_cds/gb=af006087\_/ntyp  
 d10511cds\_860-1256:in\_reversesequence,\_165-  
 243,gene\_for\_mitochondrial\_acetoacetyl-coa\_thiolase  
 d26308\_241-691,mrna\_for\_nadph-flavin\_reductase,\_complete\_cds\_  
 d26598\_187-571,mrna\_for\_proteasome\_subunit\_hsc10-ii,\_complete\_cds  
 d31764\_1478-1982,mrna\_for\_kiaa0064\_gene,\_complete\_cds  
 d38047\_327-825,mrna\_for\_26s\_proteasome\_subunit\_p31,\_complete\_cds\_  
 d38751\_1539-1868:not\_in\_gb\_record,mrna\_for\_kid\_(kinesin-like\_dna\_binding\_protein),\_complete\_cds\_  
 d43947\_6379-6901,mrna\_for\_kiaa0100\_gene,\_complete\_cds  
 d50645\_502-1006,mrna\_for\_sdf2,\_complete\_cds  
 d85433\_109-439,murrl\_mrna,\_sequence/gb=d85433\_/ntype=rna\_  
 hg3638-ht3849\_s\_at\_hg3638-  
 ht3849\_amyloid\_beta\_(a4)\_precursor\_protein,\_altsplince\_2,\_a4(751)\_  
 j04444cds\_596-944:in\_reversesequence,\_3590-3740,cytochrome\_c-1\_gene,\_complete\_cds\_  
 l20320cds\_605-  
 953:in\_reversesequence,\_1218,protein\_serine/threonine\_kinase\_stk1\_mrna,\_complet  
 e\_cds  
 l37042mrna\_960-1314,casein\_kinase\_i\_alpha\_isoform\_(csnk1a1)\_mrna,\_complete\_cds  
 l40410mrna\_296-803,thyroid\_receptor\_interactor\_(trip3)\_mrna,\_3'\_end\_of\_cds  
 l41559mrna\_61-475,pterin-4a-carbinolamine\_dehydratase\_(pcbd)\_mrna,\_complete\_cds\_  
 m15661mrna\_3-338,ribosomal\_protein\_mrna,\_complete\_cds  
 m19483cds\_1127-1559:in\_reversesequence,\_2162-  
 2204,atp\_synthase\_beta\_subunit\_gene  
 m29971\_282-750,6-o-methylguanine-dna\_methyltransferase\_(mgmt)\_mrna,\_complete\_cds\_  
 m55153\_2794-3232,transglutaminase\_(tgase)\_mrna,\_complete\_cds\_

u34343\_110-560,13kd\_differentiation-associated\_protein\_mrna,\_partial\_cds/gb=u34343\_/ntype=rna  
u43923\_888-1410,transcription\_factor\_supt4h\_mrna,\_complete\_cds\_  
u65093\_466-838,msg1-related\_gene(mrg1)\_mrna,\_complete\_cds\_  
u79262\_878-1007,deoxyhypusine\_synthase\_mrna,\_complete\_cds\_  
u79718\_532-1012,endonuclease\_iii\_homolog(octs3)\_mrna,\_complete\_cds\_  
all\_x90857\_2739-3184,mrna\_for\_-14\_gene,\_containing\_globin\_regulatory\_element\_  
x94910\_333-861:not\_in\_gb\_record,mrna\_for\_erp31\_protein  
y08766cds\_1803-1893:in\_reversesequence,\_2190-  
2239,mrna\_for\_splicing\_factor,\_sf1-bo\_isoform  
y12478\_210-750,mrna\_for\_chd5\_protein\_

Metagene 464

d16593\_290-812,bdr-2\_mrna\_for\_hippocalcin,\_complete\_cds  
d88460\_1233-1695,mrna\_for\_n-wasp,\_complete\_cds\_  
d89016\_1618-2116,mrna\_for\_neuroblastoma,\_complete\_cds  
hg2280-ht2376\_at\_hg2280-ht2376\_d-amino-acid\_oxidase  
hg908-ht908\_at\_hg908-ht908\_mg61\_protein  
l00635\_1029-1437,farnesyl-protein\_transferase\_beta-subunit\_mrna,\_complete\_cds  
l34355\_827-961,(clone\_p4)\_50\_kd\_dystrophin-associated\_glycoprotein\_mrna,\_complete\_cds\_  
l36818\_4098-4608,(clone\_51c-3)\_51c\_protein\_mrna,\_complete\_cds  
l44140exon#61-62\_44-  
221:not\_in\_gb\_record,\_dnll1\_gene\_extracted\_fromchromosome\_x\_region\_from\_filamin  
-  
m38258\_2000-2486,retinoic\_acid\_receptor\_gammamrna,\_complete\_cds\_  
m77348mrna\_1757-1786,pmelmrna,\_complete\_cds\_  
m92432\_3098-3566,retinal\_guanylyl\_cyclase\_(retgc)\_mrna,\_complete\_cds  
m96759mrna\_783-1299,rod\_outer\_segment\_membrane\_protein(rom1)\_gene\_exons\_1-  
3,\_complete\_cds  
all\_s58733\_264-  
357,\_pp52=b\_lymphocyte\_signal\_transduction\_gene\_{group\_3,\_inverted\_repeat}\_[hum  
an,\_tu  
u07418\_2004-2454,dna\_mismatch\_repair\_(hmlh1)\_mrna,\_complete\_cds  
u37529\_556-1030,substance\_p\_beta-ppt-a\_mrna,\_complete\_cds  
u43177exon#1\_62-464,urocortin\_gene,\_complete\_cds\_  
u49928\_2513-3035,tak1\_binding\_protein(tab1)\_mrna,\_complete\_cds  
u62966\_2137-2635,na+/nucleoside\_cotransporter\_(hcnt1a)\_mrna,\_complete\_cds  
u68536\_1918-2410,zinc\_finger\_protein\_mrna,\_complete\_cds  
u71087\_1092-1126,map\_kinase\_kinase\_mek5b\_mrna,\_complete\_cds  
u92314\_840-  
1415,hydroxysteroid\_sulfotransferase\_sult2b1a\_(hsst2)\_mrna,\_complete\_cds.  
all\_x06256\_3681-4180,mrna\_for\_fibronectin\_receptor\_alpha\_subunit\_  
all\_x13589\_2395-2936,mrna\_for\_aromatase\_(estrogen\_synthetase)  
all\_x54871\_1059-1612,mrna\_for\_ras-related\_protein\_rab5b  
all\_x86681\_1848-2257,mrna\_for\_nucleolar\_protein,\_hnp36\_  
all\_x94453\_2396-2907,mrna\_for\_pyrroline\_5-carboxylate\_synthetase\_

Metagene 360

d28137\_395-743,mrna\_for\_bst-2,\_complete\_cds  
j04164\_366-804,interferon-inducible\_protein\_27-sep\_mrna,\_complete\_cds

l22342\_672-810,nuclear\_phosphoprotein\_mrna,\_complete\_cds\_  
 m13755mrna\_33-591,interferon-induced\_17-kda/15-kda\_protein\_mrna,\_complete\_cds\_  
 m31724mrna\_2694-3168,phosphotyrosyl-protein\_phosphatase\_(ptp-  
 1b)\_mrna,\_complete\_cds\_  
 m62505\_1952-2240,c5a\_anaphylatoxin\_receptor\_mrna,\_complete\_cds\_  
 u12255\_905-1391,igg\_fc\_receptor\_hfcrn\_mrna,\_complete\_cds\_  
 u50648mrna\_2211-2751,interferon-inducible\_rna-  
 dependent\_protein\_kinase\_(pkr)\_gene  
 u72882\_448-1009,interferon-  
 induced\_leucine\_zipper\_protein\_(ifp35)\_mrna,\_partial\_cds  
 u95006\_114-654,d9\_splice\_variant\_a\_mrna,\_complete\_cds\_  
 x00371mrna\_495-1011,myoglobin\_gene\_(exon\_1)\_(and\_joined\_cds)  
 all\_x02874\_1063-1298,mrna\_for\_(2'-5')\_oligo\_a\_synthetase\_e\_(1,6\_kb\_rna)  
 all\_x02875\_158-628,mrna\_(3'--fragment)\_for\_(2'--  
 5')\_oligo\_a\_synthetase\_e\_(1,8\_kb\_rna)\_  
 all\_x57351\_294-891,1-8d\_gene\_from\_interferon-inducible\_gene\_family,1-  
 8d\_gene\_from\_interferon-inducib  
 x79882cds\_2116-2656:in\_reversesequence,\_2773,lrp\_mrna\_  
 x85116\_rna1\_s\_at\_x85116\_x85116,not\_in\_gb\_record,epb72\_gene\_exon\_1\_

Metagene 335

k02882cds\_660-1098,\_ighd\_gene\_(immunoglobulin\_delta-  
 chain)\_extracted\_fromgermline\_igd\_chain\_gene,\_c-  
 m61199\_1227-1689,cleavage\_signalprotein\_mrna,\_complete\_cds

Metagene 328

d25274\_727-1177,randomly\_sequenced\_mrna  
 d49396\_948-1446,mrna\_for\_apo1(mer5(aop1-mouse)-like\_protein),\_complete\_cds  
 l04731\_13654-14152,translocation\_t(4:11)\_of\_all-1\_gene\_to\_chromosome\_4  
 l25081\_595-1015,gtpase\_(rhoc)\_mrna,\_complete\_cds\_  
 m22538\_286-778,nuclear-encoded\_mitochondrial\_nadh-  
 ubiquinone\_reductase\_24kd\_subunit\_mrna,\_complete\_c  
 m31951exon#2\_671-  
 1061:in\_reversesequence,\_6169,perforin\_(prf1)\_gene,\_complete\_cds\_  
 m63138mrna\_1545-2007,cathepsin\_d\_(catd)\_gene\_  
 s65738\_1061-  
 1373,\_actin\_depolymerizing\_factor\_[human,\_fetal\_brain,\_mrna,\_1452\_nt]\_  
 u09848\_2904-3474,zinc\_finger\_protein\_(znf139)\_mrna,\_partial\_cds  
 u43901mrna#1\_429-  
 557,37\_kd\_laminin\_receptor\_precursor/p40\_ribosome\_associated\_protein\_gene,\_comp  
 lete  
 u83908cds\_941-1295:in\_reversesequence,\_1589-  
 1649,nuclear\_antigen\_h731\_mrna,\_complete\_cds  
 u90878\_693-1179,lim\_domain\_protein\_clp-36\_mrna,\_complete\_cds.  
 u90902\_939-1407,clone\_23612\_mrna\_sequence  
 u94855\_696-1176,translation\_initiation\_factor47\_kda\_subunit\_mrna,\_complete\_cds  
 all\_x16416\_4998-5497,c-abl\_mrna\_encoding\_p150\_protein  
 all\_x51466\_2702-3057,mrna\_for\_elongation\_factor\_2  
 x70218\_771-1203,\_hsapiens\_mrna\_for\_protein\_phosphatase\_x  
 all\_x74929\_1365-1706,krt8\_mrna\_for\_keratin\_8\_  
 all\_x76228\_677-1242,mrna\_for\_vacuolar\_h+\_atpase\_e\_subunit

x78136cds\_688-1060:in\_reversesequence,\_1130-1244,hnrnp-e2\_mrna  
 x82207cds\_876-1098:in\_reversesequence,\_1166-1412,mrna\_for\_beta-contractin\_(pc3)  
 y08999cds\_583-1045:in\_reversesequence,\_1132,mrna\_for\_sop2p-like\_protein\_  
 all\_z14000\_958-1463,ring1\_gene\_  
 all\_z49835\_1354-1805,mrna\_for\_protein\_disulfide\_isomerase

Metagene 213

hg4321-ht4591\_at\_hg4321-ht4591\_ahnak-related\_sequence  
 j04449\_2290-2776,(clone\_nf\_10)\_cytochrome\_p-  
 450\_nifedipine\_oxidase\_mrna,\_complete\_cds\_  
 j05459mrna\_695-1187,glutathione\_transferase\_m3\_(gstm3)\_mrna,\_complete\_cds  
 l17325\_73-451,pre-t/nk\_cell\_associated\_protein\_(ld12a2)\_mrna,\_complete\_cds\_  
 l32164\_630-1158,zinc\_finger\_protein\_mrna,\_3'\_end  
 m16714exon#8\_627-  
 747,mhc\_i\_divergent\_lymphocyte\_antigen\_gene,\_complete\_cds,\_clone\_rs5  
 all\_m37457\_334-371,na+,k+\_#name?\_catalytic\_subunit\_alpha-  
 iii\_isoform\_gene,na+,k+\_#name?\_catalytic\_su  
 all\_m86808\_2578-2977,pyruvate\_dehydrogenase\_complex\_(pdha2)\_gene,\_complete\_cds\_  
 all\_x58723\_1862-2049,mdr1\_(multidrug\_resistance)\_gene\_for\_p-glycoprotein\_  
 x92368mrna\_5695-6187,ncx1\_gene\_(exon\_1)/gb=x92368\_/ntype=dna\_/annot=mrna\_

Metagene 92

d14826\_834-1163,mrna\_for\_hcrem\_(cyclic\_amp-  
 responsive\_element\_modulator)\_typeprotein,\_complete\_cds  
 hg2591-ht2687\_s\_at\_hg2591-ht2687\_transcription\_factor\_itf-1  
 u13696cds\_2138-2563:in\_reversesequence,\_2600-  
 2669,homolog\_of\_yeast\_mut1\_(hpms2)\_gene,\_complete\_cds  
 u60269cds#3\_237-447:in\_reversesequence,\_1593-1737,endogenous\_retrovirus\_herv-  
 k(hm16)\_proviral\_clone\_  
 x84740mrna\_2847-3309,mrna\_for\_dna\_ligase\_iii\_  
 y10275cds\_363-633:in\_reversesequence,\_880-1060,mrna\_for\_l-3-  
 phosphoserine\_phosphatase\_

Metagene 64

hg2702-ht2798\_r\_at\_hg2702-ht2798\_serine/threonine\_kinase\_  
 s79781mrna\_31-  
 169,\_wt1\_{antisense\_promoter,\_intron\_1}\_[human,\_kidney,\_genomic,\_780\_nt]/gb=s79  
 781\_/nt  
 x54162mrna\_3362-  
 3818,mrna\_for\_a\_64\_kd\_autoantigen\_expressed\_in\_thyroid\_and\_extra-ocular\_muscle\_  
 x61118mrna\_1457-1955,\_ttg-2a\_gene\_extracted\_fromttg-  
 2\_mrna\_for\_a\_cysteine\_rich\_protein\_with\_lim\_moti  
 y13896\_4-  
 179,skeletal\_muscle\_alternate\_5'\_end\_of\_gene\_kir4.2\_5'\_utr/gb=y13896\_/ntype=rna

Metagene 45

d38163\_3117-3661,mrna\_for\_a1(xix)\_collagen\_chain,\_complete\_cds\_  
 all\_x03066\_787-1268,mrna\_for\_hla-d\_ii\_antigen\_do\_beta\_chain  
 x14766mrna\_1363-1711,mrna\_for\_gaba-a\_receptor,\_alphasubunit\_  
 x76104cds\_4113-4257:in\_reversesequence,\_4629-4827,dap-kinase\_mrna\_  
 z34974cds\_1816-2144:in\_reversesequence,\_2439-  
 2515,mrna\_for\_plakophilin\_(partial)

Metagene 447

af006084\_935-1277,arp2/3\_protein\_complex\_subunit\_p41-  
 arc\_(arc41)\_mrna,\_complete\_cds/gb=af006084\_/nty  
 d00017\_851-1319,lipocortin\_ii\_mrna\_  
 d26129\_1145-1577,mrna\_for\_ribonuclease\_a\_(rnase\_a),\_complete\_cds\_  
 d42043\_2329-2863,mrna\_for\_kiaa0084\_gene,\_partial\_cds\_  
 d87292\_572-1052,mrna\_for\_rhodanese,\_complete\_cds\_  
 d88152\_2081-2639,mrna\_for\_acetyl-coenzyme\_a\_transporter,\_complete\_cds  
 j04456\_31-469,\_humankd\_lectin\_mrna,\_complete\_cds  
 l13720\_1860-2436,growth-arrest-specific\_protein\_(gas)\_mrna,\_complete\_cds  
 l25080\_1212-1692,gtp-binding\_protein\_(rhoa)\_mrna,\_complete\_cds\_  
 l33075\_6978-7530,ras\_gtpase-activating-  
 like\_protein\_(iqgap1)\_mrna,\_complete\_cds\_  
 l40379mrna\_181-541,thyroid\_receptor\_interactor\_(trip10)\_mrna,\_3'\_end\_of\_cds\_  
 l41147mrna\_1383-1959,5-ht6\_serotonin\_receptor\_mrna,\_complete\_cds  
 m13450\_636-1020,esterase\_d\_mrna,\_3'\_end  
 all\_m14338\_2740-3281,mrna\_for\_protein\_s\_and\_intron\_  
 all\_m14949\_1905-2423,r-ras\_gene  
 m23294mrna#1\_1219-1651,beta-hexosaminidase\_beta-subunit\_(hexb)\_gene  
 m26576exon\_43-289:not\_in\_gb\_record,col4a1\_gene\_(alpha-  
 1\_type\_iv\_collagen)\_extracted\_fromalpha-1\_col  
 m27492\_4336-4864,interleukinreceptor\_mrna,\_complete\_cds\_  
 m28713exon\_536-1052,nadh-cytochrome\_b5\_reductase\_(b5r)\_gene\_  
 m33680\_879-1431,26-kda\_cell\_surface\_protein\_tapa-1\_mrna,\_complete\_cds  
 m36341\_912-1458,adp-ribosylation\_factor(arf4)\_mrna,\_complete\_cds  
 m63256\_1975-2497,major\_yo\_paraneoplastic\_antigen\_(cdr2)\_mrna,\_3'\_end\_  
 m64571mrna\_4553-4931,microtubule-associated\_proteinmrna,\_complete\_cds\_  
 m76378mrna\_1294-1768,cysteine-rich\_protein\_(crp)\_gene  
 m82809\_1465-1915,annexin\_iv\_(anx4)\_mrna,\_complete\_cds  
 m83751\_539-1013,arginine-rich\_protein\_(arp)\_gene,\_complete\_cds\_  
 u01691mrna\_1257-1743,annexin\_v\_(anx5)\_gene,\_5'\_-untranslated\_region  
 u02570\_2792-3290,cdc42\_gtpase-activating\_protein\_mrna,\_partial\_cds\_  
 u44378\_2091-  
 2655,homozygous\_deletion\_target\_in\_pancreatic\_carcinoma\_(dpc4)\_mrna,\_complete\_c  
 ds  
 u46006\_140-620,smooth\_muscle\_lim\_protein\_(h-  
 smlim)\_mrna,\_complete\_cds/gb=u46006\_/ntype=rna\_  
 u46499\_at\_u46499\_u46499,not\_in\_gb\_record,microsomal\_glutathione\_transferase\_(gs  
 t12)\_gene,\_5'\_sequenc  
 u93205\_588-1020,nuclear\_chloride\_ion\_channel\_protein\_(ncc27)\_mrna,\_complete\_cds  
 x04412cds\_2047-2305:in\_reversesequence,\_2421-2529,mrna\_for\_plasma\_gelsolin  
 all\_x05610\_1701-2098,mrna\_for\_type\_iv\_collagen\_alpha\_-2\_chain  
 all\_x07979\_3223-3596,mrna\_for\_fibronectin\_receptor\_beta\_subunit  
 all\_x54304\_391-878,mrna\_for\_myosin\_regulatory\_light\_chain  
 y00433cds\_233-581:in\_reversesequence,\_905-  
 1109,mrna\_for\_glutathione\_peroxidase\_(ec\_1.11.1.9.)\_

## Metagene 70

u02687\_2874-3312,growth\_factor\_receptor\_tyrosine\_kinase\_(stk-1)\_mrna,\_complete\_cds\_  
u79271\_596-1130,clones\_23920\_and\_23921\_mrna\_sequence\_

## Metagene 191

hg3415-ht3598\_at\_hg3415-ht3598\_poliovirus\_receptor\_j00124exon#8\_14-  
227:not\_in\_gb\_record,50\_kda\_type\_i\_epidermal\_keratin\_gene,\_complete\_cds\_  
all\_100205\_358-503,k6b\_(epidermal\_keratin,\_type\_ii)\_gene\_  
135594mrna\_3002-3178,autotaxin\_mrna,\_complete\_cds\_  
142611\_1374-1954,keratinisoform\_k6e\_(krt6e)\_mrna,\_complete\_cds\_  
m14676\_1864-2332,src-like\_kinase\_(slk)\_mrna,\_complete\_cds\_  
m95585mrna\_3253-3805,hepatic\_leukemia\_factor\_(hlf)\_mrna,\_complete\_cds\_  
u41518\_1761-2253,channel-like\_integral\_membrane\_protein\_(aqp-1)\_mrna,\_clone\_aqp-1-2344,\_partial\_cds\_  
u77180\_55-511,macrophage\_inflammatory\_proteinbeta\_(mip-3beta)\_mrna,\_complete\_cds\_  
all\_x06182\_4474-5069,c-kit\_proto-oncogene\_mrna\_  
x61123mrna\_1212-1608,btg1\_mrna\_

## Metagene 27

ac002073cds#1\_507-759:in\_reversesequence,\_23812-24010,\_wugsc:dj515n1.2\_gene\_extracted\_frompac\_clone\_  
hg3345-ht3522\_at\_hg3345-ht3522\_pou\_domain-containing\_protein\_137036exon#2\_29-92:in\_reversesequence,\_1754-1971,neutrophil-activating\_peptide\_78\_(ena-78)\_gene,\_com  
m15169mrna#1\_1704-1950:in\_reversesequence,\_3390-3408,beta-2-adrenergic\_receptor\_mrna,\_complete\_cds\_  
m25756\_1777-2287,secretogranin\_ii\_gene,\_complete\_cds\_  
m28983\_1823-2369,interleukinalpha\_(il\_1)\_mrna,\_complete\_cds\_  
m33317mrna\_1158-1693,cytochrome\_p450iia4\_(cyp2a4)\_mrna,\_complete\_cds\_  
m62486exon\_17-359:not\_in\_gb\_record,c4b-binding\_protein\_gene\_  
u66580cds\_510-1026:in\_reversesequence,\_1075-1081,putative\_g\_protein-coupled\_receptor\_(gpr21)\_gene,\_c  
u79242\_1043-1589,clone\_23560\_mrna\_sequence\_  
all\_x02404\_227-750,mrna\_fragment\_for\_second\_calcitonin\_gene\_related\_peptide\_(cgrp)\_from\_medullary\_th  
x55005mrna\_2002-2230,c-erba-1\_mrna\_for\_thyroid\_hormone\_receptor\_alpha\_  
x77533cds\_982-1390:in\_reversesequence,\_1532-1544,mrna\_for\_activin\_type\_ii\_receptor\_  
all\_z11933\_1730-1942,mrna\_for\_n-oct\_3,\_n-oct5a,\_and\_n-oct\_5b\_proteins

## Metagene 444

af014958\_1175-  
 1619,chemokine\_receptor\_x\_(ckrx)\_mrna,\_complete\_cds/gb=af014958\_/ntype=rna  
 d16688\_876-1448,ltg9/mlt3\_mrna,\_c-terminal  
 d29956\_3758-4328,mrna\_for\_kiaa0055\_gene,\_complete\_cds  
 d31888\_4700-5186,mrna\_for\_kiaa0071\_gene,\_partial\_cds\_  
 d38037\_292-826,mrna\_for\_fk506-binding\_protein\_12kda\_(hfkbp-  
 12)\_homologue,\_complete\_cds\_  
 d63135mrna\_31-499,mrna\_for\_ets-like\_30\_kda\_protein/gb=d63135\_/ntype=rna  
 d79987\_6109-6523,mrna\_for\_kiaa0165\_gene,\_complete\_cds  
 d86957\_3869-4265,mrna\_for\_kiaa0202\_gene,\_partial\_cds\_  
 d88213\_2085-2481,mrna\_for\_retina-specific\_amine\_oxidase,\_complete\_cds  
 hg2383-ht4824\_s\_at\_hg2383-ht4824\_cystathionine\_beta\_synthase,\_altsplice\_3  
 hg25930-ht26386\_at\_hg25930-ht26386\_estradiol\_17-beta\_dehydrogenase  
 hg2841-ht2968\_s\_at\_hg2841-ht2968\_albumin,\_altsplice\_1  
 hg2987-ht3136\_s\_at\_hg2987-ht3136\_vasoactive\_intestinal\_peptide\_  
 hg3264-ht3441\_at\_hg3264-ht3441\_af-6  
 hg4027-ht4297\_f\_at\_hg4027-ht4297\_beta-1-  
 glycoprotein,\_domains\_n\_and\_iaa,\_pregnancy-specific  
 hg4390-ht4660\_at\_hg4390-ht4660\_ribosomal\_protein\_l18a\_homolog  
 l06133\_7979-8435,putative\_cu++-transporting\_p-type\_atpase\_mrna,\_complete\_cds\_  
 all\_l08904\_1372-1667,h2k\_binding\_factor(kbf2)\_mrna,\_complete\_cds\_  
 l12468\_3246-3780,aminopeptidase\_a\_mrna,\_complete\_cds  
 l14812\_3349-3936,retinoblastoma\_related\_protein\_(p107)\_mrna,\_complete\_cds  
 l20826\_3074-3572,i-plastin\_mrna,\_complete\_cds  
 l22569\_1685-2243,cathepsin\_b\_mrna,\_3'\_utr\_with\_a\_stem-  
 loop\_structure\_providing\_mrna\_stability\_  
 l39060mrna\_1037-1547,transcription\_factor\_sl1\_mrna,\_complete\_cds  
 m11025mrna\_783-1263,asialoglycoprotein\_receptor\_h2\_mrna,\_complete\_cds  
 m17252mrna\_934-1198,cytochrome\_p450c21\_mrna,\_3'\_end  
 all\_m24364\_1059-  
 1435,mhc\_ii\_lymphocyte\_antigen\_dqb\_mrna,\_complete\_cds,\_haplotype\_dr7,\_dqw9\_  
 m29581\_1469-1853,zinc-finger\_protein(zfp8)\_mrna,\_3'\_end\_  
 m57464\_3899-4439,ret\_proto-oncogene\_mrna,\_complete\_cds\_  
 m63962mrna\_2985-3507,gastric\_h,k-atpase\_catalytic\_subunit\_gene,\_complete\_cds  
 m74525\_2002-2536,hhr6b\_(yeast\_radhomologue)\_mrna,\_complete\_cds  
 m87860cds\_25-331:in\_reversesequence,\_176-212,s-lac\_lectin\_l1-14-  
 ii\_(lgals2)\_gene\_  
 m89955cds\_635-1085:in\_reversesequence,\_1391-1439,5-ht1d-  
 type\_serotonin\_receptor\_gene,\_complete\_cds  
 s48983cds\_36-282:in\_reversesequence,\_204-  
 408,\_saa4=serum\_amyloid\_a\_[human,\_genomic,\_858\_ntsegments]  
 s59184\_2487-  
 2979,\_ryk=related\_to\_receptor\_tyrosine\_kinase\_[human,\_hepatoma,\_mrna,\_3068\_nt]  
 s61953\_516-798,\_c-  
 erbb3=receptor\_tyrosine\_kinase\_{alternatively\_spliced}\_[human,\_gastric\_cancer\_c  
 ell  
 u16811\_1491-2034,bak\_mrna,\_complete\_cds  
 all\_u18914\_2694-3199,19.8\_kda\_protein\_mrna,\_complete\_cds\_  
 u28758\_45-626,nmda\_receptor\_subtype\_2b\_subunit\_(grin2b)\_mrna,\_partial\_cds  
 u40215\_1479-2049,synapsin\_iib\_mrna,\_complete\_cds\_  
 u40763\_2251-2803,clk-associated\_rs\_cyclophilin\_cars-cyp\_mrna,\_complete\_cds\_  
 u43286\_1633-2155,selenophosphate\_synthetase(sps2)\_mrna,\_complete\_cds  
 u44848\_7-  
 187,nuclear\_respiratory\_factor(nrfl1)\_mrna,\_3'\_utr/gb=u44848\_/ntype=rna\_  
 u48807\_1652-2156,map\_kinase\_phosphatase\_(mkp-2)\_mrna,\_complete\_cds\_



u49974cds\_444-  
 1017,mariner2\_transposable\_element,\_complete\_consensus\_sequence/gb=u49974\_/ntyp  
 e=dna\_  
 u52518\_399-825,grb2-related\_adaptor\_protein\_(grap)\_mrna,\_complete\_cds  
 u71092cds\_954-1158:in\_reversesequence,\_1611-1767,somatostatin\_receptor-  
 like\_protein\_(slc1)\_gene,\_com  
 u79257\_952-1432,clone\_23932\_mrna\_sequence  
 u88666\_3113-3653,serine\_kinase\_srp\_k2\_mrna,\_complete\_cds  
 all\_u90552\_3170-  
 3242,butyrophilin\_(btf5)\_mrna,\_complete\_cds,butyrophilin\_(btf5)\_mrna,\_complete\_  
 cds  
 u90912\_1074-1584,clone\_23865\_mrna\_sequence\_  
 u94332\_761-1331,osteoprotegerin\_(opg)\_mrna,\_complete\_cds.  
 all\_x06268\_1159-1337,mrna\_for\_pro-alpha(ii)\_collagen\_3'\_end\_c-  
 termtriple\_helical\_and\_c-terminal\_non-  
 all\_x13956\_694-  
 1163,12s\_rna\_induced\_by\_poly(ri),\_poly(rc)\_and\_newcastle\_disease\_virus  
 x15954mrna\_729-1240,mbp1\_gene,\_exon(and\_joined\_cds)  
 x16707cds\_379-733:in\_reversesequence,\_869-923,fra-1\_mrna  
 x17360mrna\_4536-5034,hox\_5.1\_gene\_for\_hox\_5.1\_protein\_  
 all\_x63575\_3903-4466,mrna\_for\_plasma\_membrane\_calcium\_atpase\_  
 all\_x64838\_5256-5833,mrna\_for\_restin\_  
 x66171cds\_341-623:in\_reversesequence,\_892-1108,cmrf35\_mrna,\_complete\_cds  
 all\_x77383\_1094-1599,mrna\_for\_cathepsin-o  
 x78031\_1113-1629,alpha-1,\_3-fucosyltransferase\_mrna  
 all\_x95289\_48-625,mrna\_for\_hcgix\_protein\_  
 y11651cds\_750-960:in\_reversesequence,\_1250-1466,mrna\_for\_phosphate\_cyclase

## Metagene 369

d86966\_4491-5031,mrna\_for\_kiaa0211\_gene,\_complete\_cds  
 d87074\_6650-7184,mrna\_for\_kiaa0237\_gene,\_complete\_cds  
 hg1862-ht1897\_at\_hg1862-ht1897\_calmodulin\_type\_i\_  
 hg825-ht825\_at\_hg825-ht825\_guanine\_nucleotide-binding\_protein,\_alpha\_12  
 108424\_1124-1586,achaete\_scute\_homologous\_protein\_(ash1)\_mrna,\_complete\_cds\_  
 l23116\_3296-3644,galactocerebrosidase\_(galc)\_mrna,\_complete\_cds\_  
 m34715mrna\_1750-2206,pregnancy-specific\_beta-1-  
 glycoprotein\_mrna\_psg95,\_complete\_cds\_  
 m57423\_485-  
 1016,phosphoribosylpyrophosphate\_synthetase\_subunit\_iii\_mrna,\_3'\_end.  
 m80359\_2409-2835,protein\_p78\_mrna,\_complete\_cds  
 s69370\_234-  
 761,\_pax3b=transcription\_factor\_{alternatively\_spliced}\_[human,\_adult\_cerebellu  
 m,\_mrna,\_8  
 u25750\_3002-3380,chromosome\_17q21\_mrna\_clone\_1046:1-1  
 u35139\_1111-1507,necdin\_related\_protein\_mrna,\_complete\_cds\_  
 u39447\_3452-3980,placenta\_copper\_monamine\_oxidase\_mrna,\_complete\_cds\_  
 u42390\_8359-8863,trio\_mrna,\_complete\_cds  
 u82130\_1151-1451,tumor\_susceptibility\_protein\_(tsg101)\_mrna,\_complete\_cds\_  
 x53793cds\_873-  
 1227,ade2h1\_mrna\_showing\_homologies\_to\_saicar\_synthetase\_and\_air\_carboxylase\_of  
 \_the\_pu  
 x54150mrna\_978-1530,mrna\_for\_fc\_receptor\_  
 x63422cds\_305-461:in\_reversesequence,\_688-916,mrna\_for\_delta-  
 subunit\_of\_mitochondrial\_f1f0\_atp-synth

all\_x63546\_7261-7856,mrna\_for\_tre\_oncogene\_(clone\_210)\_  
all\_z25535\_4922-5463,mrna\_for\_nuclear\_pore\_complex\_protein\_hnup153\_

Metagene 441

d16350\_1280-1826,sa\_mrna\_for\_sa\_gene\_product,\_complete\_cds\_  
d38073\_2590-3022,mrna\_for\_hrlf\_beta\_subunit\_(p102\_protein),\_complete\_cds\_  
d63481\_4350-4890,mrna\_for\_kiaa0147\_gene,\_partial\_cds\_  
l42373mrna\_2651-3071,protein\_phosphatase\_2a\_b56-alpha\_mrna,\_complete\_cds  
m29277\_2335-  
2901,isolate\_juso\_muc18\_glycoprotein\_mrna\_(3'\_variant),\_complete\_cds,isolate\_ju  
so\_muc18\_  
m34458mrna\_1900-2463,lamin\_b\_mrna,\_complete\_cds\_  
u33286\_2642-3092,chromosome\_segregation\_gene\_homolog\_cas\_mrna,\_complete\_cds  
u37426\_4269-4815,kinesin-like\_spindle\_protein\_hksp\_(hksp)\_mrna,\_complete\_cds\_  
u53204\_14286-14721,plectin\_(plec1)\_mrna,\_complete\_cds  
u56816\_1376-1838,kinase\_myt1\_(myt1)\_mrna,\_complete\_cds.  
u73843\_1356-1860,epithelial-specific\_transcription\_factor\_ese-1b\_(ese-  
1)\_mrna,\_complete\_cds  
all\_x74331\_1801-2288,mrna\_for\_dna\_primase\_(subunit\_p58)  
all\_x99459\_1516-1799,mrna\_for\_sigma\_3b\_protein\_  
y00486mrna\_252-  
786,\_adenine\_phosphoribosyltransferase\_(aprt)\_gene\_extracted\_fromaprt\_gene\_for\_  
adenin  
all\_z22555\_2041-2516,encoding\_cla-1\_mrna\_  
z37986cds\_409-631:in\_reversesequence,\_826-  
1000,mrna\_for\_phenylalkylamine\_binding\_protein

Metagene 407

d28539\_4017-  
4549,mrna\_for\_metabotropic\_glutamate\_receptor\_subtype\_5b,\_complete\_cds\_  
d83195cds\_448-802:in\_reversesequence,\_3957-  
3963,dnase1\_gene\_for\_deoxyribonuclease\_i,\_complete\_cds\_  
m21665mrna\_1535-1621,beta-myosin\_heavy\_chain\_mrna,\_3'\_end  
m32315\_3202-3604,tumor\_necrosis\_factor\_receptor\_mrna,\_complete\_cds\_  
z70295exon#2-3\_7-252:not\_in\_gb\_record,gcap-ii\_gene

Metagene 390

d88795\_13-379,mrna\_for\_cadherin,\_partial\_cds/gb=d88795\_/ntype=rna\_  
d88797\_49-379,mrna\_for\_cadherin,\_partial\_cds/gb=d88797\_/ntype=rna\_  
hg273-ht273\_s\_at\_hg273-ht273\_lymphocyte\_antigen\_hla-g3\_  
hg3454-ht3647\_at\_hg3454-ht3647\_zinc\_finger\_protein\_  
hg644-ht644\_at\_hg644-ht644\_histone\_h1.1  
l35251mrna\_801-1281,extracellular\_matrix\_protein\_(mfap3)\_gene,\_complete\_cds  
all\_m11437\_1562-  
2440,\_kng\_gene\_(kininogen)\_extracted\_fromkininogen\_gene,\_kng\_gene\_(kininogen)\_e  
xtrac  
u28727\_7835-8357,pregnancy-associated\_plasma\_protein-  
a\_preproform\_(pappa)\_mrna,\_complete\_cds\_

u43279\_3409-3955,nucleoporin\_nup\_36\_mrna,\_complete\_cds/gb=u43279\_/ntype=rna  
 x05615cds\_7824-8238:in\_reversesequence,\_8327-8423,mrna\_for\_thyroglobulin  
 x51823cds\_5-34,mrna\_for\_b-  
 subunit\_of\_coagulation\_factor\_xiii\_(fxiiib)\_(partial)/gb=x51823\_/ntype=rna  
 x82279exon\_54-169,fas,\_apo-  
 1\_gene\_(promoter\_and\_exon\_i)/gb=x82279\_/ntype=dna\_/annot=exon\_

Metagene 254

d28118\_1807-2263,mrna\_for\_db1,\_complete\_cds  
 d45370mrna\_13-  
 337,apm2\_mrna\_for\_gs2374\_(unknown\_product\_specific\_to\_adipose\_tissue),\_complete  
 \_cds  
 hg2465-ht4871\_at\_hg2465-ht4871\_dna-binding\_protein\_ap-2,\_altsplice\_3\_  
 m31682mrna\_2130-2526,testicular\_inhibin\_beta-b-subunit\_mrna,\_3'\_end  
 m86933\_220-  
 681,amelogenin\_(amely)\_mrna,\_complete\_cds,amelogenin\_(amely)\_mrna,\_complete\_cds  
 u28249\_919-1405,11kd\_protein\_mrna,\_complete\_cds  
 u68031\_91-301,g\_protein-  
 coupled\_receptor\_(strl22)\_mrna,\_alternatively\_spliced\_5'\_utr\_sequence/gb=u68  
 x76732cds\_975-1221:in\_reversesequence,\_1464-  
 1518:not\_in\_gb\_record,nefa\_protein\_mrna,\_complete\_cds\_(d

Metagene 399

d87328\_5900-6404,mrna\_for\_hcs,\_complete\_cds  
 j05096mrna\_5006-5456,na,k-atpase\_subunit\_alpha(atp1a2)\_gene,\_complete\_cds  
 reverse\_176568\_31050-  
 31356,\_s26\_fromexcision\_and\_cross\_link\_repair\_protein\_(ercc4)\_gene,\_complete\_ge  
 all\_u67092\_1093-1868:not\_in\_gb\_record,ataxia-  
 telangiectasia\_locus\_protein\_(atm)\_gene,\_exons\_1a,\_1b,\_  
 all\_x13227\_1080-1567,mrna\_for\_d-amino\_acid\_oxidase\_(ec\_1.4.3.3)  
 x59710cds\_75-585:in\_reversesequence,\_714,mrna\_for\_caat-  
 box\_dna\_binding\_protein\_subunit\_b\_(nf-yb)  
 x64559cds\_202-580:in\_reversesequence,\_679-823,mrna\_for\_tetranectin

Metagene 275

j04168\_1867-2263,leukosialin\_mrna,\_complete\_cds  
 l05515\_2108-2594,camp\_response\_element-binding\_protein\_(cre-  
 bp1)\_mrna,\_complete\_cds\_  
 l09190mrna\_6480-6930,trichohyalin\_(trhy)\_gene,\_complete\_cds\_  
 m26602\_181-469,defensinprotein\_mrna,\_complete\_cds\_  
 u79245\_1139-1541,clone\_23586\_mrna\_sequence\_  
 u82668mrna#2\_1298-  
 1820,\_shox\_gene\_(shoxb)\_extracted\_fromshox\_gene,\_alternatively\_spliced\_products  
 ,\_c  
 z18954exon#1-4\_126-240:in\_reversesequence,\_246-  
 264,mrna\_for\_s100d\_calcium\_binding\_protein\_

Metagene 268

d63483\_2777-3304,mrna\_for\_kiaa0149\_gene,\_complete\_cds  
 l04510\_2769-3285,nucleotide\_binding\_protein\_mrna,\_complete\_cds\_  
 m25322mrna\_2577-3039,granule\_membrane\_protein-140\_mrna,\_complete\_cds\_  
 s76978\_29-224,\_prostate-  
 specific\_membrane\_antigen\_{alternatively\_spliced}\_[human,\_primary\_prostatic\_  
 u33429\_2481-2994,k+\_channel\_betasubunit\_mrna,\_complete\_cds

Metagene 250

d00760\_277-781,mrna\_for\_proteasome\_subunit\_hc3\_  
 d14710\_1298-1808,mrna\_for\_atp\_synthase\_alpha\_subunit,\_complete\_cds\_  
 d15057\_162-576,mrna\_for\_dad-1,\_complete\_cds  
 d78151\_2321-2825,mrna\_for\_26s\_proteasome\_subunit\_p97,\_complete\_cds\_  
 d78275\_959-1511,mrna\_for\_proteasome\_subunit\_p42,\_complete\_cds  
 hg1112-ht1112\_at\_hg1112-ht1112\_ras-like\_protein\_tc4  
 hg2855-ht2995\_at\_hg2855-ht2995\_heat\_shock\_protein,\_70\_kda  
 hg3214-ht3391\_at\_hg3214-ht3391\_metallopanstimulin\_  
 j02683mrna\_629-1066,adp/atp\_carrier\_protein\_mrna,\_complete\_cds\_  
 j02902mrna\_1694-2156,protein\_phosphatase\_2a\_regulatory\_subunit\_alpha-  
 isotype\_(alpha-pr65)\_mrna,\_comp  
 j04173\_1114-1648,phosphoglycerate\_mutase\_(pgam-b)\_mrna,\_complete\_cds  
 j04973mrna\_1023-1485,cytochrome\_bc-1\_complex\_core\_protein\_ii\_mrna,\_complete\_cds  
 l03532\_1898-2372,m4\_protein\_mrna,\_complete\_cds\_  
 l07633\_396-870,(clone\_1950.2)\_interferon-gamma\_ief\_ssp\_5111\_mrna,\_complete\_cds  
 l26247\_131-617,sui1iso1\_mrna,\_complete\_cds  
 l41351mrna\_1269-1695,prostasin\_mrna,\_complete\_cds\_  
 l76159mrna\_471-957,frgl\_mrna,\_complete\_cds  
 m17733mrna\_13-505,thymosin\_beta-4\_mrna,\_complete\_cds\_  
 m38690\_584-1106,cd9\_antigen\_mrna,\_complete\_cds\_  
 m55265mrna\_1612-2116,casein\_kinase\_ii\_alpha\_subunit\_mrna,\_complete\_cds\_  
 m57730mrna\_975-1437,b61\_mrna,\_complete\_cds\_  
 m63488\_1834-2344,replication\_protein\_a\_70kda\_subunit\_mrna\_complete\_cds\_  
 m93651\_1973-2519,set\_gene,\_complete\_cds  
 s80343\_1609-2077,\_argrs=arginyl-trna\_synthetase\_[human,\_ataxia-  
 telangiectasia\_patients,\_ebv-lymphobl  
 u03100\_2985-3501,alpha2(e)-catenin\_mrna,\_complete\_cds  
 u06155cds\_43-  
 495,chromosome\_1q\_subtelomeric\_sequence\_d1s553/gb=u06155\_/ntype=dna\_/annot=cds,  
 chromoso  
 u15008\_25-433,snrnp\_core\_protein\_sm\_d2\_mrna,\_complete\_cds  
 u18919\_408-948,chromosome\_17q12-21\_mrna,\_clone\_pov-2,\_partial\_cds  
 u25849mrna\_1717-2137,red\_cell-  
 type\_low\_molecular\_weight\_acid\_phosphatase\_(acp1)\_gene,\_5'\_flanking\_re  
 u30825\_528-1014,splicing\_factor\_srp30c\_mrna,\_complete\_cds  
 u32944\_162-540,cytoplasmic\_dynein\_light\_chain(hdlc1)\_mrna,\_complete\_cds\_  
 u38846\_1294-1732,stimulator\_of\_tar\_rna\_binding\_(srb)\_mrna,\_complete\_cds  
 u39317\_16-  
 484,e2\_ubiquitin\_conjugating\_enzyme\_ubch5b\_(ubch5b)\_mrna,\_complete\_cds\_  
 u51678\_276-756,small\_acidic\_protein\_mrna,\_complete\_cds\_  
 u52427mrna\_239-773,rna\_polymerase\_ii\_seventh\_subunit\_(rpb-  
 7)\_gene,\_complete\_cds.  
 u60276\_645-1191,hasna-i\_mrna,\_complete\_cds\_

u73514\_376-892,short-chain\_alcohol\_dehydrogenase\_(xh98g2)\_mrna,\_complete\_cds.  
 u73824\_3202-3766,p97\_mrna,\_complete\_cds  
 u77396\_at\_u77396\_u77396,not\_in\_gb\_record,tnf-  
 alpha\_inducible\_responsive\_element\_mrna,\_complete\_cds  
 x00351cds\_855-1065:in\_reversesequence,\_1154-1376,mrna\_for\_beta-actin  
 all\_x15183\_2479-2894,mrna\_for\_90-kda\_heat-shock\_protein  
 all\_x53331\_31-590,mrna\_for\_matrix\_gla\_protein  
 all\_x57206\_3916-4487,mrna\_for\_1d-myo-inositol-trisphosphate\_3-  
 kinase\_b\_isoenzyme\_  
 x57959cds\_264-714,mrna\_for\_ribosomal\_protein\_17  
 x60036cds\_683-1037:in\_reversesequence,\_1163-  
 1223,mrna\_for\_mitochondrial\_phosphate\_carrier\_protein  
 x63563cds\_3176-3500,mrna\_for\_rna\_polymerase\_ii\_140\_kda\_subunit\_  
 x75091cds\_300-653:in\_reversesequence,\_848-892,mrna\_for\_hla-  
 dr\_associated\_protein\_ii\_(phapii)  
 all\_x81817\_933-1240,bap31\_mrna\_  
 x83218cds\_215-539,mrna\_for\_atp\_synthase  
 all\_x96752\_1367-1818,mrna\_for\_l-3-hydroxyacyl-coa\_dehydrogenase  
 y12711\_336-864,mrna\_for\_putative\_progesterone\_binding\_protein  
 z35402mrna\_3912-4402,gene\_encoding\_e-cadherin,\_exonand\_joined\_cds  
 z50853cds\_556-802:in\_reversesequence,\_833-1001,mrna\_for\_clpp

Metagene 67

hg2171-ht2241\_at\_hg2171-ht2241\_12-lipoxygenase\_  
 m97347\_1499-2060,beta-1,6-n-acetylglucosaminyltransferase\_mrna,\_complete\_cds\_  
 u46116mrna\_5907-6477,receptor\_tyrosine\_phosphatase\_gamma\_(ptprg)\_gene  
 all\_u83600\_202-  
 527,death\_domain\_receptor(DDR3)\_mrna,\_alternatively\_spliced\_form\_2,\_partial\_cds  
 /gb=u8  
 all\_x95715\_1306-1901,mrna\_for\_anthracycline\_resistance\_associated\_protein

Metagene 293

102320\_1463-1997,radixin\_mrna,\_complete\_cds  
 m86868\_1189-1585,gamma\_amino\_butyric\_acid\_(gaba\_rho2)\_gene\_mrna,\_complete\_cds

Metagene 448

ab000449\_1091-1607,mrna\_for\_vrk1,\_complete\_cds\_  
 d14689\_6077-6557,mrna\_for\_kiaa0023\_gene,\_complete\_cds  
 x55668mrna\_550-940,mrna\_for\_proteinase\_3\_  
 all\_x75917\_1064-1602,mrna\_for\_fetal\_beta-mhc\_binding\_factor

Metagene 127

124470\_1905-2403,prostanoid\_fp\_receptor\_mrna,\_complete\_cds  
 all\_m36089\_2244-2797,dna-repair\_protein\_(xrccl)\_mrna,\_complete\_cds\_  
 m74161\_2469-2991,inositol\_polyphosphate\_5-phosphatase\_(5ptase)\_mrna,\_3'\_end

s57235\_1085-  
 1664,\_cd68=110kda\_transmembrane\_glycoprotein\_[human,\_promonocyte\_cell\_line\_u937  
 ,\_mrna,\_1  
 u48231exon#2\_1478-2015,bradykinin\_b1\_receptor\_(bdkrb1)\_gene,\_first\_  
 x51630mrna\_2403-2955:in\_reversesequence,\_2961-  
 2979,wilms\_tumor\_wt1\_mrna\_for\_zinc\_finger\_protein,\_kru  
 x98261cds\_121-352:in\_reversesequence,\_388-583,mrna\_for\_m-  
 phase\_phosphoprotein,\_mpps5\_

Metagene 134

hg4128-ht4398\_at\_hg4128-ht4398\_anion\_exchanger\_3,\_cardiac\_isoform  
 j03934\_1835-2371,\_human,\_nad(p)h:menadione\_oxidoreductase\_mrna,\_complete\_cds  
 100634\_734-1246,farnesyl-protein\_transferase\_alpha-subunit\_mrna,\_complete\_cds  
 109717mrna\_1316-1778,lysosomal\_membrane\_glycoprotein-  
 2\_(lamp2)\_gene,\_5'\_end\_and\_flanking\_region  
 110413\_1331-1589,farnesyltransferase\_alpha-subunit\_mrna,\_complete\_cds  
 120852\_2574-3150,leukemia\_virus\_receptor(glv2)\_mrna,\_complete\_cds  
 137199\_977-1313,(clone\_cd24-  
 1)\_huntington\_disease\_candidate\_region\_mrna\_fragment  
 142025mrna\_1988-2504,cellular\_co-factor\_(rab)\_gene,\_complete\_cds\_  
 m23114mrna\_3623-4085,calcium-atpase\_(hkl)\_mrna,\_complete\_cds  
 m55150mrna\_978-1422,fumarylacetoacetate\_hydrolase\_mrna,\_complete\_cds\_  
 m91592\_1971-2325,zinc-finger\_protein\_(znf76)\_gene,\_partial\_cds\_  
 s82447\_42-397,\_gcn5-  
 like\_1=gcn5\_homolog/putative\_regulator\_of\_transcriptional\_activation\_{clone\_gcn  
 5  
 u10324\_2934-3444,nuclear\_factor\_nf90\_mrna,\_complete\_cds  
 u24169\_723-1197,jtv-1\_(jtv-1)\_mrna,\_complete\_cds\_  
 u24183\_2457-3031,phosphofructokinase\_(pfkm)\_mrna,\_complete\_cds\_  
 u29091\_960-1368,selenium-  
 binding\_protein\_(hsbp)\_mrna,\_complete\_cds/gb=u29091\_/ntype=rna  
 u29463mrna\_2121-2681,cytochrome\_b561\_gene  
 u40462\_3034-3574,ikaros/lyf-1\_homolog\_(hik-1)\_mrna,\_complete\_cds\_  
 u52153\_2069-  
 2513,inwardly\_rectifying\_potassium\_channel\_kir3.2\_mrna,\_complete\_cds\_  
 u65676\_3144-3648,hermansky-pudlak\_syndrome\_protein\_(hps)\_mrna,\_complete\_cds  
 u66669\_785-1240:not\_in\_gb\_record,3-hydroxyisobutyryl-  
 coenzyme\_a\_hydrolase\_mrna,\_complete\_cds  
 u68063\_1453-1915,transformer-2\_beta\_(htra-2\_beta)\_mrna,\_complete\_cds\_  
 u74612\_2915-3425,hepatocyte\_nuclear\_factor-3/fork\_head\_homolog\_11a\_(hfh-  
 11a)\_mrna\_complete\_cds.  
 u75370\_3396-  
 3732,mitochondrial\_rna\_polymerase\_mrna,\_nuclear\_gene\_encoding\_mitochondrial\_pro  
 tein,\_com  
 u76272mrna\_161-689,diadenosine\_triphosphate\_(ap3a)\_hydrolase\_(fhit)\_gene,\_5'\_of  
 u91316\_891-1461,acyl-coa\_thioester\_hydrolase\_mrna,\_complete\_cds  
 all\_x06825\_679-1154,mrna\_for\_skeletal\_beta-tropomyosin\_  
 x15187cds\_2089-2380:in\_reversesequence,\_2521-  
 2737,tra1\_mrna\_forhomologue\_of\_murine\_tumor\_rejection\_a  
 x61970cds\_299-677:in\_reversesequence,\_758-860,mrna\_for\_macropain\_subunit\_zeta\_  
 all\_x70944\_2459-3030,mrna\_for\_ptb-associated\_splicing\_factor\_  
 all\_x77922\_1492-2000,gd3\_synthase\_mrna\_  
 x85134mrna\_2737-3007,rbq-3\_mrna\_  
 all\_x87176\_2148-2593,mrna\_for\_17-beta-hydroxysteroid\_dehydrogenase\_

all\_x91788\_857-1284,mrna\_for\_icln\_protein  
 x95586exon#3\_56-248:in\_reversesequence,\_5872-6088:not\_in\_gb\_record,mb1\_gene  
 x97795cds\_1954-2218:in\_reversesequence,\_2342-  
 2564,mrna\_homologous\_to\_scerevisiae\_rad54  
 y08682mrna\_2358-2552,mrna\_for\_carnitine\_palmitoyltransferase\_i\_type\_i\_  
 y11251\_4297-4822,mrna\_for\_novel\_member\_of\_serine-  
 arginine\_domain\_protein,\_srrp129  
 z17227\_1268-1850,mrna\_for\_transmembrane\_receptor\_protein\_  
 z68129mrna#1\_3-469:in\_fullsequence,\_16183-16321:not\_in\_gb\_record,\_h-  
 idh\_gamma\_gene\_(nad(h)-specific\_

Metagene 466

hg3920-ht4521\_s\_at\_hg3920-ht4521\_homeotic\_protein\_a1,\_i,\_altsplice\_1\_  
 hg4517-ht4920\_s\_at\_hg4517-  
 ht4920\_immunoglobulin\_recombination\_signal\_sequence\_binding\_protein,\_altsp  
 l34155\_4838-5306,laminin-related\_protein\_(lama3)\_mrna,\_complete\_cds\_  
 m21305cds\_39-  
 119,alpha\_satellite\_and\_satellitejunction\_dna\_sequence/gb=m21305\_/ntype=dna\_/an  
 not=cds\_  
 u60808\_1423-2000,cdp-diacylglycerol\_synthase\_(cds)\_mrna,\_complete\_cds  
 x60673mrna\_1091-1649,ak3\_mrna\_for\_adenylate\_kinase\_3

Metagene 100

d28423\_53-100,mrna\_for\_pre-  
 mrna\_splicing\_factor\_srp20,\_5'\_utr\_(sequence\_from\_the\_5'\_cap\_to\_the\_start  
 all\_d89377\_1587-2173,mrna\_for\_msx-2,\_complete\_cds,mrna\_for\_msx-2,\_complete\_cds  
 l13943\_1963-2019,glycerol\_kinase\_(gk)\_mrna\_exons\_1-4,\_complete\_cds\_  
 m37197mrna\_2687-3065,ccaat-box-binding\_factor\_(cbf)\_mrna,\_complete\_cds\_  
 m68520\_1708-2170,cdc2-related\_protein\_kinase\_mrna,\_complete\_cds  
 s67970\_962-  
 1538,\_znf75=krab\_zinc\_finger\_[human,\_lung\_fibroblast,\_mrna,\_1563\_nt]\_  
 s70585mrna\_138-612,\_thyroid-  
 stimulating\_hormone\_alpha\_subunit\_[human,\_genomic,\_1327\_ntsegments]\_  
 s82471\_77-298,\_ssx3=kruppel-  
 associated\_box\_containing\_ssx\_gene\_[human,\_testis,\_mrna\_partial,\_675\_nt]  
 u04209\_1396-1834,associated\_microfibrillar\_protein\_mrna,\_complete\_cds  
 u12978\_1713-2247,sperm\_membrane\_protein\_bs-84\_(hsd-1)\_mrna,\_partial\_cds  
 u15555\_1003-1489,serine\_palmitoyltransferase\_(lcb2)\_mrna,\_partial\_cds  
 u18271\_cds1\_at\_u18271\_u18271,not\_in\_gb\_record,thymopoietin\_(tmpo)\_gene,thymopoi  
 etin\_(tmpo)\_gene  
 u39226\_6864-7440,myosin\_viia\_(ush1b)\_mrna,\_complete\_cds  
 u43843\_813-1374,h-neuro-d4\_protein\_mrna,\_complete\_cds  
 u82321\_1608-2112,clone\_14.9b\_mrna\_sequence\_  
 all\_x59618\_1970-2475,rr2\_mrna\_for\_small\_subunit\_ribonucleotide\_reductase\_  
 x98482mrna\_2-  
 46,tnnt2\_gene\_exon/gb=x98482\_/ntype=dna\_/annot=mrna,tnnt2\_gene\_exon/gb=x98482\_/n  
 ttype=dn

Metagene 59

af001548mrna\_6079-  
 6385,\_815a9.1\_gene\_(myosin\_heavy\_chain)\_extracted\_fromchromosomebac\_clone\_cit98  
 7sk  
 d15049\_3317-3845,mrna\_for\_protein\_tyrosine\_phosphatase\_  
 l36531mrna\_2573-3059,integrin\_alphasubunit\_mrna,\_3'\_end  
 l41680\_1371-1869,alpha-2,8-polysialyltransferase\_(pst)\_gene,\_complete\_cds\_  
 m17316exon\_3-249:in\_reversesequence,\_260-338:not\_in\_gb\_record,gamma-a-  
 crystallin\_gene\_(gamma-g5)\_  
 m26061mrna\_2449-  
 2890:not\_in\_gb\_record,cgmp\_phosphodiesterase\_alpha\_subunit\_(cgpr-  
 a)\_mrna,\_complete\_c  
 m73482mrna\_757-1279,neuromedin\_b\_receptor\_(nmb-r)\_mrna,\_complete\_cds\_  
 u43916\_147-698,tumor-  
 associated\_membrane\_protein\_homolog\_(tmp)\_mrna,\_complete\_cds  
 u46744\_2358-2493,dystrobrevin-alpha\_mrna,\_complete\_cds\_  
 u94747\_838-1276,wd\_repeat\_protein\_han11\_mrna,\_complete\_cds/gb=u94747\_/ntype=rna  
 all\_x74142\_1952-2535,hbf-1\_mrna\_for\_transcription\_factor\_  
 y09445cds\_1175-1517:in\_reversesequence,\_2206-  
 2368,mrna\_for\_transcription\_factor\_tbx5\_

Metagene 87

j05070\_1805-2303,type\_iv\_collagenase\_mrna,\_complete\_cds  
 u22028utr#1\_47-  
 168:in\_reversesequence,\_8031,cytochrome\_p450\_(cyp2a13)\_gene,\_complete\_cds,cytoc  
 hrome\_  
 u77968\_1294-1879,neuronal\_pas1\_(npas1)\_mrna,\_complete\_cds  
 x87767exon\_4-148,cd89\_gene,\_exon\_s1/gb=x87767\_/ntype=dna\_/annot=exon\_

Metagene 195

d87461\_2959-3517,mrna\_for\_kiaa0271\_gene,\_complete\_cds  
 m26004\_3326-3894,cr2/cd21/c3d/epstein-barr\_virus\_receptor\_mrna,\_complete\_cds\_  
 m65254\_1710-2184,\_protein\_phosphatase\_2a\_65\_kda\_regulatory\_subunit-  
 beta\_mrna,\_complete\_cds  
 s81243\_2102-  
 2660,\_chn=steroid/thyroid\_orphan\_receptor\_homolog\_gene\_[human,\_fetal\_brain,\_mrn  
 a\_partial  
 u04847\_1262-1802,inil\_mrna,\_complete\_cds\_  
 u18383mrna\_2319-2587,nuclear\_respiratory\_factor(nrf-1)\_gene\_  
 u19147\_34-66,gage-6\_protein\_mrna,\_complete\_cds\_  
 u51920\_1447-1927,signal\_recognition\_particle\_(srp54)\_mrna,\_complete\_cds  
 u79290\_1380-1770,clone\_23908\_mrna\_sequence\_  
 u97502mrna\_2736-3126,butyrophilin\_(bt3.3)\_gene\_  
 all\_x51757\_1909-2414,heat-shock\_protein\_hsp70b'\_gene\_  
 x95152mrna\_10974-11274,brca2\_gene\_exon(and\_joined\_coding\_region)\_  
 y10812\_767-1253,mrna\_for\_fructose-bisphosphatase\_

Metagene 489



m92287\_1531-1999,cyclin\_d3\_(ccnd3)\_mrna,\_complete\_cds\_  
 u32989\_1109-1559,tryptophan\_oxygenase\_(tdo)\_mrna,\_complete\_cds\_  
 u90907\_1150-1612,clone\_23907\_mrna\_sequence\_  
 all\_x99268\_928-1367,mrna\_for\_b-hlh\_dna\_binding\_protein\_

Metagene 451

d10923\_1452-1962,mrna\_for\_hm74\_  
 d42038\_3730-4216,mrna\_for\_kiaa0087\_gene,\_complete\_cds\_  
 d50917\_4943-5489,mrna\_for\_kiaa0127\_gene,\_complete\_cds\_  
 d50918\_4053-4563,mrna\_for\_kiaa0128\_gene,\_partial\_cds\_  
 hg2530-ht2626\_at\_hg2530-ht2626\_adenylyl\_cyclase-associated\_protein  
 hg2796-ht2904\_at\_hg2796-ht2904\_neural\_cell\_adhesion\_molecule\_  
 hg3248-ht3425\_at\_hg3248-ht3425\_fibroblast\_growth\_factor,\_antisense\_mrna  
 all\_k01884\_587-888,blym-1\_transforming\_gene,\_complete\_coding\_region  
 l05568\_1937-2459,na+/cl-\_dependent\_serotonin\_transporter\_mrna,\_complete\_cds\_  
 l10374\_1461-1977,(clone\_ctg-a4)\_mrna\_sequence  
 l11695\_1767-2247,activin\_receptor-like\_kinase\_(alk-5)\_mrna,\_complete\_cds\_  
 l13436mrna\_3522-4020,guanylate\_cyclase\_mrna,\_complete\_mature\_peptide  
 l20321\_3112-3655,protein\_serine/threonine\_kinase\_stk2\_mrna,\_complete\_cds\_  
 l22206exon#3\_63-639,vasopressin\_receptor\_v2\_gene,\_complete\_cds\_  
 l38500cds\_1574-2102,na+/myo-  
 inositol\_cotransporter\_(slc5a3)\_gene,\_complete\_cds/gb=l38500\_/ntype=dna\_  
 l77563mrna\_129-591,dgs-f\_partial\_mrna/gb=l77563\_/ntype=rna  
 reverse\_l78833\_2267-  
 2337,\_brca1\_gene\_extracted\_frombrca1,\_rho7\_and\_vati\_genes,\_complete\_cds,\_and\_ip  
 f  
 m17863mrna\_242-822,preproinsulin-like\_growth\_factor\_ii\_(igf-  
 ii)\_variant\_mrna,\_complete\_cds\_  
 all\_m19720\_2034-2557,\_l-myc\_gene\_(l-myc\_protein)\_extracted\_froml-  
 myc\_protein\_gene,\_complete\_cds,\_l-m  
 m25164cds\_5-383:in\_reversesequence,\_265-1170,thyrotropin\_beta\_subunit\_gene  
 m55268mrna\_1094-1556,casein\_kinase\_ii\_alpha'\_subunit\_mrna,\_complete\_cds  
 m62302\_1939-2485,growth/differentiation\_factor(gdf-1)\_mrna,\_complete\_cds  
 m64788\_2759-3209,gtpase\_activating\_protein\_(rap1gap)\_mrna,\_complete\_cds  
 m65290\_1957-  
 2215,natural\_killer\_cell\_stimulatory\_factor\_(nksf)\_mrna,\_complete\_cds,\_clone\_p4  
 0\_  
 m95549\_1774-2194,sodium/glucose\_cotransporter-like\_protein\_mrna,\_complete\_cds\_  
 m98776mrna\_1864-2266,keratogene,\_complete\_cds\_  
 s78432mrna#1\_3-87,\_un-named-transcript-  
 1\_from\_sas=transmembraneprotein\_{5'\_region}\_[human,\_sarcomas,  
 u10686exon#2\_730-1267,mage-11\_antigen\_(magell)\_gene,\_complete\_cds  
 u12897\_1564-1870:in\_reversesequence,\_1900-1996,non-translated\_mrna\_sequence\_  
 u15173\_1781-2303,nip2\_(nip2)\_mrna,\_complete\_cds  
 u23736\_779-1348,gata-3\_binding\_protein\_g3b\_mrna,\_partial\_cds.  
 u28831\_532-964,protein\_immuno-reactive\_with\_anti-  
 pth\_polyclonal\_antibodies\_mrna,\_partial\_cds\_  
 u37352\_3505-  
 3961,protein\_phosphatase\_2a\_b'alpha1\_regulatory\_subunit\_mrna,\_complete\_cds\_  
 u37431mrna#1\_2114-  
 2540,hoxa1\_mrna,\_long\_transcript\_and\_alternatively\_spliced\_forms,\_complete\_cds\_  
 u43527\_180-728:not\_in\_gb\_record,malignant\_melanoma\_metastasis-suppressor\_(kiss-  
 1)\_gene,\_mrna,\_comple

u43944\_1705-1978,breast\_cancer\_cytosolic\_nadp(+)-  
 dependent\_malic\_enzyme\_mrna,\_partial\_cds  
 u47931mrna\_63-537,g-protein\_beta-  
 3\_subunit\_alternatively\_spliced\_form\_mrna\_sequence/gb=u47931\_/ntype  
 u52830\_19-271,cri-du-chat\_region\_mrna,\_clone\_csc8.  
 u55209\_3812-3977,myosin\_viiia\_transcriptmrna,\_complete\_cds\_  
 u63329cds\_1128-  
 1554:in\_reversesequence,\_1814,muty\_homolog\_(hmyh)\_gene,\_complete\_cds\_  
 u84011\_6566-  
 7127,glycogen\_debranching\_enzyme\_isoform(agl)\_mrna,\_alternatively\_spliced\_isofo  
 rm,\_compl  
 x04145cds\_286-454:in\_reversesequence,\_593-689,mrna\_for\_t-  
 cell\_receptor\_t3\_gamma\_polypeptide\_  
 x14690cds\_1150-1604:in\_reversesequence,\_1636-1676,mrna\_for\_plasma\_inter-alpha-  
 trypsin\_inhibitor\_heav  
 all\_x16983\_3252-3787,mrna\_for\_integrin\_alpha-4\_subunit\_  
 all\_x65962\_1115-1174,mrna\_for\_cytochrome\_p-450\_  
 all\_x79984\_16-269,aa1\_mrna/gb=x79984\_/ntype=rna  
 x89398exon#7\_695-1121,\_ung\_gene\_(uracil-dna-  
 glycosylase,\_ung2)\_extracted\_fromung\_gene\_for\_uracil\_dna  
 all\_z48541\_4517-5100,mrna\_for\_protein\_tyrosine\_phosphatase\_  
 z48579cds\_1852-2050:in\_reversesequence,\_2062-2392,mrna\_for\_disintegrin-  
 metalloprotease\_(partial)\_  
 reverse\_z84722\_11257-  
 11453,dna\_sequence\_from\_cosmid\_gg4\_from\_a\_contig\_from\_the\_tip\_of\_the\_short\_arm\_

Metagene 252

d10326\_1427-1981,mrna\_for\_pyruvate\_kinase  
 d49372\_197-755,mrna\_for\_eotaxin,\_complete\_cds  
 all\_d83407\_2601-3184,\_zaki-4\_mrna\_inskin\_fibroblast,\_complete\_cds  
 d87467\_5371-5857,mrna\_for\_kiaa0277\_gene,\_complete\_cds  
 hg167-ht167\_s\_at\_hg167-ht167\_hypothetical\_protein\_npiiy20  
 hg2810-ht2921\_at\_hg2810-ht2921\_homeotic\_protein\_pl2  
 hg3162-ht3339\_at\_hg3162-ht3339\_transcription\_factor\_iaa  
 hg3627-ht3836\_at\_hg3627-ht3836\_calcium\_channel,\_voltage-  
 gated,\_betasubunit,\_l\_type,\_altsplce\_2,\_ske  
 hg3638-ht3993\_s\_at\_hg3638-  
 ht3993\_amyloid\_beta\_(a4)\_precursor\_protein,\_altsplce\_4  
 hg4169-ht4439\_s\_at\_hg4169-ht4439\_syntaxin\_1b\_  
 hg830-ht830\_at\_hg830-ht830\_potassium\_channel\_  
 j02645mrna\_882-1314,translational\_initiation\_factor\_(eif-  
 2),\_alpha\_subunit\_mrna,\_complete\_cds  
 k02777\_139-621,t-cell\_receptor\_active\_alpha-chain\_mrna\_from\_jurkat\_cell\_line\_  
 100354exon\_7-361:not\_in\_gb\_record,cholecystokinin\_(cck)\_gene  
 l43821mrna\_3222-3774,enhancer\_of\_filamentation\_(hef1)\_mrna,\_complete\_cds  
 all\_m15517\_182-  
 480,\_ttr\_gene\_extracted\_frommutant\_prealbumin\_gene\_directly\_linked\_to\_familial\_  
 amyloi  
 all\_m17183\_531-752,parathyroid\_hormone-related\_protein\_mrna,\_complete\_cds  
 all\_m17466\_3487-4040,blood\_coagulation\_factor\_xii\_(f12)\_gene\_  
 m20642mrna\_369-898,alkali\_myosin\_light\_chainmrna,\_complete\_cds  
 m69238\_2033-  
 2579,aryl\_hydrocarbon\_receptor\_nuclear\_translocator\_(arnt)\_mrna,\_complete\_cds  
 m90299mrna\_2142-2628,glucokinase\_(gck)\_mrna,\_complete\_cds

s43646\_1904-2402,\_cytokeratin[human,\_epidermis,\_mrna,\_2427\_nt]\_  
 s77582\_2-  
 55,\_hervk10/hummtv\_reverse\_transcriptase\_homolog\_{clone\_rt240}\_{human,\_multiple  
 \_sclerosis,\_  
 s78798\_1252-1687,\_1-phosphatidylinositol-4-phosphate\_5-  
 kinase\_isoform\_c\_[human,\_peripheral\_blood\_leu  
 s79219\_344-902,\_metastasis-  
 associated\_gene\_[human,\_highly\_metastatic\_lung\_cell\_subline\_anip[937],\_mr  
 s82592\_357-861,\_evi-1=evi-  
 1\_protein\_{3'\_region,\_deletion\_region}\_{human,\_megakaryoblastoid\_cell\_line  
 u13219\_1945-2473,forkhead\_protein\_freac-1\_mrna,\_complete\_cds\_  
 u18549exon#2\_1091-1571,gpr6\_g\_protein-coupled\_receptor\_gene,\_complete\_cds  
 u40317\_5400-  
 5965,protein\_tyrosine\_phosphatase\_ptpsigma\_(ptpsigma)\_mrna,\_complete\_cds\_  
 u49250\_2323-2851,putative\_cerebral\_cortex\_transcriptional\_regulator\_t-brain-  
 1\_(tbr-1)\_mrna,\_complete  
 u58130\_2887-3301,bumetanide-sensitive\_na-k-  
 2cl\_cotransporter\_(nkcc2)\_mrna,\_complete\_cds  
 u67615\_12883-13381,beige\_protein\_homolog\_(chs)\_mrna,\_complete\_cds  
 u77846mrna\_979-  
 1356,elastin\_gene,\_partial\_cds\_and\_partial\_3'\_utr,elastin\_gene,\_partial\_cds\_and  
 \_parti  
 u79277\_986-1520,clone\_23548\_mrna\_sequence  
 u89995\_3040-3460,dna\_binding\_protein\_fkhl15\_(fkhl15)\_mrna,\_complete\_cds  
 u92015\_605-1031,clone\_143789\_defective\_mariner\_transposon\_hsmar2\_mrna\_sequence\_  
 all\_x07876\_1706-2205,mrna\_for\_irp\_protein\_(int-1\_related\_protein)  
 x16706cds\_541-931:in\_reversesequence,\_970,fra-2\_mrna  
 x54380mrna\_4050-4590,mrna\_for\_pregnancy\_zone\_protein\_  
 all\_x64269\_2501-2754,gene\_mttf1\_for\_mitochondrial\_transcription\_factor\_1\_  
 x68561cds\_2234-2324:in\_reversesequence,\_2547-2943,spr-  
 1\_mrna\_for\_gt\_box\_binding\_protein\_  
 all\_x69920\_2736-3249,mrna\_for\_calcitonin\_receptor  
 all\_x73079\_2348-2919,encoding\_polymeric\_immunoglobulin\_receptor\_  
 all\_x77737\_992-  
 1431,mrna\_for\_red\_cell\_anion\_exchanger\_(epb3,\_ae1,\_band\_3)\_3'\_non-  
 coding\_region\_  
 all\_x78342\_1655-1857,pisslre\_mrna  
 x78711cds\_1553-1638:in\_reversesequence,\_1665-  
 1735,mrna\_for\_glycerol\_kinase\_testis\_specific\_1  
 x87871cds\_939-1367:in\_reversesequence,\_1472-  
 1588,mrna\_for\_hepatocyte\_nuclear\_factor\_4b  
 all\_x90846\_2935-  
 3407,mrna\_for\_mixed\_lineage\_kinase\_2,mrna\_for\_mixed\_lineage\_kinase\_2  
 x91220\_3940-4165,mrna\_for\_na-cl\_electroneutral\_thiazide-sensitive\_cotransporter  
 all\_z11502\_886-1451,mrna\_for\_intestine-specific\_annexin  
 z48051mrna\_1733-2303,gene\_for\_myelin\_oligodendrocyte\_glycoprotein\_(mog)\_  
 all\_z70218\_2-333,mrna\_for\_mn1\_protein\_(clone\_icrfp507i0498)  
 all\_z73903\_5001-5554,mrna\_for\_trpcla.  
 z96810cds\_482-968,dna\_sequence\_from\_pac\_452h17\_on\_chromosome\_x\_contains\_sodium-  
 and\_chloride-dependen

Metagene 334

d13146mrna#1\_2083-2551,\_2'\_3'-cyclic-nucleotide\_3'\_-  
 phosphodiesterase\_gene\_extracted\_from2'\_3'\_-c

d21235\_1418-1673,mrna\_for\_hhr23a\_protein,\_complete\_cds\_  
d83702\_2392-2902,brain\_mrna\_for\_photolyase\_homolog,\_complete\_cds\_  
d87452\_3950-4418,mrna\_for\_kiaa0263\_gene,\_complete\_cds\_  
d87459\_2144-2564,mrna\_for\_kiaa0269\_gene,\_complete\_cds\_  
l13848\_3675-4161,rna\_helicase\_a\_mrna,\_complete\_cds\_  
l20591exon\_1-295:not\_in\_gb\_record,annexin\_iii\_(anx3)\_gene,\_alternative  
m22348\_3-494,mitochondrial\_ubiquinone-binding\_protein\_mrna,\_complete\_cds\_  
s74017\_1721-2213,\_nrf2=nf-e2-  
like\_basic\_leucine\_zipper\_transcriptional\_activator\_[human,\_hemin-induc  
s75313\_1197-  
1387,\_mjd1=mjd1\_protein\_{cag\_repeats}\_[human,\_brain,\_mrna,\_1776\_nt]\_  
u19765exon#5\_630-1194,nucleic\_acid\_binding\_protein\_gene,\_complete\_cds\_  
u64105\_2540-3104,guanine\_nucleotide\_exchange\_factor\_p115-  
rhogef\_mrna,\_partial\_cds  
u67156\_4641-5151,mitogen-  
activated\_kinase\_kinase\_kinase(mapkkk5)\_mrna,\_complete\_cds\_  
all\_x06318\_2381-2541,mrna\_for\_protein\_kinase\_c\_(pkc)\_type\_beta\_i\_  
x55740mrna\_2940-3516,placental\_cdna\_coding\_for\_5'\_nucleotidase\_(ec\_3.1.3.5)  
all\_x76648\_338-777,mrna\_for\_glutaredoxin\_  
z78291\_28-223,mrna\_(clone\_1d8).

Metagene 311

d13305\_1572-1992,mrna\_for\_brain\_cholecystokinin\_receptor\_  
d55640\_110-635,monocyte\_pabl\_(pseudoautosomal\_boundary-  
like\_sequence)\_mrna,\_clone\_mo2/gb=d55640\_/nty  
l19063exon\_79-451,glial-  
derived\_neurotrophic\_factor\_gene,\_complete\_cds/gb=l19063\_/ntype=dna\_/annot=e  
l39211\_1877-  
2399,mitochondrial\_carnitine\_palmitoyltransferase\_i\_mrna,\_complete\_cds  
m10051\_4111-4651,insulin\_receptor\_mrna,\_complete\_cds\_  
m69203cds\_4-254:in\_reversesequence,\_122-144,cytokine\_(scya2)\_gene\_  
u03644\_1050-1452,recepin\_mrna,\_complete\_cds  
u17566\_2214-2754,65\_kda\_hydrophobic\_protein\_mrna,\_complete\_cds\_  
u78628\_7-  
199,leukemia\_inhibitory\_factor\_receptor\_mrna,\_5'\_untranslated\_region/gb=u78628\_  
/ntype=rna\_  
x66363cds\_1279-1459:in\_reversesequence,\_1594-1702,mrna\_pctaire-  
1\_for\_serine/threonine\_protein\_kinase  
x85785mrna\_1060-1498,darc\_gene  
x99076mrna\_736-1234,nrgn\_gene,\_exons\_2,3\_&(joined\_cds)\_  
y00451cds\_1461-1890:in\_reversesequence,\_2009-2037,mrna\_for\_5-  
aminolevulinate\_synthase\_

Metagene 175

m31661\_2134-2674,prolactin\_(prl)\_receptor\_mrna,\_complete\_cds\_  
u12139exon\_13-  
151,alpha1(xi)\_collagen\_(col11a1)\_gene,\_5'\_region\_and\_exon/gb=u12139\_/ntype=dna  
\_/annot

Metagene 43

d11086\_976-1408,mrna\_for\_interleukinreceptor\_gamma\_chain  
 hg2090-ht2152\_s\_at\_hg2090-ht2152\_external\_membrane\_protein,\_130\_kda  
 hg2639-ht2735\_s\_at\_hg2639-ht2735\_single-stranded\_dna-binding\_protein\_mssp-1  
 m30257\_2214-2709,vascular\_cell\_adhesion\_moleculermrna,\_complete\_cds  
 m33600\_581-1109,mhc\_ii\_hla-dr-beta-1\_(hla-drb1)\_mrna,\_complete\_cds\_  
 m37033\_915-1395,cd53\_glycoprotein\_mrna,\_complete\_cds\_  
 m60830exon\_1480-2020,evi2b3p\_gene,\_exon\_and\_complete\_cds\_  
 m83221\_1788-2262,i-rel\_mrna,\_complete\_cds\_  
 s73813\_1337-  
 1775,\_cd39=lymphoid\_cell\_activation\_antigen\_[human,\_b\_lymphoblastoid\_cell\_line,  
 \_mp-1,\_mr  
 u95626mrna#3\_2792-  
 3278,\_ccr2\_gene\_(ccr2a)\_extracted\_fromccr2b\_(ccr2),\_ccr2a\_(ccr2),\_ccr5\_(ccr5)\_a  
 nd\_  
 x04500exon#7\_244-778,gene\_for\_prointerleukinbeta  
 x56841mrna\_1269-1713,hla-e\_gene  
 all\_x57522\_2229-2788,ring4\_cdna  
 x64072cds\_1948-2281:not\_in\_gb\_record,\_hsapiens\_cd18\_exon\_2\_  
 all\_x99687\_221-732,mrna\_for\_methyl-cpg-  
 binding\_protein\_2,\_intron/gb=x99687/\_ntype=rna\_  
 all\_y00062\_3996-4597,mrna\_for\_t200\_leukocyte\_common\_antigen\_(cd45,\_lc-a)\_  
 y09561cds\_1238-1676:in\_reversesequence,\_1798,mrna\_for\_p2x7\_receptor\_  
 z14982mrna#1\_616-1150,\_mhc-encoded\_proteasome\_subunit\_gene\_lamp7-  
 e1\_gene\_(proteasome\_subunit\_lmp7)\_e

Metagene 458

hg2339-ht2435\_at\_hg2339-ht2435\_nuclear\_factor\_1,\_variant\_hepatic\_  
 l11702\_2837-3335,phospholipase\_d\_mrna,\_complete\_cds  
 l38820exon\_170-620,hmc\_i\_antigen-like\_glycoprotein\_(cd1d)\_gene  
 m93119\_2345-2777,zinc-finger\_dna-binding\_motifs\_(ia-1)\_mrna,\_complete\_cds  
 all\_u34301\_1497-  
 1528,nonmuscle\_myosin\_heavy\_chain\_iib\_gene,\_promoter\_region\_and\_exon/gb=u34301\_  
 /ntyp  
 u66497\_3549-4047,leptin\_receptor\_splice\_variant\_form\_13.2\_mrna,\_complete\_cds.  
 u73191\_1078-1582,inward\_rectifier\_potassium\_channel\_(kir1.3),\_complete\_cds\_  
 all\_x75756\_3248-3699,mrna\_for\_protein\_kinase\_c\_mu

Metagene 222

d87444\_3517-3823,mrna\_for\_kiaa0255\_gene,\_complete\_cds  
 d89859\_2331-2841,mrna\_for\_zinc\_fingerprotein,\_complete\_cds  
 hg162-ht3165\_at\_hg162-ht3165\_tyrosine\_kinase,\_receptor\_axl,\_altsplice\_2  
 hg33-ht33\_at\_hg33-ht33\_ribosomal\_protein\_s4,\_x-linked  
 l06147\_1586-2042,(clone\_sy11)\_golgin-95\_mrna,\_complete\_cds\_  
 l10910\_2084-2552,splicing\_factor\_(cc1.3)\_mrna,\_complete\_cds\_  
 m18737mrna\_269-  
 815,\_gjalp1\_gene\_extracted\_fromhanukah\_factor\_serine\_protease\_(huhf)\_mrna,\_comp  
 lete\_c

all\_m29277\_2842-  
 2926, isolate\_juso\_muc18\_glycoprotein\_mrna\_(3'\_variant),\_complete\_cds, isolate\_ju  
 so\_mu  
 m33493\_504-792, tryptase-iii\_mrna, \_3'\_end\_  
 m83822\_6791-7253, beige-like\_protein\_(bgl)\_mrna, \_partial\_cds  
 s52969\_cds1\_s\_at\_s52969\_s52969, not\_in\_gb\_record, \_description:\_alpha-  
 1,3\_fucosyltransferase\_gene\_extr  
 u07620\_1861-2215, map\_kinase\_mrna, \_complete\_cds\_  
 u48705mrna\_3326-3867, receptor\_tyrosine\_kinase\_ddr\_gene, \_complete\_cds  
 u63295\_1285-1795, seven\_in\_absentia\_homolog\_mrna, \_complete\_cds  
 u67122\_469-728, ubiquitin-related\_protein\_sumo-1\_mrna, \_complete\_cds.  
 u70660\_31-463, copper\_transport\_protein\_hah1\_(hah1)\_mrna, \_complete\_cds  
 x80907\_2095-2557, mrna\_for\_p85\_beta\_subunit\_of\_phosphatidyl-inositol-3-kinase\_  
 x84707mrna\_73-511, mia\_gene  
 x89211cds\_1571-  
 2129, dna\_for\_endogenous\_retroviral\_like\_element/gb=x89211\_/ntype=dna\_/annot=cds  
 -  
 all\_z21966\_1647-2182, mpou\_homeobox\_protein\_mrna  
 z36715cds\_1026-1200:in\_reversesequence, \_1491-  
 1557, mrna\_for\_net\_transcription\_factor\_

Metagene 249

m15780cds\_13-  
 304, dna/endogenouspapillomavirus\_type(hpv)\_dna, \_right\_flank\_and\_viral\_host\_junc  
 tion/gb=  
 m22092exon\_6-42, neural\_cell\_adhesion\_molecule\_(n-  
 cam)\_gene, \_exon\_sec\_and\_partial\_cds/gb=m22092\_/ntyp  
 u18004\_31-205, \_hsu18004cdna\_

Metagene 432

ac002115\_66940-67151:in\_ac002115cds#2\_675-  
 1000, \_cox6b\_gene\_(coxg)\_extracted\_fromdna\_from\_overlapping  
 hg371-ht26388\_s\_at\_hg371-ht26388\_mucin\_1, \_epithelial, \_altsplise\_9  
 j05252\_1611-2178, kex2-like\_endoprotease\_mrna, \_complete\_cds.  
 j05556mrna\_1640-2198, collagenase\_mrna, \_complete\_cds\_  
 all\_m18255\_18-408:in\_m18255cds\_47, \_prkacb\_gene\_(protein\_kinase\_c-beta-  
 2)\_extracted\_fromprotein\_kinas  
 m60614\_1996-2060, wilms\_tumor\_(wit-1)\_associated\_protein\_mrna, \_complete\_cds\_  
 s75213\_1727-2087, \_type-  
 iva\_cyclic\_amp\_specific\_phosphodiesterase\_hpde4a\_[human, \_t-cells, \_mrna\_partia  
 u00954\_738-1224, clone\_ce29\_7.2\_(cac)n/(gtg)n\_repeat-containing\_mrna  
 u38904\_1210-1744, zinc\_finger\_protein\_c2h2-25\_mrna, \_complete\_cds  
 u45976\_1748-  
 2210, clathrin\_assembly\_protein\_lymphoid\_myeloid\_leukemia\_(calm)\_mrna, \_complete\_  
 cds\_  
 u52682\_4755-  
 5241, lymphocyte\_specific\_interferon\_regulatory\_factor/interferon\_regulatory\_fac  
 tor(lsirf  
 u58096\_798-1056, testis-specific\_protein\_(tspy)\_mrna, \_complete\_cds  
 u65406mrna#1\_1860-2370, \_kcnj1\_gene\_(potassium\_channel\_rom-  
 k3)\_extracted\_fromalternatively\_spliced\_po

u71203\_339-753,rit\_mrna,\_complete\_cds  
u89336exon#13\_173-  
695,\_unknown\_gene\_extracted\_fromhla\_iii\_region\_containing\_notch4\_gene,\_partial\_  
seq  
all\_x16660\_1795-2049,\_open\_reading\_frame\_p25\_(aa\_1-  
223)\_gene\_extracted\_fromhtlv-i\_related\_endogenous  
x71877cds\_587-767:in\_reversesequence,\_783-1089,mrna\_for\_chymotrypsin-  
like\_protease\_ctrl-1  
all\_x89894\_2017-2486,mrna\_for\_nuclear\_receptor\_  
x93498mrna\_589-1117,mrna\_for\_21-glutamic\_acid-rich\_protein\_(21-garp)\_  
x93512cds\_61-157:in\_reversesequence,\_175-  
211,mrna\_for\_telomeric\_dna\_binding\_protein\_(orf2)  
y00067mrna\_2655-3207,gene\_for\_neurofilament\_subunit\_m\_(nf-m)  
y10262cds\_1163-1693,eya3\_gene/gb=y10262\_/ntype=dna\_/annot=cds

Metagene 453

d16481\_1438-1942,mrna\_for\_mitochondrial\_3-ketoacyl-coa\_thiolase\_beta-  
subunit\_of\_trifunctional\_protei  
d50914\_1543-2077,mrna\_for\_kiaa0124\_gene,\_partial\_cds\_  
d82060\_1801-  
2215,kidney\_mrna\_for\_putative\_membrane\_protein\_with\_histidine\_rich\_charge\_clust  
ers,\_comp  
d83778\_4662-5154,mrna\_for\_kiaa0194\_gene,\_partial\_cds\_  
d87443\_5442-5988,mrna\_for\_kiaa0254\_gene,\_complete\_cds  
hg1400-ht1400\_s\_at\_hg1400-  
ht1400\_carboxyl\_methyltransferase,\_aspartate,\_altsplise\_1  
hg2463-ht2559\_at\_hg2463-ht2559\_guanine\_nucleotide-binding\_protein\_g25k\_  
106845\_1728-2268,cysteinyl-trna\_synthetase\_mrna,\_partial\_cds\_  
113278\_1231-1753,zeta-crystallin/quinone\_reductase\_mrna,\_complete\_cds\_  
113773\_8844-9252,af-4\_mrna,\_complete\_cds\_  
121954exon\_36-384:not\_in\_gb\_record,peripheral\_benzodiazepine\_receptor\_gene  
125085\_103-361,sec61-complex\_beta-subunit\_mrna,\_complete\_cds\_  
138961\_1919-  
2429,putative\_transmembrane\_protein\_precursor\_(b5)\_mrna,\_complete\_cds  
142572mrna\_2192-2648,p87/89\_gene,\_complete\_cds  
m14200mrna\_139-469,diazepam\_binding\_inhibitor\_(dbi)\_mrna,\_complete\_cds  
m24400mrna\_282-840,chymotrypsinogen\_mrna,\_complete\_cds  
m31899\_2318-2708,dna\_repair\_helicase\_(ercc3)\_mrna,\_complete\_cds  
m64992\_741-1185,prosomeal\_protein\_p30-33k\_(pros-30)\_mrna,\_complete\_cds  
m65131mrna\_2187-2709,methylmalonyl-coa\_mutase\_(mcm)\_mrna,\_complete\_cds  
m73547\_2649-3153,polyposis\_locus\_(dpl\_gene)\_mrna,\_complete\_cds\_  
m83233\_3488-3974,transcription\_factor\_(htf4a)\_mrna,\_complete\_cds  
s74728\_1245-  
1773,\_antiquitin=26g\_turgor\_protein\_homolog\_[human,\_kidney,\_mrna,\_1809\_nt]  
s78569\_5723-6161,\_laminin\_alphachain\_[human,\_fetal\_lung,\_mrna,\_6204\_nt]  
u10117mrna\_474-954,endothelial-  
monocyte\_activating\_polypeptide\_ii\_mrna,\_complete\_cds\_  
u10439\_5983-6529,double-stranded\_rna\_adenosine\_deaminase\_mrna,\_complete\_cds  
u12535\_3273-  
3783,epidermal\_growth\_factor\_receptor\_kinase\_substrate\_(eps8)\_mrna,\_complete\_cd  
s\_  
u14193\_135-687,tfiia\_gamma\_subunit\_mrna,\_complete\_cds  
u15009\_25-541,snrnp\_core\_protein\_sm\_d3\_mrna,\_complete\_cds  
u26312\_166-686,heterochromatin\_protein\_hplhs-gamma\_mrna,\_complete\_cds

u28686\_973-1486,putative\_rna\_binding\_protein\_rnpl\_mrna,\_complete\_cds\_  
 u41654\_1159-1525,adenovirus\_protein\_e3-14.7k\_interacting\_protein(fip-  
 1)\_mrna,\_complete\_cds  
 u41740\_7119-7635,trans-golgi\_p230\_mrna,\_complete\_cds\_  
 u43899\_2320-2740,signal\_transducing\_adaptor\_molecule\_stam\_mrna,\_complete\_cds\_  
 u50523\_858-1344,brca2\_region,\_mrna\_sequence\_cg037  
 u50950\_1546-2074,infant\_brain\_unknown\_product\_mrna,\_complete\_cds\_  
 u57099\_666-1158,apeg-1\_mrna,\_complete\_cds  
 u67319\_2133-2529,lice2\_beta\_cysteine\_protease\_mrna,\_complete\_cds.  
 u69645\_551-1037,zinc\_finger\_protein\_mrna,\_complete\_cds\_  
 u70987\_1308-1830,gap\_binding\_protein\_p62dok\_(dok)\_mrna,\_complete\_cds\_  
 u93237mrna#1\_2162-  
 2738,\_men1\_gene\_(menin)\_extracted\_frommenin\_(men1)\_gene,\_complete\_cds.  
 all\_x12791\_311-870,mrna\_for\_19kd\_protein\_of\_signal\_recognition\_particle\_(srp)  
 x52151cds\_1148-1394:in\_reversesequence,\_1884-  
 1980,arylsulphatase\_a\_mrna,\_complete\_cds  
 x52730mrna#1\_455-911,\_phenylethanolamine\_n-  
 methyltransferase\_gene\_extracted\_fromgene\_for\_phenylethan  
 x54326cds\_4149-4299:in\_reversesequence,\_4363-4507,mrna\_for\_glutaminyll-  
 trna\_synthetase\_  
 all\_x63469\_962-1467,mrna\_for\_transcription\_factor\_tfiie\_beta\_  
 all\_x65644\_8589-9100,mrna\_mbp-2\_for\_mhc\_binding\_protein\_2  
 x75535exon#8\_2216-2768,mrna\_for\_pxf\_protein  
 all\_x75962\_913-1340,mrna\_for\_ox40\_homologue  
 all\_x77548\_2835-3418,\_hsapiens\_cdna\_for\_rfg\_  
 all\_x84195\_230-723,mrna\_for\_acylphosphatase,\_muscle\_type\_(mt)\_isoenzyme  
 x99296exon#1\_28-  
 223,\_rd\_fromrd\_gene\_(5'\_partial)\_and\_g11a\_gene\_(5'\_partial)/gb=x99296/\_ntype=dn  
 a\_/an  
 all\_y00264\_2984-3321,mrna\_for\_amyloid\_a4\_precursor\_of\_alzheimer\_disease  
 all\_z22551\_4012-4595,kinectin\_gene\_  
 z46973cds\_2460-2634:in\_reversesequence,\_2711-  
 2891,mrna\_for\_phosphatidylinositol\_3-kinase  
 z97074\_852-1176,mrna\_for\_rab9\_effector\_p40,\_complete\_cds

Metagene 415

d83657exon#1-3\_13-  
 167:in\_reversesequence,\_2025:not\_in\_gb\_record,dna\_for\_caaf1\_(calcium-  
 binding\_prote  
 hg4740-ht5187\_at\_hg4740-ht5187\_transcription\_factor\_eb\_  
 m64925\_1400-  
 1940,palmitoylated\_erythrocyte\_membrane\_protein\_(mpp1)\_mrna,\_complete\_cds  
 u18088\_1188-1742,3',5'--  
 cyclic\_amp\_phosphodiesterase\_inactive\_splice\_variant\_hspde4a8a\_mrna,\_comple  
 u22377\_5634-6168,zn-15\_related\_zinc\_finger\_protein\_(rlf)\_mrna,\_complete\_cds  
 u41766\_3235-3653,metalloprotease/disintegrin/cysteine-  
 rich\_protein\_precursor\_(mdc9)\_mrna,\_complete\_c  
 u43185\_3667-  
 4243,signal\_transducer\_and\_activator\_of\_transcription\_stat5a\_mrna,\_complete\_cds  
 u53476\_841-1351,proto-oncogene\_wnt7a\_mrna,\_complete\_cds  
 v00536mrna\_811-1135,\_ifng\_gene\_extracted\_fromimmune\_interferon\_(ifn-  
 gamma)\_gene\_  
 y00282cds\_1657-1849:in\_reversesequence,\_2341-2383,mrna\_for\_ribophorin\_ii



## Metagene 257

ac002115cds#4\_474-750:in\_reversesequence,\_100047-  
 100269,\_cox6b\_gene\_(coxg)\_extracted\_fromdna\_from\_ov  
 af001620\_1478-2000,trabecular\_meshwork-  
 induced\_glucocorticoid\_response\_protein\_(tigr)\_mrna,\_complete  
 hg4185-ht4455\_at\_hg4185-ht4455\_estrogen\_sulfotransferase,\_ste  
 hg537-ht537\_at\_hg537-ht537\_collagen,\_type\_viii,\_alpha\_2  
 l19183mrna\_1533-1959,mac30\_mrna,\_3'\_end  
 l27584cds\_1093-1400:in\_reversesequence,\_1464-  
 1677,ca\_channel\_b3\_subunit\_(cal\_bet\_3)\_mrna,\_complete\_c  
 l39009mrna\_109-  
 475,iv\_alcohol\_dehydrogenase(adh7)\_gene,\_5'\_flanking\_region/gb=l39009/\_ntype=dn  
 a/\_ann  
 m10058mrna\_706-1252,asialoglycoprotein\_receptor\_h1\_mrna,\_complete\_cds  
 m18700cds\_288-784,elastase\_iii\_a\_gene,\_exon\_8  
 m24122mrna\_309-774,myosin\_alkali\_light\_chain\_(ventricular)\_mrna,\_complete\_cds  
 m26679exon#2\_505-925,homeobox\_protein\_(hox-1.3)\_gene,\_complete\_cds  
 m73047\_4025-4565,tripectidyl\_peptidase\_ii\_mrna,\_complete\_cds  
 s67156\_876-1368,\_asp=aspartoacylase [human,\_kidney,\_mrna,\_1435\_nt]  
 u07225\_1430-1958,p2u\_nucleotide\_receptor\_mrna,\_complete\_cds  
 u18288\_2804-3314,clone\_ciita-10\_mhc\_ii\_transactivator\_ciita\_mrna,\_complete\_cds\_  
 u19878\_1137-1647,transmembrane\_protein\_mrna,\_complete\_cds  
 x52479cds\_1689-1995:in\_reversesequence,\_2040-  
 2202,pkc\_alpha\_mrna\_for\_protein\_kinase\_c\_alpha\_  
 x99802\_1983-2463,mrna\_for\_zyg\_homologue  
 z33642mrna\_2763-3291,v7\_mrna\_for\_leukocyte\_surface\_protein\_

## Metagene 321

all\_d13315\_1488-1975,mrna\_for\_lactoyl\_glutathione\_lyase  
 d14812\_1345-1747,mrna\_for\_kiaa0026\_gene,\_complete\_cds  
 d16469\_2264-2738,mrna\_for\_orf,\_xq\_terminal\_portion\_  
 d23662\_61-565,mrna\_for\_ubiquitin-like\_protein,\_complete\_cds  
 d30756\_4053-4611,mrna\_for\_kiaa0049\_gene,\_complete\_cds  
 d31767\_1338-1812,mrna\_for\_kiaa0058\_gene,\_complete\_cds  
 d50495mrna\_493-1033,mrna\_for\_transcription\_elongation\_factor\_s-ii,\_hs-ii-  
 t1,\_complete\_cds  
 d86985\_5502-5946,mrna\_for\_kiaa0232\_gene,\_complete\_cds  
 d87438\_3322-3808,mrna\_for\_kiaa0251\_gene,\_partial\_cds\_  
 hg1595-ht4788\_s\_at\_hg1595-  
 ht4788\_heterogeneous\_nuclear\_ribonucleoprotein\_i,\_altsplice\_2,\_ptb-1\_  
 hg4683-ht5108\_s\_at\_hg4683-  
 ht5108\_tumor\_necrosis\_factor\_receptorassociated\_protein\_trap3\_  
 hg998-ht998\_s\_at\_hg998-ht998\_sulfotransferase,\_phenol-preferring\_  
 j03805\_926-1491,phosphatase\_2a\_mrna,\_partial\_cds\_  
 l19686mrna\_61-  
 493,macrophage\_migration\_inhibitory\_factor\_(mif)\_gene,\_complete\_cds  
 l36151\_2433-2907,phosphatidylinositol\_4-kinase\_mrna,\_complete\_cds\_  
 l38810mrna\_706-1246,thyroid\_receptor\_interactor\_(trip1)\_mrna,\_complete\_cds  
 l40391mrna\_889-1435,(clone\_s153)\_mrna\_fragment  
 l43964\_1671-2211,(clone\_f-t03796)\_stm-2\_mrna,\_complete\_cds  
 l77213mrna\_479-959,phosphomevalonate\_kinase\_mrna,\_complete\_cds

m34175mrna\_5100-5670,beta\_adaptin\_mrna,\_complete\_cds\_  
 m62762\_681-1083,vacuolar\_h+\_atpase\_proton\_channel\_subunit\_mrna,\_complete\_cds\_  
 m63959\_1030-1444,alpha-2-macroglobulin\_receptor-associated\_protein\_mrna,\_complete\_cds\_  
 m69023\_524-1088,globin\_gene  
 m98343\_2695-3163,amplaxin\_(ems1)\_mrna,\_complete\_cds\_  
 u02556\_1579-2101,rp3\_mrna,\_complete\_cds\_  
 u17969exon#6\_165-663,initiation\_factor\_eif-5a\_gene,\_complete\_cds\_  
 u19796\_406-760,melanoma\_antigen\_p15\_mrna,\_complete\_cds\_  
 u22897\_1798-2338,nuclear\_domainprotein\_(ndp52)\_mrna,\_complete\_cds\_  
 u25435\_3227-3737,transcriptional\_repressor\_(ctcf)\_mrna,\_complete\_cds\_  
 u31930\_411-963,deoxyuridine\_nucleotidohydrolase\_mrna,\_complete\_cds\_  
 u36341mrna#1\_3376-3862,\_slc6a8\_gene\_(creatine\_transporter)\_extracted\_fromxq28\_cosmid,\_creatine\_trans  
 ans  
 u49869mrna\_785-887,ubiquitin\_gene,\_complete\_cds\_  
 u64444\_633-1113,ubiquitin\_fusion-degradation\_protein\_(ufd1l)\_mrna,\_complete\_cds\_  
 u72342mrna\_5025-5499,platelet\_activating\_factor\_acetylhydrolase,\_brain\_isoform,\_45\_kda\_subunit\_(lis1)  
 u78095\_942-1434,placental\_bikunin\_mrna,\_complete\_cds\_  
 u80017mrna#2\_5760-6039,\_btf2p44\_gene\_(basic\_transcription\_factorp44)\_extracted\_frombasic\_transcripti  
 pti  
 u81556\_1541-1925,hypothetical\_protein\_a4\_mrna,\_complete\_cds\_  
 all\_x04526\_2577-2968,liver\_mrna\_for\_beta-subunit\_signal\_transducing\_proteins\_gs/gi\_(beta-g)  
 x13546mrna\_657-1137,\_puthmg-17\_protein\_gene\_extracted\_fromhmg-17\_gene\_for\_non-histone\_chromosomal\_pr  
 x15341cds\_13-235:in\_reversesequence,\_374-500,cox\_via-l\_mrna\_for\_cytochrome\_c\_oxidase\_liver-specific  
 all\_x55330\_1609-2120,mrna\_for\_aspartylglucosaminidase  
 x56681mrna\_1311-1835,jund\_mrna\_  
 all\_x64330\_3792-4243,mrna\_for\_atp-citrate\_lyase  
 all\_x64364\_1014-1561,mrna\_for\_m6\_antigen\_  
 all\_x75593\_679-1202,mrna\_for\_rab\_13  
 x82103cds\_660-840:in\_reversesequence,\_954-1128,mrna\_for\_beta-cop  
 all\_x84709\_1088-1683,mrna\_for\_mediator\_of\_receptor-induced\_toxicity  
 z35093cds\_674-842:in\_reversesequence,\_898-976,mrna\_for\_surf-1\_

Metagene 473

j00219cds\_110-467:in\_reversesequence,\_4721-4823,immune\_interferon\_(ifn-gamma)\_gene,\_complete\_cds\_  
 s78873\_291-835,\_mss4=zn2+\_binding\_protein/guanine\_nucleotide\_exchange\_factor\_[human,\_brain  
 ,\_mrna\_par  
 all\_s83366\_910-2840,\_region\_centromeric\_to\_t(12;17)\_brakepoint:\_orf1/unknown\_43\_amino\_acid\_transcrip  
 y10515mrna\_79-307,mrna\_for\_cd58\_t7\_protein/gb=y10515\_/ntype=rna  
 z83800\_115-505,mrna\_for\_cytoplasmic\_dynein\_heavy\_chain\_(partial,\_id\_hdhc11)

Metagene 470

d49677\_905-1445,u2af1-rs2\_mrna,\_complete\_cds\_  
 hg2797-ht2905\_s\_at\_hg2797-ht2905\_clathrin,\_light\_polypeptide\_altsplice\_1  
 122548\_2914-3334,collagen\_type\_xviii\_alpha(coll18a1)\_mrna,\_partial\_cds\_  
 127624\_373-917,tissue\_factor\_pathway\_inhibitor-2\_mrna,\_complete\_cds\_  
 m57710\_355-865,ige-binding\_protein\_(epsilon-bp)\_mrna,\_complete\_cds\_  
 s54005\_2-197,\_thymosin\_beta-  
 10\_[human,\_metastatic\_melanoma\_cell\_line,\_mrna,\_453\_nt]\_  
 s75295\_2339-  
 2915,\_nucleoprotein\_interactor\_1=srp1\_homolog\_[human,\_cervical\_carcinoma\_hela\_c  
 ells,\_mrn  
 s81578\_13-271,\_dioxin-  
 responsive\_gene\_{putative\_polyadenylation\_signal\_region}\_[human,\_hepatoma\_g2\_c  
 u09410\_1481-2003,zinc\_finger\_protein\_znf131\_mrna,\_partial\_cds  
 u26648\_936-1482,syntaxinmrna,\_complete\_cds  
 u46025cds\_2254-2710:in\_reversesequence,\_2777-  
 2843,translation\_initiation\_factor\_eif-3\_p110\_subunit\_g  
 all\_x57348\_844-1377,mrna\_(clone\_9112)  
 all\_x66087\_3046-3563,a-myb\_mrna  
 all\_x69433\_1312-1733,mrna\_for\_mitochondrial\_isocitrate\_dehydrogenase\_(nadp+)\_  
 x70476mrna\_2526-3024,subunit\_of\_coatomer\_complex  
 x98507cds\_2790-3018:in\_reversesequence,\_3131-3293,mrna\_for\_myosin-i\_beta  
 y08136cds\_292-496:in\_reversesequence,\_520-820,mrna\_for\_asm-  
 like\_phosphodiesterase\_3a

Metagene 462

d88155cds\_1025-1357:in\_reversesequence,\_439-576,dna\_for\_ad4bp\_(sf-1)\_gene\_  
 hg3925-ht4195\_at\_hg3925-ht4195\_surfacant\_protein\_sp-a2\_delta\_  
 j02960cds#1\_394-729:in\_reversesequence,\_1015-  
 1252,\_unknown\_protein\_gene\_extracted\_frombeta-2-adrener  
 178833exon#24\_1038-  
 1476,\_brca1\_gene\_extracted\_frombrca1,\_rho7\_and\_vati\_genes,\_complete\_cds,\_and\_ip  
 f3  
 m16937\_806-1310,homeo\_box\_c1\_protein,\_mrna,\_complete\_cds\_  
 all\_m21064\_1360-1426,migration\_inhibitory\_factor-  
 related\_protein(mrp14)\_gene,\_complete\_cds\_  
 m76558\_7124-7592,neuronal\_dhp-sensitive,\_voltage-  
 dependent,\_calcium\_channel\_alpha-1d\_subunit\_mrna,\_c  
 u18548exon\_620-1046,gpr12\_g\_protein\_coupled-receptor\_gene,\_complete\_cds  
 u29195exon\_927-1443,neuronal\_pentraxin\_ii\_(nptx2)\_gene\_  
 u32324\_1353-1671,interleukin-11\_receptor\_alpha\_chain\_mrna,\_complete\_cds  
 u92027\_524-1028,clone\_61501\_defective\_mariner\_transposon\_hsmar2\_mrna\_sequence  
 all\_x15218\_3012-3511,ski\_oncogene\_mrna\_  
 x51954exon\_10-  
 148,ucp\_gene\_for\_uncoupling\_protein\_exon/gb=x51954\_/ntype=dna\_/annot=exon\_  
 x52282cds\_1092-  
 1597,mrna\_for\_atrial\_natriuretic\_peptide\_clearance\_receptor\_(anp-c\_receptor)  
 all\_x96698\_662-1245,mrna\_for\_d1075-like\_gene\_  
 y09615cds\_891-1131:in\_reversesequence,\_1268-  
 1472,mrna\_for\_mitochondrial\_transcription\_termination\_fa  
 y13618\_7553-7895,mrna\_for\_dffry\_protein,\_abundant\_transcript  
 z73677mrna\_91-137,gene\_encoding\_plakophilin\_1b.

## Metagene 445

ab002314\_6334-6898,mrna\_for\_kiaa0316\_gene,\_complete\_cds/gb=ab002314\_/ntype=rna\_  
hg2600-ht2696\_at\_hg2600-ht2696\_guanine\_nucleotide-binding\_protein\_rap2b,\_ras-  
oncogene\_related  
hg2602-ht2698\_at\_hg2602-ht2698\_succinate\_dehydrogenase,\_flavoprotein\_subunit\_  
l27586\_1755-2205,tr4\_orphan\_receptor\_mrna,\_complete\_cds  
all\_m24748\_1170-1531,\_thra1\_gene\_(thyroid\_receptor\_alpha-  
1)\_extracted\_fromthyroid\_hormone\_receptor\_a  
u45983cds\_789-1005:in\_reversesequence,\_1304-1496,g\_protein-  
coupled\_receptor\_gpr-cy6\_gene,\_complete\_c  
u49187\_1780-2206,placenta\_(diff48)\_mrna,\_complete\_cds  
u66464\_2131-2701,hematopoietic\_progenitor\_kinase\_(hpk1)\_mrna,\_complete\_cds\_  
u70321\_1127-1643,herpesvirus\_entry\_mediator\_mrna,\_complete\_cds\_  
x66360cds\_1134-1518:in\_reversesequence,\_1629-1689,mrna\_pctaire-  
2\_for\_serine/threonine\_protein\_kinase  
all\_x90840\_6383-6942,mrna\_for\_axonal\_transporter\_of\_synaptic\_vesicles  
all\_z80777\_449-807,h2a/k\_gene

## Metagene 442

hg2075-ht2137\_s\_at\_hg2075-ht2137\_camp-responsive\_element\_modulator,\_altsplce\_1  
m30135cds\_139-361:in\_reversesequence,\_4255-4303,p40\_t-  
cell\_and\_mast\_cell\_growth\_factor\_(hp40)\_gene,\_  
u13680\_767-1160,lactate\_dehydrogenase-c\_(ldh-c)\_mrna,\_complete\_cds\_  
u66033\_1937-2495,glypican-5\_(gpc5)\_mrna,\_complete\_cds  
all\_x51420\_2264-2781,mrna\_for\_tyrosinase-related\_protein\_  
x58298cds\_824-1371:in\_reversesequence,\_1441,mrna\_for\_interleukin-6-receptor\_

## Metagene 425

ab000410mrna\_947-1442,hogg1\_mrna,\_complete\_cds\_  
d13118\_61-  
523:in\_reversesequence,\_529,mrna\_for\_atp\_synthase\_subunit\_c\_encoded\_by\_p1\_gene  
d16611\_1726-2299,mrna\_for\_coproporphyrinogen\_oxidase,\_complete\_cds\_  
d85418\_875-1403,mrna\_for\_phosphatidylinositol-glycan-class\_c\_(pig-  
c),\_complete\_cds\_  
d86519\_1368-1932,mrna\_for\_neuropeptide\_y/peptide\_yy\_y6\_receptor,\_complete\_cds  
d87845\_1946-2216,mrna\_for\_platelet-  
activating\_factor\_acetylhydrolase\_2,\_complete\_cds\_  
hg3491-ht3685\_at\_hg3491-ht3685\_zinc\_finger\_protein\_zfp-36  
j03925\_4110-4656,mac-  
1\_gene\_encoding\_complement\_receptor\_type\_3,\_cd11b,\_complete\_cds\_  
j04970\_1397-1715,carboxypeptidase\_m,\_3'\_end  
l14595\_1801-  
2077,alanine/serine/cysteine/threonine\_transporter\_(asct1)\_mrna,\_complete\_cds  
l34657mrna\_2757-3219,platelet/endothelial\_cell\_adhesion\_molecule-1\_(pecam-  
1)\_gene\_  
m28212\_175-691,gtp-binding\_protein\_(rab6)\_mrna,\_complete\_cds  
m55543mrna\_1356-1872,guanylate\_binding\_protein\_isoform\_ii\_(gbp-  
2)\_mrna,\_complete\_cds\_

m55683\_2732-3242, cartilage\_matrix\_protein\_(cmp)\_mrna, \_exons\_8-mar  
 m62424\_2868-3117, thrombin\_receptor\_mrna, \_complete\_cds  
 m63154\_977-1541, intrinsic\_factor\_mrna, \_complete\_cds  
 m95809\_1310-1850, basic\_transcription\_factor\_62kd\_subunit\_(btf2), \_complete\_cds  
 s83249\_19-349, \_ng-  
 tra=transporter\_protein/putative\_hormone\_extrusion\_pump\_[human, \_liver\_and\_vario  
 us\_  
 u03270\_626-1136, centrin\_mrna, \_complete\_cds\_  
 u20938\_3946-4348, lymphocyte\_dihydropyrimidine\_dehydrogenase\_mrna, \_complete\_cds.  
 u40992\_839-1175, heat\_shock\_protein\_hsp40\_homolog\_mrna, \_complete\_cds  
 u68133\_4-133, scc-  
 s4\_mrna\_expressed\_in\_primary\_and\_relatively\_radiosensitive\_squamous\_cell\_carcin  
 oma,  
 u88667\_6771-7251, atp\_binding\_cassette\_transporter\_(abcr)\_mrna, \_complete\_cds  
 all\_x00088\_334-787, histone\_h2b\_gene  
 all\_x67081\_578-810, histone\_h4\_gene\_  
 x69089\_4333-4849, mrna\_for\_skeletal\_muscle\_165kd\_protein  
 x89101\_exon#3\_8-96:in\_reversesequence, \_183-188, mrna\_for\_fas\_(apo-  
 1, \_cd95)/gb=x89101/\_ntype=rna\_  
 x90530\_cds\_632-1100:in\_reversesequence, \_1548-1554, mrna\_for\_ragb\_protein  
 z68747\_cds\_656-1106:in\_reversesequence, \_1177, mrna\_for\_imogen\_38  
 z69915\_mrna\_31-244, mrna\_(clone\_icrfp507l1876).

Metagene 389

j05125\_1038-1422, triglyceride\_lipase\_mrna, \_complete\_cds  
 m68840\_1558-1924, monoamine\_oxidase\_a\_(maoa)\_mrna, \_complete\_cds\_  
 u85707\_1922-2426, leukemogenic\_homolog\_protein\_(meis1)\_mrna, \_complete\_cds\_  
 u90916\_1309-1825, clone\_23815\_mrna\_sequence\_

Metagene 363

hg1496-ht1496\_s\_at\_hg1496-ht1496\_adrenal-specific\_protein\_pg2  
 s73205\_2183-  
 2573, \_insulin\_activator\_factor\_[human, \_pancreatic\_insulinoma, \_mrna\_partial, \_262  
 2\_nt]/gb=  
 u00930\_2705-3191, clone\_c4e\_1.63\_(cac)n/(gtg)n\_repeat-containing\_mrna\_  
 x59131\_2735-  
 3119:not\_in\_gb\_record, d13s106\_mrna\_for\_a\_highly\_charged\_amino\_acid\_sequene

Metagene 350

d14497\_2222-2726, mrna\_for\_proto-oncogene\_protein, \_complete\_cds\_  
 d64015\_1126-1222, mrna\_for\_t-  
 cluster\_binding\_protein, \_complete\_cds/gb=d64015/\_ntype=rna  
 l00352\_exon\_1952-2492, low\_density\_lipoprotein\_receptor\_gene\_  
 l07493\_193-631, replication\_protein\_a\_14kda\_subunit\_(rpa)\_mrna, \_complete\_cds\_  
 u20980\_1596-2118, chromatin\_assembly\_factor-i\_p60\_subunit\_mrna, \_complete\_cds  
 u34962\_1074-1560, transcription\_factor\_hcsx\_(hcsx)\_mrna, \_complete\_cds\_  
 u46571\_1183-1687, tetratricopeptide\_repeat\_protein\_(tpr2)\_mrna, \_complete\_cds  
 x56088\_mrna\_2240-2794, mrna\_for\_cholesterol\_7-alpha-hydroxylase

## Metagene 344

m57293mrna#1\_4-289,parathyroid\_hormone-  
 related\_peptide\_(pthrp)\_gene,\_exons\_1a,\_1b,\_1c,\_and/gb=m57293  
 m85276exon#2-5\_5-  
 92:in\_reversesequence,\_5295:not\_in\_gb\_record,nkg5\_gene,\_complete\_cds\_  
 all\_x69116\_2-434,znf37a\_gene\_for\_zinc\_finger\_protein\_  
 z80345mrna\_4931-5457,scad\_gene,\_5'\_utr\_exonand(and\_joined\_cds)

## Metagene 315

d83018\_2645-3149,mrna\_for\_nel-related\_protein\_2,\_complete\_cds  
 all\_l31860\_2084-2589,glycophorin\_mn-types\_(gypa)\_mrna,\_complete\_cds\_  
 m16961\_937-1477,alpha-2-hs-glycoprotein\_alpha\_and\_beta\_chain\_mrna,\_complete\_cds\_  
 all\_u01317\_19502-63478,\_epsilon-  
 globin\_gene\_extracted\_frombeta\_globin\_region\_on\_chromosome\_11,\_epsil  
 u01877\_8517-8997,p300\_protein\_mrna,\_complete\_cds\_

## Metagene 314

104656\_370-856,carbonic\_anhydrase\_related\_protein\_(carp)\_mrna,\_complete\_cds\_  
 l49209exon\_25-  
 92,retinoblastoma\_susceptibility\_protein\_(rb1)\_i66dbp\_deletion\_mutant\_(resultin  
 g\_in\_pr  
 m84605\_4280-4766,putative\_opioid\_receptor\_mrna,\_complete\_cds\_  
 u14747\_410-944,visinin-like\_peptidehomolog\_mrna,\_complete\_cds\_  
 u21556\_709-1204,membrane\_protein-  
 like\_protein\_mrna,\_partial\_cds/gb=u21556\_/ntype=rna\_  
 u50929\_1910-2330,betaine:homocysteine\_methyltransferase\_mrna,\_complete\_cds\_  
 u83326cds\_538-1010,cc\_chemokine\_receptor-5\_(ccr5)\_gene,\_complete\_cds.

## Metagene 259

m57471exon\_13-  
 59,urate\_oxidase\_(uox)\_gene,\_exon/gb=m57471\_/ntype=dna\_/annot=exon\_  
 m99439\_1082-1385,transducin-like\_enhancer\_protein\_(tle4)\_mrna,\_3'\_end  
 u46024\_2801-3377,myotubularin\_(mtm1)\_mrna,\_partial\_cds\_  
 all\_u57341\_2-  
 129,neurofilament\_triplet\_l\_protein\_mrna,\_partial\_cds/gb=u57341\_/ntype=rna,neur  
 ofilamen  
 u82468\_1566-2091,tubby\_related\_protein(tulp1)\_mrna,\_complete\_cds  
 x56741cds\_85-595:in\_reversesequence,\_617,mrna\_for\_rab8\_gene\_  
 x74328mrna\_1175-  
 1745,\_cb2\_(peripheral)\_cannabinoid\_receptor\_gene\_extracted\_frommrna\_for\_cb2\_(pe  
 riphe

## Metagene 232

all\_d38024\_2639-  
 3228, facioscapulohumeral\_muscular\_dystrophy\_(fshd)\_gene\_region,\_d4z4\_tandem\_repeat\_u  
 hg2260-ht2349\_s\_at\_hg2260-ht2349\_duchenne\_muscular\_dystrophy\_protein\_(dmd)\_  
 hg4020-ht4290\_s\_at\_hg4020-ht4290\_transglutaminase  
 m13994mrna\_4482-5005,b-cell\_leukemia/lymphoma(bcl-2)\_proto-oncogene\_mrna\_encoding\_bcl-2-alpha\_protein  
 u27516\_2109-2555,recombination\_protein\_rad52\_mrna,\_complete\_cds  
 u82970\_2601-3009,metalloendopeptidase\_homolog\_(pex)\_mrna,\_complete\_sequence  
 x03168cds\_926-1400:in\_reversesequence,\_1497-1509,mrna\_for\_s-protein  
 all\_x89067\_751-1136,mrna\_for\_trpc2\_transcript\_(possible\_pseudogene)

## Metagene 226

ab001325\_967-1387,aqp3\_gene\_for\_aquaporine(water\_channel),\_partial\_cds  
 all\_d31784\_3804-4249,mrna\_for\_cadherin-6  
 d42087\_1034-1388,mrna\_for\_kiaa0118\_gene,\_partial\_cds  
 d87436\_5660-6116,mrna\_for\_kiaa0249\_gene,\_complete\_cds  
 all\_l32866\_67-452,effector\_cell\_protease\_receptor-1\_(epr-1)\_gene,\_partial\_cds  
 all\_m17262\_16806-  
 26862:in\_m17262cds\_1666,prothrombin\_(f2)\_gene,\_complete\_cds,\_and\_alu\_and\_kpni\_repeats  
 m26692exon#1\_37-195,lymphocyte-specific\_protein\_tyrosine\_kinase\_(lck)\_gene,\_exon\_1,\_and\_downstream\_p  
 m30269\_4417-4849,nidogen\_mrna,\_complete\_cds  
 s55606\_718-1228,\_betacellulin\_[human,\_mrna,\_1271\_nt]  
 u02019\_1958-2462,au-rich\_element\_rna-binding\_protein\_auf1\_mrna,\_complete\_cds  
 u18934\_4229-4311,receptor\_tyrosine\_kinase\_(dtk)\_mrna,\_complete\_cds  
 u58034cds\_38-  
 224,myotubularin\_related\_protein(mtmr3)\_gene,\_partial\_cds/gb=u58034\_/ntype=rna  
 u79246\_1346-1748,clone\_23799\_mrna\_sequence  
 u79289\_1287-1809,clone\_23695\_mrna\_sequence  
 x71125utr#1\_20-398:in\_reversesequence,\_985-  
 1093,mrna\_for\_glutamine\_cyclotransferase  
 all\_x97261\_25-  
 333,mrna\_for\_metallothionein\_isoform\_1r,mrna\_for\_metallothionein\_isoform\_1r  
 x97674cds\_4092-4326:in\_reversesequence,\_4536-  
 4758,mrna\_for\_transcriptional\_intermediary\_factor\_2

## Metagene 188

d10537\_1359-1876,mrna\_for\_major\_structural\_protein\_of\_myelin,\_complete\_cds  
 d26443\_3282-3822,mrna\_for\_glutamate\_transporter,\_complete\_cds  
 d31897\_1050-1548,mrna\_for\_doc2\_(double\_c2),\_complete\_cds  
 d38081\_2769-2853,mrna\_for\_thromboxane\_a2\_receptor,\_complete\_cds  
 d43767\_43-505,mrna\_for\_chemokine,\_complete\_cds  
 d50855\_2772-3309,mrna\_for\_ca-sensing\_receptor,\_complete\_cds  
 d63940\_153-656,mrna\_for\_mx11\_protein,\_complete\_cds  
 d80007\_5240-5768,mrna\_for\_kiaa0185\_gene,\_partial\_cds  
 d82344\_2434-2986,mrna\_for\_nbphox,\_complete\_cds  
 d89501exon#3\_206-441,pbi\_gene,\_complete\_cds

hg3405-ht3586\_at\_hg3405-ht3586\_zinc\_finger\_protein\_hzf3  
 hg3495-ht3689\_at\_hg3495-ht3689\_collagen\_type\_ix\_alpha\_1  
 hg358-ht358\_at\_hg358-ht358\_homeotic\_protein\_7\_notch\_group  
 hg3921-ht4191\_f\_at\_hg3921-ht4191\_homeotic\_protein\_c6\_i  
 hg3962-ht4232\_at\_hg3962-ht4232\_sialyltransferase\_stx  
 hg4069-ht4339\_s\_at\_hg4069-ht4339\_monocyte\_chemotactic\_protein  
 hg4318-ht4588\_s\_at\_hg4318-ht4588\_lim-domain\_transcription\_factor\_lim-1  
 l07738\_717-1125,dhp-  
 sensitive\_calcium\_channel\_gamma\_subunit\_cacnlg\_mrna\_complete\_cds\_  
 l07765\_1443-1923,carboxylesterase\_mrna\_complete\_cds\_  
 l10403\_834-  
 l254,dna\_binding\_protein\_for\_surfactant\_protein\_b\_mrna\_complete\_cds\_  
 l31881\_929-1385,nuclear\_factor\_i-x\_mrna\_complete\_cds  
 l38517mrna\_766-1228,indian\_hedgehog\_protein\_ihh\_mrna\_5'\_end  
 l43338mrna\_25-151,(clone\_jj1a)\_cadherin\_mrna\_fragment/gb=l43338\_/ntype=rna  
 l43366mrna\_13-157,(clone\_jj1b)\_cadherin\_mrna\_fragment/gb=l43366\_/ntype=rna  
 m15059mrna\_1025-1487,fc-  
 epsilon\_receptor\_ige\_receptor\_mrna\_complete\_cds\_h107\_epitope  
 all\_m19878\_1799-  
 l946,calbindin\_27\_gene\_exonsand\_2\_and\_alu\_repeat/gb=m19878\_/ntype=dna\_/annot=  
 exon,  
 m20203cds\_242-364,neutrophil\_elastase\_gene\_  
 m55047\_2637-3207,synaptotagmin\_mrna\_complete\_cds  
 m55067\_754-1324,47-  
 kd\_autosomal\_chronic\_granulomatous\_disease\_protein\_mrna\_complete\_cds\_  
 m59488mrna\_536-1016,s100\_protein\_beta-subunit\_gene\_  
 all\_m60752\_611-863,histone\_h2a.1\_h2a\_gene\_complete\_cds  
 m64676mrna\_1619-1892,k+\_channel\_subunit\_gene\_complete\_cds\_  
 m80647\_1317-1857,thromboxane\_synthase\_mrna\_complete\_cds  
 m84371mrna\_1318-1824,cd19\_gene\_complete\_cds  
 m85247mrna\_141-  
 597,dopamine\_d1a\_receptor\_gene\_complete\_exon\_1\_and\_exon\_2\_5'\_end/gb=m85247\_/ntype=  
 all\_m86528\_954-1357,neurotrophin-4\_nt-4\_gene\_complete\_cds\_  
 m97639\_3533-4037,transmembrane\_receptor\_ror2\_mrna\_complete\_cds  
 m97675\_2799-3309,transmembrane\_receptor\_ror1\_mrna\_complete\_cds  
 m97925mrna\_121-409,defensingene\_complete\_cds  
 s71824\_2437-2881,n-  
 cam=145\_kda\_neural\_cell\_adhesion\_molecule\_human\_small\_cell\_lung\_cancer\_cell\_l  
 i  
 u05659\_581-1049,17beta-hydroxysteroid\_dehydrogenase\_typemrna\_complete\_cds  
 u06698\_3269-3779,neuronal\_kinesin\_heavy\_chain\_mrna\_complete\_cds\_  
 u10485\_1906-2326,lymphoid-restricted\_membrane\_protein\_jaw1\_mrna\_complete\_cds  
 u11037\_19-499,sel-1\_like\_mrna\_complete\_cds  
 u11875\_48-144,interleukin-  
 8\_receptor\_type\_b\_il8rb\_mrna\_splice\_variant\_il8rb4\_partial\_cds/gb=u118  
 all\_u12471\_1014-1255\_thrombospondin-p50\_gene\_extracted\_fromthrombospondin-  
 1\_gene\_partial\_cds  
 u16861\_1076-1610,inward\_rectifying\_potassium\_channel\_mrna\_complete\_cds  
 u28131\_88-283,hmgi-c\_chimeric\_transcript\_mrna\_partial\_cds.  
 u29700cds\_1308-1644:in\_reversesequence\_8352-8382,anti-  
 mullerian\_hormone\_type\_ii\_receptor\_precursor\_  
 u35340\_442-868,beta\_b1-crystallin\_mrna\_complete\_cds\_  
 u38227\_3-411,testis-specific\_hexokinase(hhk1-  
 tb)\_mrna\_partial\_cds/gb=u38227\_/ntype=rna\_  
 u45982cds\_759-1035:in\_reversesequence\_1110-1338,g\_protein-  
 coupled\_receptor\_gpr-9-6\_gene\_complete\_c



u49742cds\_744-984:in\_reversesequence,\_5287-5473,rhodopsin\_gene,\_complete\_cds  
 u50146mrna\_39-543,typeneuropeptide\_y\_receptor\_(npv\_y2)\_gene,\_partial  
 u62433\_2748-  
 3318,nicotinic\_acetylcholine\_receptor\_alpha4\_subunit\_precursor,\_mrna,\_complete\_cds\_  
 u76366\_4225-4720,treachner\_collins\_syndrome\_(tcof1)\_mrna,\_complete\_cds  
 u79303\_939-1479,clone\_23882\_mrna,\_complete\_cds.  
 u83171\_2313-2865,macrophage-derived\_chemokine\_precursor\_(mdc)\_mrna,\_complete\_cds\_  
 x05323cds\_426-792:in\_gb\_record,mrc\_ox-2\_gene\_signal\_sequence  
 x14830cds\_1033-1423:in\_reversesequence,\_1547-  
 1571,mrna\_for\_muscle\_acetylcholine\_receptor\_beta-subuni  
 x16666cds\_422-841:in\_reversesequence,\_894-984,hox2i\_mrna\_from\_the\_hox2\_locus  
 x64044cds\_1066-1402:in\_reversesequence,\_1538-  
 1592,mmrna\_for\_large\_subunit\_of\_splicing\_factor\_u2af\_  
 x71135cds\_1083-1308:in\_reversesequence,\_1752-1977,sox3\_gene  
 x73113cds\_2973-3339:in\_reversesequence,\_3430-3520,mrna\_for\_fast\_mybp-c  
 all\_x74496\_1967-2520,mrna\_for\_prolyl\_oligopeptidase  
 x76770mrna\_1421-1931,pap\_mrna  
 x78710mrna\_2773-3247,mtf-1\_mrna\_for\_metal-regulatory\_transcription\_factor  
 all\_x79200\_380-600,mrna\_for\_syt-  
 ssx,\_synovial\_sarcoma\_translocation\_junction/gb=x79200\_/ntype=rna,mr  
 x83572\_1392-1920,arsd\_mrna\_  
 all\_x93921\_942-1471,mrna\_for\_protein-tyrosine-phosphatase\_(tissue\_type:\_testis)  
 y09321cds\_1961-2375:in\_reversesequence,\_2423-2501,tafi1105\_mrna,\_partial  
 y09392exon#4\_364-884,mrna\_for\_wsl-lr,\_wsl-s1\_and\_wsl-s2\_proteins\_  
 y10141cds\_56-286,datl\_gene,\_partial,\_vntr/gb=y10141\_/ntype=dna\_/annot=cds  
 z47038cds\_267-698,partial\_cdna\_sequence,\_clone\_x101,\_putative\_microtubule-  
 associated;\_protein\_1a\_(ma  
 z48510exon#5-7\_47-  
 6:in\_reversesequence,\_471,xg\_mrna\_(clone\_fb1)/gb=z48510\_/ntype=rna  
 z68274cds\_182-  
 632,dna\_sequence\_from\_cosmid\_l129h7,\_huntington\_disease\_region,\_chromosome\_4p16  
 .3\_cont

## Metagene 182

d16626\_2478-3006,mrna\_for\_histidase,\_complete\_cds  
 d84424\_1603-2053,fetal\_brain\_mrna\_for\_hyaluronan\_synthase,\_complete\_cds  
 hg2999-ht4756\_s\_at\_hg2999-ht4756\_thyroid\_peroxidase,\_altsplise\_2\_  
 l31529cds\_1308-1578:in\_reversesequence,\_1945-2053,beta1-  
 syntrophin\_(snt\_b1)\_gene,\_complete\_cds\_  
 m81650mrna\_1200-1566,semenogelin\_i\_(semgi)\_gene,\_complete\_cds\_  
 u46023\_4040-4544,xq28\_mrna,\_complete\_cds\_  
 all\_z48570\_1408-1991,sp17\_gene\_

## Metagene 181

af000545cds\_461-  
 983,putative\_purinergic\_receptor\_p2y10\_gene,\_complete\_cds/gb=af000545\_/ntype=dn  
 a\_/an  
 d79995\_4440-4806,mrna\_for\_kiaa0173\_gene,\_complete\_cds  
 hg2314-ht2410\_at\_hg2314-ht2410\_4-beta-galactosyltransferase

hg2325-ht2421\_at\_hg2325-ht2421\_retinoic\_acid\_receptor\_gamma\_2\_ j00212mrna\_393-761, leukocyte\_interferon\_(ifn-alpha)\_alpha-f\_mrna, \_complete\_cds\_ 140394mrna\_1312-1750, (clone\_s194)\_mrna, \_3'\_end\_of\_cds\_ 177566mrna\_1103-1655, dgs-i\_mrna, \_3'\_end\_ m15517cds#3\_155-419:in\_reversesequence, \_803- 923, \_ttr\_gene\_extracted\_frommutant\_prealbumin\_gene\_direct m55267mrna\_573-1035, ev12\_protein\_gene m77235\_7902-8418, cardiac\_tetrodotoxin-insensitive\_voltage-dependent\_sodium\_channel\_alpha\_subunit\_(hh m80899\_3582-4002, novel\_protein\_ahnak\_mrna, \_partial\_sequence all\_m81780\_3896- 4359, \_smpd1\_gene\_(acid\_sphingomyelinase)\_extracted\_fromacid\_sphingomyelinase\_(s mpd1) m86934\_1529-1973, gs1\_(protein\_of\_unknown\_function)\_mrna, \_complete\_cds m90820\_1286-1742, rapamycin-binding\_protein\_(fkbp25)\_mrna, \_complete\_cds\_ s77415cds\_660-948:in\_reversesequence, \_1449-1617, \_melanocortin- 4\_receptor\_[human, \_genomic, \_1671\_nt]\_ u01212cds\_153-411:in\_reversesequence, \_1715- 1943, olfactory\_marker\_protein\_(omp)\_gene, \_complete\_cds\_ u03187\_1505-2015, il12\_receptor\_component\_mrna, \_complete\_cds u09607\_3463-3730, jak\_family\_protein\_tyrosine\_kinase\_(jak3)\_mrna, \_complete\_cds u11717\_3500-3743, calcium\_activated\_potassium\_channel\_(hslo)\_mrna, \_complete\_cds\_ u12779\_1685-1959, map\_kinase\_activated\_protein\_kinase\_mrna, \_complete\_cds all\_u13061\_518-1020, dehydroepiandrosterone\_sulfotransferase\_(std)\_gene u20325exon#3\_57- 477, cocaine\_and\_amphetamine\_regulated\_transcript\_cart\_(hcart)\_gene, \_complete\_cd s\_ u27330\_1474- 1933, alpha\_(1,3)\_fucosyltransferase\_(fut5)\_mrna, \_minor\_transcript\_ii, \_complete\_ cds\_ u30185\_1981-2485, orphan\_opioid\_receptor\_mrna, \_complete\_cds\_ u32331\_1974-2526, rig\_mrna, \_complete\_sequence\_ u46901mrna#1\_1088-1640, nacp\_gene\_ u48437\_1855-2293, amyloid\_precursor-like\_protein\_mrna, \_complete\_cds\_ u57057cds\_1239-1515:in\_reversesequence, \_1871- 2069, wd\_protein\_ir10\_mrna, \_complete\_cds\_ u63312exon#1\_4-199:not\_in\_gb\_record, cosmid\_1112nc01- 242e1, \_etv6\_gene, \_exons\_1b\_andand\_partial\_cds/gb u79266\_972-1482, clone\_23627\_mrna, \_complete\_cds. u79302\_1414-1906, clone\_23855\_mrna, \_partial\_cds. u80987\_438- 948, transcription\_factor\_tbx5\_mrna, \_complete\_cds/gb=u80987/\_ntype=rna\_ u82759\_406-571, homeodomain\_protein\_hoxa9\_mrna, \_complete\_cds all\_x04201\_619-1073, skeletal\_muscle\_1.3\_kb\_mrna\_for\_tropomyosin x66364cds\_454- 814:in\_reversesequence, \_922, mrna\_pssalre\_for\_serine/threonine\_protein\_kinase all\_x67734\_4037-4470, mrna\_for\_transient\_axonal\_glycoprotein\_(tag-1) all\_x69699\_2155-2654, pax8\_mrna\_ all\_x83378\_4940-5523, mrna\_for\_putative\_chloride\_channel

Metagene 151

ac002464cds\_799- 1345, bac\_clone\_rg331p03, \_complete\_sequence/gb=ac002464/\_ntype=dna/\_annot=cds\_ d87457\_1568-2060, mrna\_for\_kiaa0281\_gene, \_complete\_cds

hg4109-ht4379\_at\_hg4109-ht4379\_olfactory\_receptor\_or17-30  
 u31215\_3797-  
 4037,metabotropic glutamate receptoralpha\_(mglur1alpha)\_mrna,\_complete\_cds  
 x03473cds\_270-552:in\_reversesequence,\_1054-1150,gene\_for\_histone\_h1(0)  
 x06948cds\_482-680:in\_reversesequence,\_918-  
 1146,mrna\_for\_high\_affinity\_ige\_receptor\_alpha-subunit\_(fc  
 all\_z12173\_1808-2361,gns\_mrna\_encoding\_glucosamine-6-sulphatase

Metagene 124

all\_x00038\_599-718,h4\_histone\_gene\_

Metagene 102

d25215\_4320-4839,mrna\_for\_kiaa0032\_gene,\_complete\_cds  
 d86974\_5077-5308,mrna\_for\_kiaa0220\_gene,\_partial\_cds\_  
 hg3123-ht3299\_at\_hg3123-ht3299\_homeotic\_protein\_gbx2\_  
 l20861\_3555-4089,proto-oncogene\_(wnt-5a)\_mrna,\_complete\_cds\_  
 l29339mrna\_1862-2324,na+/glucose\_co-transporter\_(sglt1)\_gene  
 m91083mrna\_989-1469,dna-binding\_protein\_(hrc1)\_mrna,\_complete\_cds  
 m96684\_609-867,pur\_(pur-alpha)\_mrna,\_complete\_cds  
 s90469\_1802-  
 2300,\_cytochrome\_p450\_reductase\_[human,\_placenta,\_mrna\_partial,\_2403\_nt]  
 u05237\_2192-2570,fetal\_alz-50-reactive\_clone(fac1)\_mrna,\_complete\_cds\_  
 u13896\_2487-3015,homolog\_of\_drosophila\_discs\_large\_protein,\_isoform(hdlg-  
 2)\_mrna,\_complete\_cds  
 u47054\_853-1357,putative\_mono-  
 ribosyltransferase\_(htmart)\_mrna,\_complete\_cds\_  
 u50327mrna\_1463-2020,protein\_kinase\_c\_substrate\_80k-h\_gene\_(prkcsh)  
 u66615\_4601-5165,swi/snf\_complex\_155\_kda\_subunit\_(baf155)\_mrna,\_complete\_cds\_  
 u79288\_1035-1509,clone\_23682\_mrna\_sequence\_  
 all\_x69878\_3909-4372,flt4\_mrna\_for\_transmembrane\_tyrosine\_kinase\_  
 all\_x83618\_1574-1995,mrna\_for\_3-hydroxy-3-methylglutaryl\_coenzyme\_a\_synthase\_  
 x96506cds\_96-441:in\_reversesequence,\_600-631,mrna\_for\_nc2\_alpha\_subunit\_

Metagene 90

m16653mrna\_652-742,pancreatic\_elastase\_iib\_mrna,\_complete\_cds  
 s83513\_1328-  
 1840,\_pituitary\_adenylate\_cyclase\_activating\_polypeptide\_[human,\_mrna,\_1940\_nt]  
 \_  
 u08049exon\_19-475,peripheral\_myelin\_protein-22\_(pmp22)\_gene,\_non-  
 coding\_exon\_1a/gb=u08049\_/ntype=dna  
 u24056\_1237-1787,inward\_rectifier\_k+\_channel\_protein\_(hirk2)\_mrna,\_complete\_cds  
 u43885\_1914-2442,grb2-associated\_binder-1\_mrna,\_complete\_cds\_  
 z49105mrna\_1064-1259,hd21\_mrna\_

Metagene 56

ab000467\_1590-2118, clone\_res4-25, partial\_cds  
 d16181exon\_1310-1712, pmp2\_gene\_for\_peripheral\_myelin\_protein\_2\_  
 hg4165-ht4435\_at\_hg4165-ht4435\_hpc-1\_  
 l17328\_1400-1868, pre-t/nk\_cell\_associated\_protein\_(3cl)\_mrna, complete\_cds\_  
 l22650\_84-636, early\_lymphoid\_activation\_protein\_(epag)\_mrna\_sequence\_  
 m24902mrna\_2694-3018, prostatic\_acid\_phosphatase\_mrna, complete\_cds\_  
 m82882\_3023-3503, cis-acting\_sequence\_  
 s76617\_2203-  
 2569, blk=protein\_tyrosine\_kinase\_[human, b\_lymphocytes, mrna, 2608\_nt]\_  
 s78467\_987-1384, pig-a-  
 ii=glycoinositol\_phospholipid\_anchor\_synthetic\_element\_[human, paroxysmal\_noc  
 u20350\_2697-3045, g\_protein-coupled\_receptor\_v28\_mrna, complete\_cds\_  
 u46194\_1466-1997, renal\_cell\_carcinoma\_antigen\_rage-  
 4\_mrna, complete\_putative\_cds\_  
 u66726\_2378-  
 2846, testis\_specific\_rna\_binding\_protein\_(spgyla)\_mrna, complete\_cds, testis\_spe  
 cific\_rna  
 u85265\_7-  
 63, down\_syndrome\_critical\_region(dscr1)\_gene, alternative\_exon/gb=u85265\_/ntype  
 =rna\_

Metagene 35

af012024\_658-1175, integrin\_cytoplasmic\_domain\_associated\_protein\_(icap-  
 1b)\_mrna, complete\_cds/gb=af0  
 d23660\_889-1369, mrna\_for\_ribosomal\_protein, complete\_cds\_  
 d31883\_6153-6711, mrna\_for\_kiaa0059\_gene, complete\_cds  
 d78361\_504-942, mrna\_for\_ornithine\_decarboxylase\_antizyme, orfand\_orf\_2  
 d86331\_1281-1777, mt2\_mmp\_gene\_for\_matrix\_metalloprotein, complete\_cds  
 hg1103-ht1103\_at\_hg1103-ht1103\_guanine\_nucleotide-binding\_protein\_ral, ras-  
 oncogene\_related  
 hg180-ht180\_at\_hg180-ht180\_ahnak-a\_nucleoprotein\_ahnak-a\_  
 hg2873-ht3017\_at\_hg2873-ht3017\_ribosomal\_protein\_l30\_homolog\_  
 hg3362-ht3539\_s\_at\_hg3362-ht3539\_chromosomal-  
 translocation\_associated\_gene\_ltg19/enl\_  
 hg3395-ht3573\_s\_at\_hg3395-ht3573\_dnaj\_homolog, altsplice\_form\_2  
 hg3549-ht3751\_at\_hg3549-ht3751\_wilm\_tumor-related\_protein  
 hg4319-ht4589\_at\_hg4319-ht4589\_ribosomal\_protein\_l5  
 hg821-ht821\_at\_hg821-ht821\_ribosomal\_protein\_s13\_  
 j03592\_707-1085, adp/atp\_translocase\_mrna, 3'\_end, clone\_phat8  
 j04617cds\_1069-1364:in\_reversesequence, 3823-4030, elongation\_factor\_ef-1-  
 alpha\_gene, complete\_cds\_  
 l04483\_39-272, ribosomal\_protein\_s21\_(rps21)\_mrna, complete\_cds\_  
 l06499mrna\_4-301, ribosomal\_protein\_l37a\_(rpl37a)\_mrna, complete\_cds\_  
 l06505mrna\_259-553, ribosomal\_protein\_l12\_mrna, complete\_cds  
 l07868\_4919-5429, receptor\_tyrosine\_kinase\_(erbb4)\_gene, complete\_cds  
 l11566\_77-521, ribosomal\_protein\_l18\_(rpl18)\_mrna, complete\_cds  
 all\_m10277\_3236-3578, cytoplasmic\_beta-actin\_gene, complete\_cds\_  
 m17886mrna\_7-475, acidic\_ribosomal\_phosphoprotein\_p1\_mrna, complete\_cds\_  
 m18000cds\_78-360, ribosomal\_protein\_s17\_gene, complete\_cds  
 m19828exon#8\_1305-1576:in\_reversesequence, 14367-14518, apolipoprotein\_b-  
 100\_(apob)\_gene\_  
 m24194mrna\_504-  
 l023, mhc\_protein\_homologous\_to\_chicken\_b\_complex\_protein\_mrna, complete\_cds\_

all\_m31520\_25-  
 590,ribosomal\_protein\_s24\_mrna,ribosomal\_protein\_s24\_mrna,ribosomal\_protein\_s24\_mrna  
 m31520mrna\_2-  
 106,ribosomal\_protein\_s24\_mrna,ribosomal\_protein\_s24\_mrna,ribosomal\_protein\_s24\_mrna  
 m36072\_368-770,ribosomal\_protein\_17a\_(surf\_3)\_large\_subunit\_mrna,\_complete\_cds\_  
 m55409\_556-1069,pancreatic\_tumor-related\_protein\_mrna,\_3'\_end  
 m58603\_3120-3600,nuclear\_factor\_kappa-b\_dna\_binding\_subunit\_(nf-kappa-b)\_mrna,\_complete\_cds  
 m60854\_19-373,ribosomal\_protein\_s16\_mrna,\_complete\_cds\_  
 m64098\_3873-  
 4305,high\_density\_lipoprotein\_binding\_protein\_(hbp)\_mrna,\_complete\_cds\_  
 m64716mrna\_31-451,ribosomal\_protein\_s25\_mrna,\_complete\_cds\_  
 m81757\_49-421,s19\_ribosomal\_protein\_mrna,\_complete\_cds\_  
 s79522\_19-481,ubiquitin\_carboxyl\_extension\_protein\_[human,\_mrna,\_540\_nt]\_  
 u07804\_1857-2384,dna\_topoisomerase\_i\_mrna,\_partial\_cds\_  
 u07806\_2865-  
 3382,camptothecin\_resistant\_clone\_cem/c2\_dna\_topoisomerase\_i\_mrna,\_partial\_cds\_  
 u09953\_153-621,ribosomal\_protein\_l9\_mrna,\_complete\_cds\_  
 u14968\_133-451,ribosomal\_protein\_l27a\_mrna,\_complete\_cds\_  
 u14969\_43-451,ribosomal\_protein\_l28\_mrna,\_complete\_cds\_  
 u14971\_91-661,ribosomal\_protein\_s9\_mrna,\_complete\_cds\_  
 u14973\_13-235,ribosomal\_protein\_s29\_mrna,\_complete\_cds\_  
 u25789\_19-481,ribosomal\_protein\_l21\_mrna,\_complete\_cds\_  
 u49352\_548-1106,liver\_2,4-dienoyl-coa\_reductase\_mrna,\_complete\_cds\_  
 u49785\_311-641,d-dopachrome\_tautomerase\_mrna,\_complete\_cds.  
 u78027mrna#3\_3-350,\_l44l\_gene\_(l44-like\_ribosomal\_protein)\_extracted\_frombruton\_tyrosine\_kinase\_(btk  
 u79273\_851-1127,clone\_23933\_mrna\_sequence  
 u83461\_1235-  
 1619,putative\_copper\_uptake\_protein\_(hctr2)\_mrna,\_complete\_cds/gb=u83461/\_ntype=rna  
 x01677cds\_629-983:in\_reversesequence,\_1109-1229,liver\_mrna\_for\_glyceraldehyde-3-phosphate\_dehydrogen  
 x03342cds\_51-375:in\_reversesequence,\_439-445,mrna\_for\_ribosomal\_protein\_l32\_  
 x06617mrna\_31-475,mrna\_for\_ribosomal\_protein\_s11\_  
 x16064cds\_147-483:in\_reversesequence,\_625-745,mrna\_for\_translationally\_controlled\_tumor\_protein  
 x17206cds\_111-585:in\_reversesequence,\_885,mrna\_for\_llrep3\_  
 x52966cds\_11-299:in\_reversesequence,\_19-373,mrna\_for\_ribosomal\_protein\_l35a\_  
 x55715cds\_228-618:in\_reversesequence,\_748-784,hums3\_mrna\_for\_40s\_ribosomal\_protein\_s3\_  
 x56932cds\_114-576:in\_reversesequence,\_611-623,mrna\_for\_23\_kd\_highly\_basic\_protein\_  
 x56997mrna#1\_19-475:not\_in\_gb\_record,uba52\_gene\_coding\_for\_ubiquitin-52\_amino\_acid\_fusion\_protein  
 all\_x64707\_401-888,bbc1\_mrna\_  
 x67247mrna\_116-662,rps8\_gene\_for\_ribosomal\_protein\_s8\_  
 x69150mrna\_25-403,\_l06432mrna\_for\_ribosomal\_protein\_s18  
 x79234cds\_115-511,mrna\_for\_ribosomal\_protein\_l11\_  
 z26876\_43-328,gene\_for\_ribosomal\_protein\_l38\_  
 z28407cds\_220-703:in\_reversesequence,\_809-818,mrna\_for\_ribosomal\_protein\_l8\_  
 z49148cds\_2-418:in\_reversesequence,\_18-589,mrna\_for\_ribosomal\_protein\_l29\_  
 z69043cds\_66-489:in\_reversesequence,\_30-598,mrna\_translocon-associated\_protein\_delta\_subunit\_precurs  
 all\_z70759\_4-251,mitochondrial\_16s\_rrna\_gene\_(partial).

## Metagene 2

d13633\_2141-2597,mrna\_for\_kiaa0008\_gene,\_complete\_cds  
 l19783\_895-1351,gpi-h\_mrna,\_complete\_cds\_  
 l33262\_1751-  
 2273,dna\_repair\_and\_recombination\_homologue\_(rad52)\_gene,\_complete\_cds  
 m29927exon\_229-703,ornithine\_aminotransferase\_gene\_  
 u09087\_2090-2543,thymopoietin\_beta\_mrna,\_complete\_cds  
 u67611\_788-  
 1130:not\_in\_gb\_record,\_mouse\_transaldolase\_gene\_mrna,\_complete\_cds/gb=u67611\_/n  
 type=rna\_  
 u72936\_9836-  
 10377,putative\_dna\_dependent\_atpase\_and\_helicase\_(atrx)\_mrna,\_alternatively\_spl  
 iced\_prod  
 all\_x67491\_839-1137,gene\_for\_glutamate\_dehydrogenase\_  
 x99586cds\_12-223:in\_reversesequence,\_329,mrna\_for\_smt3c\_protein\_  
 z46629mrna\_3352-3730,sox9\_mrna

## Metagene 1

100137cds#1\_6-234:in\_reversesequence,\_8-  
 134:not\_in\_gb\_record,\_ghrf\_gene\_(growth\_hormone\_releasing\_fa  
 m33478mrna\_653-1049,33-kda\_phototransducing\_protein\_mrna,\_complete\_cds\_  
 all\_m34344\_114-364:in\_m34344cds\_3032-  
 3069,platelet\_glycoprotein\_iib\_(gpiib)\_gene  
 m62810\_1350-1818,mitochondrial\_transcription\_factormrna,\_complete\_cds\_  
 m73239mrna\_2114-  
 2638,(clone\_sf1)\_hepatocyte\_growth\_factor\_(hgf)\_mrna,\_complete\_cds\_  
 m81758\_7258-7798,skeletal\_muscle\_voltage-  
 dependent\_sodium\_channel\_alpha\_subunit\_(skm1)\_mrna,\_complet  
 all\_u51561\_10617-28244:in\_u51561cds\_50,cosmid\_n79e2,\_complete\_sequence  
 u75309\_1813-2376,tdp-associated\_factor\_(htafii100)\_mrna,\_partial\_cds\_  
 u95090mrna\_2166-2418:in\_fullsequence,\_36716-  
 36854,chromosomecosmid\_f19541,\_complete\_sequence  
 all\_x13766\_14-551,beta-casein\_mrna\_3'--terminal\_fragment\_

## Metagene 434

all\_m26665\_267-  
 307,histatin(his2)\_mrna,\_complete\_cds,histatin(his2)\_mrna,\_complete\_cds  
 m28130mrna\_654-1002,interleukin(il8)\_gene,\_complete\_cds  
 m33684cds\_288-788,(clone\_lambda-10-2)\_non-  
 receptor\_tyrosine\_phosphatase(ptyn1)\_gene\_  
 u10492\_1894-2266,mox1\_protein\_(mox1)\_mrna,\_complete\_cds  
 u18985\_2460-2922,triadin\_mrna,\_complete\_cds  
 u48213mrna\_1031-1601,d-site\_binding\_protein\_gene,\_promoter\_region\_and

## Metagene 408

d42039\_3568-4074,mrna\_for\_kiaa0081\_gene,\_partial\_cds\_  
d55643\_443-1019,spleen\_pabl\_(pseudautosomal\_boundary-  
like\_sequence)\_mrna,\_clone\_sp2/gb=d55643\_/ntyp  
hg3993-ht4263\_at\_hg3993-ht4263\_cpg-enriched\_dna,\_clone\_s12\_  
102785\_2412-2790,colon\_mucosa-associated\_(dra)\_mrna,\_complete\_cds\_  
m28826\_976-1252,thymocyte\_antigen\_cd1b\_mrna,\_complete\_cds

Metagene 211

ab006190\_705-1179,mrna\_for\_aquaporin\_6,\_complete\_cds/gb=ab006190\_/ntype=rna\_  
d13642\_4248-4722,mrna\_for\_kiaa0017\_gene,\_complete\_cds  
d31815\_797-1295,mrna\_for\_smp-30\_(senescence\_marker\_protein-30),\_complete\_cds\_  
d31846exon#4\_179-713,gene\_for\_aquaporin-2\_water\_channel,\_exon1-4,\_complete\_cds\_  
d38305\_701-1181,mrna\_for\_tob,\_complete\_cds\_  
d63482\_1722-2226,mrna\_for\_kiaa0148\_gene,\_complete\_cds  
d82070\_285-843,ac1\_mrna,\_complete\_cds  
d85527\_37-349,mrna\_for\_lim\_domain,\_partial\_cds/gb=d85527\_/ntype=rna  
d87460\_2023-2503,mrna\_for\_kiaa0270\_gene,\_partial\_cds\_  
d87468\_2496-2886,mrna\_for\_kiaa0278\_gene,\_partial\_cds\_  
hg1649-ht1652\_at\_hg1649-ht1652\_elastase\_  
hg1800-ht1823\_at\_hg1800-ht1823\_ribosomal\_protein\_s20\_  
hg2261-ht2352\_at\_hg2261-ht2352\_antigen,\_prostate\_specific,\_altsplce\_form\_3  
hg2604-ht2700\_at\_hg2604-ht2700\_pan-2\_  
hg3432-ht3618\_at\_hg3432-ht3618\_fibroblast\_growth\_factor\_receptor\_k-  
sam,\_altsplce\_1  
hg3987-ht4257\_at\_hg3987-ht4257\_cpg-enriched\_dna,\_clone\_e06\_  
hg4036-ht4306\_at\_hg4036-ht4306\_retinoblastoma\_  
hg4051-ht4321\_at\_hg4051-ht4321\_choline\_acetyltransferase\_  
hg4662-ht5075\_at\_hg4662-  
ht5075\_omega\_light\_chain,\_immunoglobulin\_lambda\_light\_chain\_related  
hg896-ht896\_at\_hg896-ht896\_thrombospondin\_  
hg919-ht919\_at\_hg919-ht919\_dna\_polymerase,\_epsilon,\_catalytic\_subunit  
all\_k03460\_3-379,alpha-tubulin\_isotype\_h2-alpha\_gene,\_last\_exon  
120965\_3164-3680,phosphodiesterase\_mrna,\_complete\_cds  
123852mrna\_1122-1674,(clone\_z146)\_retinal\_mrna,\_3'\_end\_and\_repeat\_region  
136720\_661-1219,bystin\_mrna,\_complete\_cds\_  
142621mrna\_1775-2231,ly-9\_mrna,\_complete\_cds  
177561mrna\_583-1093,dgs-d\_mrna,\_3'\_end  
all\_m13903\_1676-2031,involucrin\_mrna\_  
m27749\_245-323,immunoglobulin-  
related\_14.1\_protein\_mrna,\_complete\_cds,immunoglobulin-related\_14.1\_pr  
m30185mrna\_1234-1666,cholesteryl\_ester\_transfer\_protein\_mrna,\_complete\_cds\_  
m34079\_830-1298,immunodeficiency\_virus\_tat\_transactivator\_binding\_protein-  
1\_(tbp-1)\_mrna,\_complete\_c  
m34182mrna#1\_1112-1517,testis-specific\_protein\_kinase\_gamma-  
subunit\_mrna,\_complete\_cds\_  
s76992\_2182-  
2710,\_vav2=vav\_oncogene\_homolog\_[human,\_fetal\_brain,\_mrna\_partial,\_2753\_nt]\_  
s78771\_1149-1661,\_nat=cpg\_island-associated\_gene\_[human,\_mrna,\_1741\_nt]\_  
s81003\_130-640,\_l-  
ubc=ubiquitin\_conjugating\_enzyme\_[human,\_odontogenic\_keratocysts,\_mrna\_partial,  
\_68  
u01157\_2506-2992,glucagon-like\_peptide-  
1\_receptor\_mrna\_with\_ca\_dinucleotide\_repeat,\_complete\_cds\_

u01922\_405-921,btk\_region\_clone\_fci-12\_mrna  
 u08336\_368-872,basic\_helix-loop-helix\_transcription\_factor\_mrna,\_complete\_cds  
 u09210\_1910-2396,vesicular\_acetylcholine\_transporter\_mrna,\_complete\_cds  
 u20908cds\_13-193,clone\_350/2\_melanoma\_ubiquitous\_mutated\_protein\_(mum-1)\_gene,\_partial\_cds/gb=u20908  
 u31903\_2052-2510,creb-rp\_(creb-rp)\_mrna,\_complete\_cds  
 u34880\_1699-2179,dph21\_mrna,\_complete\_cds  
 u37673\_2848-3412,neuron-specific\_vesicle\_coat\_protein\_and\_cerebellar\_degeneration\_antigen\_(beta-nap)  
 u39576\_2486-2852,butyrophilin\_precursor\_mrna,\_complete\_cds  
 u49089\_2571-3075,neuroendocrine-dlg\_(ne-dlg)\_mrna,\_complete\_cds  
 u52696\_703-742,adrenal\_creb-rp\_homolog\_(creb-rp),\_complete\_cds,\_and\_tenascin-x\_(xb),\_partial\_cds,\_mr  
 u59302\_4047-4617,steroid\_receptor\_coactivator-1\_f-src-1\_mrna,\_complete\_cds\_  
 u62317mrna#3\_1056-1488,\_hypothetical\_protein\_384d8gene\_extracted\_from\_chromosome\_22q13\_bac\_clone\_cit  
 u66059cds#21\_49-283:in\_reversesequence,\_207121-207343,germline\_t-cell\_receptor\_beta\_chain\_dopamine-b  
 u73328\_918-1314,dlx7\_(dlx7)\_mrna,\_complete\_cds\_  
 u76764\_2544-3054,cd97\_mrna,\_complete\_cds\_  
 u78521\_655-1111,immunophilin\_homolog\_ara9\_mrna,\_complete\_cds  
 u78678\_191-683,thioredoxin\_mrna,\_nuclear\_gene\_encoding\_mitochondrial\_protein,\_complete\_cds\_  
 u79258\_861-1407,clone\_23732\_mrna,\_partial\_cds  
 u81001\_2773-3039,snrpn\_mrna,\_3'\_utr,\_partial\_sequence  
 u90543\_2445-2739,butyrophilin\_(btfl1)\_mrna,\_complete\_cds,butyrophilin\_(btfl1)\_mrna,\_complete\_cds  
 u96629mrna#2\_3194-3722,\_2a8.2\_gene\_(unknown\_protein\_cit987sk\_2a8\_1)\_extracted\_fromchromosomebac\_clon  
 all\_x14085\_1251-1422,mrna\_for\_beta-1,4-galactosyltransferase\_(ec\_2.4.1.22)\_  
 all\_x62573\_1608-2161,rna\_for\_fc\_receptor,\_tc9  
 all\_x66785\_2930-3511,mrna\_for\_transacylase\_(dbt)\_  
 all\_x78817\_2647-3236,partial\_c1\_mrna\_  
 all\_x83368\_4789-5345,mrna\_for\_phosphatidylinositolkinase\_gamma  
 x96401\_1673-2186,mrna\_for\_rox\_protein  
 x96924mrna\_1184-1215,gene\_encoding\_mitochondrial\_citrate\_transport\_protein  
 all\_x99133\_5342-5685:in\_x99133cds\_563-597:not\_in\_gb\_record,ngal\_gene\_  
 z31560cds\_475-923:in\_reversesequence,\_953,sox-2\_mrna\_(partial)

## Metagene 145

ab000450\_1298-1730,mrna\_for\_vrk2,\_complete\_cds\_  
 ab000464\_3281-3743,\_clone\_res4-24a,\_exon\_1,\_2,\_3,\_4\_  
 ab001106\_3542-4088,mrna\_for\_glia\_maturation\_factor,\_complete\_cds\_  
 d00723\_642-1110,mrna\_for\_hydrogen\_carrier\_protein,\_a\_component\_of\_an\_enzyme\_complex,\_glycine\_synthas  
 d11151exon\_1936-2434,dna\_for\_endothelin-a\_receptor,\_5'\_flanking\_region\_and\_  
 d12625\_2036-2219,mrna\_for\_nf1\_protein\_isoform\_(neurofibromin\_isoform),\_complete\_cds  
 d12676\_1884-2220,mrna\_for\_lyosomal\_sialoglycoprotein,\_complete\_cds



d13635\_4583-5117,mrna\_for\_kiaa0010\_gene,\_complete\_cds  
 d13789\_1594-2062,mrna\_for\_n-acetylglucosaminyltransferase\_iii,\_complete\_cds  
 d14662\_1082-1592,mrna\_for\_kiaa0106\_gene,\_complete\_cds  
 d21163\_3183-3693,mrna\_for\_kiaa0031\_gene,\_complete\_cds  
 d86549\_609-969,mrna\_for\_p97\_homologous\_protein,\_partial\_cds  
 d88532\_3016-3328,mrna\_for\_p55pik,\_complete\_cds\_  
 l04733\_1785-2265,kinesin\_light\_chain\_mrna,\_complete\_cds\_  
 l08488\_1206-1644,inositol\_polyphosphate\_1-phosphatase\_mrna,\_complete\_cds\_  
 l13434\_2304-2850,chromosome\_3p21.1\_gene\_sequence,\_complete\_cds\_  
 l22009\_1642-2056,hnrnp\_h\_mrna,\_complete\_cds  
 l27476\_3901-4429,x104\_mrna,\_complete\_cds\_  
 l38933mrna\_883-  
 l393,\_the\_longest\_open\_reading\_frame\_predicts\_a\_protein\_of\_202\_amino\_acids,\_wit  
 h\_fair  
 l41939mrna\_3197-3731,(clone\_fbk\_iii\_11c)\_protein-  
 tyrosine\_kinase\_(drt)\_mrna,\_complete\_cds\_  
 m37190mrna\_1220-1796,ras\_inhibitor\_mrna,\_3'\_end  
 all\_m54968\_5180-5775,k-ras\_oncogene\_protein\_mrna,\_complete\_cds\_  
 m64936\_2808-3264,retinoic\_acid-inducible\_endogenous\_retroviral\_dna  
 m91029exon#3\_2581-2977,amp\_deaminase\_(ampd2)\_mrna\_  
 s59049\_786-1314,\_b134=b\_cell\_activation\_gene\_[human,\_mrna,\_1398\_nt]\_  
 s73149mrna\_293-827,\_insulin-  
 like\_growth\_factor\_ii\_{intron\_7}\_[human,\_genomic,\_1702\_nt]/gb=s73149\_/nt  
 u08023\_3037-3529,cellular\_proto-oncogene\_(c-mer)\_mrna,\_complete\_cds  
 u08316\_1719-2235,insulin-stimulated\_protein\_kinase\_(ispk-1)\_mrna,\_complete\_cds\_  
 u15782\_2237-2681,cleavage\_stimulation\_factor\_77kda\_subunit\_mrna,\_complete\_cds  
 u23028\_1702-2236,eukaryotic\_initiation\_factor\_2b-epsilon\_mrna,\_partial\_cds\_  
 u39487\_3877-4339,xanthine\_dehydrogenase/oxidase\_mrna,\_complete\_cds\_  
 u85658\_2310-2736,transcription\_factor\_erf-1\_mrna,\_complete\_cds\_  
 x62083\_3969-4029,mrna\_for\_drosophila\_female\_sterile\_homeotic\_(fsh)\_homologue\_  
 all\_x69962\_4188-4308,fmr-1\_mrna  
 all\_x82125\_2007-2368,hok-2\_mrna\_for\_zinc\_finger\_protein

## Metagene 143

d14663\_785-1259,mrna\_for\_kiaa0107\_gene,\_complete\_cds\_  
 d38496\_3615-4170,mrna\_for\_lztr-1,\_complete\_cds\_  
 d42084\_2112-2610,mrna\_for\_kiaa0094\_gene,\_partial\_cds\_  
 d49400\_115-655,fetus\_brain\_mrna\_for\_vacuolar\_atpase,\_complete\_cds  
 d84294mrna\_8552-9020,mrna\_for\_tprdi,\_complete\_cds  
 d86988\_4716-5220,mrna\_for\_kiaa0221\_gene,\_complete\_cds  
 d87445\_6334-6892,mrna\_for\_kiaa0256\_gene,\_complete\_cds  
 hg1322-ht5143\_s\_at\_hg1322-  
 ht5143\_small\_nuclear\_ribonucleoprotein,\_polypeptide\_altsplice\_2\_  
 hg3484-ht3678\_s\_at\_hg3484-ht3678\_protein\_kinase  
 j04794mrna\_567-1071,aldehyde\_reductase\_mrna,\_complete\_cds  
 l09209\_3114-3666,amyloid\_protein\_homologue\_mrna,\_complete\_cds\_  
 l35249mrna\_2225-2690,vacuolar\_h+-  
 atpase\_mr\_56,000\_subunit\_(ho57)\_mrna,\_complete\_cds\_  
 l49380mrna\_2916-3414,clone\_b4\_transcription\_factor\_zfml\_mrna,\_complete\_cds  
 m14483mrna\_41-  
 443,\_ptma\_gene\_extracted\_fromprothymosin\_alpha\_mrna,\_complete\_cds\_  
 m26708\_549-1008,prothymosin\_alpha\_mrna\_(prot-alpha),\_complete\_cds  
 m91432mrna\_1664-2144,medium-chain\_acyl-coa\_dehydrogenase\_(mcad)\_gene\_  
 u00115\_3001-3451,zinc-finger\_protein\_(bcl-6)\_mrna,\_complete\_cds

u09825\_3156-3522,acid\_finger\_protein\_mrna,\_complete\_cds  
 u22970mrna#1\_205-749,\_16-jun\_gene\_(interferon-  
 inducible\_peptide\_precursor)\_extracted\_frominterferon-  
 u26424\_2237-2735,ste20-like\_kinase\_(mst2)\_mrna,\_complete\_cds\_  
 u45328\_591-1079,ubiquitin-conjugating\_enzyme\_(ube2i)\_mrna,\_complete\_cds  
 u60061\_905-1325,fez2\_mrna,\_partial\_cds\_  
 u61397\_875-1173,ubiquitin-homology\_domain\_protein\_pic1\_mrna,\_complete\_cds  
 u80017mrna#3\_892-  
 1444,\_btf2p44\_gene\_(basic\_transcription\_factorp44)\_extracted\_frombasic\_transcri  
 ptio  
 u91930\_4196-4682,ap-3\_complex\_delta\_subunit\_mrna,\_complete\_cds\_  
 u91931\_3081-3489,ap-3\_complex\_beta3a\_subunit\_mrna,\_complete\_cds  
 u91932\_778-1210,ap-3\_complex\_sigma3a\_subunit\_mrna,\_complete\_cds  
 u92014\_817-1366,clone\_121711\_defective\_mariner\_transposon\_hsmar2\_mrna\_sequence\_  
 all\_x03484\_2418-2947,mrna\_for\_raf\_oncogene\_  
 x60787mrna\_2434-3000,mrna\_for\_transcription\_factor\_ilf\_  
 all\_x62534\_726-1137,hmg-2\_mrna\_  
 all\_x63692\_4825-5348,mrna\_for\_dna\_(cytosin-5)-methyltransferase  
 x65784cds\_58-399,car\_gene  
 all\_x66899\_1902-2323,ews\_mrna  
 x69838cds\_2756-2924:in\_reversesequence,\_3043-3331,mrna\_for\_g9a  
 all\_x69910\_2339-2892,p63\_mrna\_for\_transmembrane\_protein  
 all\_x70394\_2591-3156,ozf\_mrna  
 all\_x72889\_5441-5844,hbrm\_mrna\_  
 all\_x73478\_2042-2637,hptpa\_mrna  
 all\_x79536\_1005-1156,mrna\_for\_hnrnpcore\_protein\_a1.  
 all\_x86691\_5882-6399,mrna\_for\_218kd\_mi-2\_protein\_  
 all\_x89750\_1061-1512,mrna\_for\_tgif\_protein\_  
 all\_x95404\_482-1047,mrna\_for\_non-muscle\_type\_cofilin\_  
 x95735\_1628-2168,mrna\_for\_zyxin\_2  
 all\_x98743\_2619-3112,mrna\_for\_rna\_helicase\_(myc-regulated\_dead\_box\_protein)  
 all\_y00815\_7107-7684,mrna\_for\_lca-  
 homologlar\_protein\_(leukocyte\_antigen\_related)\_  
 all\_y08614\_3715-4118,mrna\_for\_crml1\_protein\_  
 all\_z24724\_1263-1840,polya\_site\_dna  
 z26491exon#5\_388-430,gene\_for\_catechol\_o-methyltransferase\_  
 all\_z29505\_1140-1468,mrna\_for\_nucleic\_acid\_binding\_protein\_sub2.3

## Metagene 108

ab003102\_956-1442,mrna\_for\_proteasome\_subunit\_p44.5,\_complete\_cds  
 d14659\_648-1134,mrna\_for\_kiaa0103\_gene,\_complete\_cds\_  
 d21260\_5600-6002,mrna\_for\_kiaa0034\_gene,\_complete\_cds  
 d31885\_1773-2169,mrna\_for\_kiaa0069\_gene,\_partial\_cds\_  
 d38551\_3082-3592,mrna\_for\_kiaa0078\_gene,\_complete\_cds  
 d38555\_3911-4421,mrna\_for\_kiaa0079\_gene,\_complete\_cds  
 d64142mrna\_625-1177,mrna\_for\_histone\_h1x,\_complete\_cds\_  
 d78129\_568-  
 1024,adult\_(34\_year\_old)\_male\_liver\_mrna\_for\_squalene\_epoxidase,\_partial\_cds/gb  
 =d78129\_/n  
 d85429exon#3\_813-1347,dna\_for\_heat\_shock\_protein\_40,\_complete\_cds  
 d86972\_4190-4610,mrna\_for\_kiaa0218\_gene,\_complete\_cds  
 d87120\_1936-2314,cancellous\_bone\_osteoblast\_mrna\_for\_gs3786,\_complete\_cds  
 hg2788-ht2896\_at\_hg2788-ht2896\_calcyclin\_  
 hg2874-ht3018\_at\_hg2874-ht3018\_ribosomal\_protein\_l39\_homolog\_

109604\_339-819,differentiation-dependent\_a4\_protein\_mrna,\_complete\_cds  
 119779\_7-496,histone\_h2a.2\_mrna,\_complete\_cds\_  
 138928mrna\_274-832,5,10-methenyltetrahydrofolate\_synthetase\_mrna,\_complete\_cds  
 142542mrna\_3353-3803,rlip76\_protein\_mrna,\_complete\_cds\_  
 m31642mrna\_802-  
 1288,hypoxanthine\_phosphoribosyltransferase\_(hprt)\_mrna,\_complete\_cds\_  
 m58460\_1311-1490,75-kd\_autoantigen\_(pm-scl)\_mrna,\_complete\_cds\_  
 all\_m59830\_2432-2661,mhc\_iii\_hsp70-2\_gene\_(hla),\_complete\_cds  
 m60922\_1971-2427,surface\_antigen\_mrna,\_complete\_cds  
 all\_m90516\_2559-3058,glutamine:fructose-6-  
 phosphate\_amidotransferase\_(gfat)\_mrna,\_complete\_cds\_  
 u76992\_2137-2533,tat-sf1\_mrna,\_complete\_cds  
 x55079mrna\_3257-3366:not\_in\_gb\_record,\_gaa\_gene\_extracted\_fromlysosomal\_alpha-  
 glucosidase\_gene\_exon\_  
 x57985mrna#1\_1652-  
 2168,\_g1105\_gene\_(histone\_h2b)\_extracted\_fromgenes\_for\_histones\_h2b.1\_and\_h2a\_  
 y07867cds\_643-787:in\_reversesequence,\_1087-1237,mrna\_for\_pirin,\_isolate\_1\_

Metagene 50

d10667\_2830-3307,mrna\_for\_smooth\_muscle\_myosin\_heavy\_chain\_  
 m72885mrna\_207-750,\_g0s2\_gene\_extracted\_fromgos2\_gene,\_5'\_flank\_and\_cds\_  
 all\_u22028\_8029-  
 8330,cytochrome\_p450\_(cyp2a13)\_gene,\_complete\_cds,cytochrome\_p450\_(cyp2a13)\_gen  
 e,\_co  
 u92459\_2702-3194,metabotropic\_glutamate\_receptormrna,\_complete\_cds

Metagene 18

u39231\_1739-1979,gip\_receptor\_(gipr)\_mrna,\_complete\_cds  
 all\_v00503\_2330-2452,mrna\_encoding\_pro-alpha-  
 2\_chain\_of\_type\_i\_procollagen(major\_part)\_  
 all\_x79200\_380-600,mrna\_for\_syt-  
 ssx,\_synovial\_sarcoma\_translocation\_junction/gb=x79200\_/ntype=rna,mr

Metagene 13

all\_d32001\_61-294,husaalg\_gene\_for\_serum\_amyloid\_a1\_gamma,\_exonand\_intron\_3\_  
 hg2059-ht2114\_at\_hg2059-ht2114\_arrestin,\_beta\_2  
 hg2480-ht2576\_at\_hg2480-ht2576\_fm1p-related\_receptor\_i\_  
 hg2809-ht2920\_s\_at\_hg2809-ht2920\_lung\_surfactant\_protein\_d\_  
 hg3107-ht3283\_s\_at\_hg3107-ht3283\_plasma\_membrane\_calcium\_pump\_hpmca2a  
 hg759-ht759\_s\_at\_hg759-ht759\_adrenergic\_receptor,\_beta\_1\_  
 j05036mrna\_1546-2119,cathepsin\_e\_mrna,\_complete\_cds  
 j05073cds\_239-641,phosphoglycerate\_mutase\_(pgam-m)\_gene,\_complete\_cds  
 k02766\_2028-2436,complement\_component\_c9\_mrna,\_complete\_cds  
 l29008\_2014-2464,1-iditol-2\_dehydrogenase\_mrna,\_complete\_cds\_  
 l33477\_3692-4142,(clone\_8b1)\_br-cadherin\_mrna,\_complete\_cds  
 l35592mrna#1\_1633-2107,germline\_mrna\_sequence\_  
 l37112mrna\_1710-1816,vasopressin\_v3\_receptor\_mrna,\_complete\_cds\_

140933cds\_1218-1470:in\_reversesequence,\_1639-1819,phosphoglucomutase-related\_protein\_(pgmrp)\_gene,\_c  
 all\_m80333\_1628-2079,m5\_muscarinic\_acetylcholine\_receptor\_gene,\_complete\_cds\_  
 m85217\_2529-2955,k+\_channel\_protein\_(hlc3)\_mrna,\_complete\_cds  
 m89473\_1394-1706,neurokininreceptor\_(nk3r)\_mrna,\_complete\_cds\_  
 m96859\_3150-3630,dipeptidyl\_aminopeptidase\_like\_protein\_mrna,\_complete\_cds\_  
 u09609\_2198-2708,p80ht\_(p80ht/nkfb-2)\_mrna,\_complete\_cds\_  
 u13737\_2046-2556,cysteine\_protease\_cpp32\_isoform\_alpha\_mrna,\_complete\_cds  
 u14910\_910-1360,rpe-retinal\_g\_protein-coupled\_receptor\_(rgr)\_mrna,\_complete\_cds  
 u18671mrna\_2702-3266,stat2\_gene,\_complete\_cds\_  
 u29615\_1098-1530,chitotriosidase\_precursor\_mrna,\_complete\_cds  
 u31929cds\_1063-1361:in\_reversesequence,\_6372-  
 6576,orphan\_nuclear\_receptor\_(dax1)\_gene,\_complete\_cds\_  
 u63336\_1666-2062,mhc\_i\_region\_proline\_rich\_protein\_mrna,\_complete\_cds  
 u65404\_1140-1530,erythroid-specific\_transcription\_factor\_eklf\_mrna,\_complete\_cds.  
 u78180\_3340-  
 3880,sodium\_channel(hbnac2)\_mrna,\_alternatively\_spliced,\_complete\_cds\_  
 u85992\_1236-1596,clone\_image:35527\_unknown\_protein\_mrna,\_partial\_cds\_  
 all\_u87408\_1441-1952,clone\_image:74593\_unknown\_protein\_mrna,\_partial\_cds\_  
 v00535mrna#1\_253-  
 692,\_interferon\_betagene\_extracted\_from\_gene\_forfibroblast\_interferon\_beta\_1  
 all\_x04729\_2-263,mrna\_for\_plasminogen\_activator\_inhibitor\_typen-terminus/gb=x04729\_/ntype=rna\_  
 x54816\_at\_x54816\_x54816,not\_in\_gb\_record,gene\_for\_alpha-1-microglobulin-bikunin,\_exons\_5-jan\_(encodi  
 all\_x54938\_1175-1752,mrna\_for\_inositol\_1,4,5-triphosphate\_3-kinase\_  
 x55889cds\_264-  
 546:not\_in\_gb\_record,gene\_for\_ciliary\_neurotrophic\_factor,\_exon\_1\_  
 x55990mrna\_163-489,ecp\_gene\_for\_eosinophil\_cationic\_protein\_  
 all\_x66141\_261-784,mrna\_for\_cardiac\_ventricular\_myosin\_light\_chain-2\_  
 x97748mrna\_59-189,ptx3\_gene\_promotor\_region/gb=x97748\_/ntype=dna\_/annot=mrna\_  
 all\_x99140\_1407-1822,mrna\_for\_hair\_keratin,\_hbb5\_  
 y10376cds\_888-1158:in\_reversesequence,\_1222-1408,mrna\_for\_sirp-beta1\_  
 y13115cds\_2477-  
 2879:in\_reversesequence,\_3061,mrna\_for\_serine/threonine\_protein\_kinase\_sak  
 z24680mrna\_3558-4044,garp\_gene\_mrna,\_complete\_cds  
 all\_z31357\_967-1502,mrna\_for\_cysteine\_dioxygenase\_type\_1\_

Metagene 486

all\_m60751\_910-1163,histone\_h2b.1\_(h2b)\_gene,\_complete\_cds\_  
 x81333cds\_1730-2078:in\_reversesequence,\_2130-  
 2220,mrna\_for\_pph\_beta\_subunit\_protein\_  
 all\_y00317\_1618-2081,mrna\_for\_liver\_microsomal\_udp-glucuronosyltransferase\_(udpgt)\_

Metagene 397

u91618\_167-671,proneurotensin/proneuromedin\_n\_mrna,\_complete\_cds.  
 x78121mrna\_1730-1940:in\_reversesequence,\_1970-2036,mrna\_for\_choroideremia\_  
 y07828cds\_345-675:in\_reversesequence,\_844-994,mrna\_for\_ring\_protein\_

## Metagene 373

d26350\_10043-10481,mrna\_for\_typeinositol\_1,4,5-  
 trisphosphate\_receptor,\_complete\_cds\_  
 hg4747-ht5195\_at\_hg4747-ht5195\_nadh-ubiquinone\_oxidoreductase,\_51\_kda\_subunit  
 m22612\_188-759,pancreatic\_trypsin(try1)\_mrna,\_complete\_cds  
 all\_x74008\_1842-2245,mrna\_for\_protein\_phosphatasegamma

## Metagene 356

d26156\_4588-5166,mrna\_for\_transcriptional\_activator\_hsnf2b,\_complete\_cds\_  
 d86964\_5449-5995,mrna\_for\_kiaa0209\_gene,\_partial\_cds\_  
 hg3141-ht3317\_f\_at\_hg3141-ht3317\_nadh-ubiquinone\_oxidoreductase,\_39\_kda\_subunit  
 k03494cds\_557-  
 1062:in\_reversesequence,\_115,green\_cone\_photoreceptor\_pigment\_gene\_1  
 l19437\_857-  
 l211,transaldolase\_mrna\_containing\_transposable\_element,\_complete\_cds\_  
 l24783\_78-624,mrna\_fragment/gb=l24783\_/ntype=rna  
 l28010\_1292-1748,hnrnp\_f\_protein\_mrna,\_complete\_cds\_  
 m80254\_492-840,cyclophilin\_isoform(hcyp3)\_mrna,\_complete\_cds  
 m88108\_2156-2636,p62\_mrna,\_complete\_cds  
 u19251\_s\_at\_u19251\_u19251,not\_in\_gb\_record,neuronal\_apoptosis\_inhibitory\_protei  
 n\_mrna,\_complete\_cds  
 u24166\_2107-2395,eb1\_mrna,\_complete\_cds  
 u33936\_578-1050,adenosine\_kinase\_mrna,\_complete\_cds/gb=u33936\_/ntype=rna\_  
 u51990\_867-1269,hprp18\_mrna,\_complete\_cds  
 u60521\_1398-1860,protease\_promch6\_(mch6)\_mrna,\_complete\_cds  
 u62389\_31-409,putative\_cytosolic\_nadp-  
 dependent\_isocitrate\_dehydrogenase\_mrna,\_partial\_cds/gb=u62389  
 u72511\_440-596,b-cell\_receptor\_associated\_protein\_(hbap)\_mrna,\_partial\_cds\_  
 x05196exon#9\_2-458:in\_reversesequence,\_3199:not\_in\_gb\_record,aldolase\_c\_gene\_  
 all\_x12953\_859-1130,rab2\_mrna,\_ypt1-related\_and\_member\_of\_ras\_family\_  
 all\_x17644\_1976-2559,gst1-hs\_mrna\_for\_gtp-binding\_protein  
 x57152mrna#1\_536-962,gene\_for\_casein\_kinase\_ii\_subunit\_beta\_(ec\_2.7.1.37)\_  
 x78338mrna\_5278-  
 5824,\_synthetic\_adenovirus\_transformedretina\_cell\_line,\_mrp\_mrna\_  
 all\_x91247\_3261-3700,mrna\_for\_thioredoxin\_reductase  
 x97065cds\_1852-2260:in\_reversesequence,\_2389-  
 2395,mrna\_for\_sec23b\_isoform,\_2450bp\_  
 x98411cds\_2016-2256:in\_reversesequence,\_2340-2490,mrna\_for\_myosin-ie  
 x99209\_1549-2053,mrna\_for\_arginine\_methyltransferase\_  
 all\_z11695\_2189-2736,40\_kda\_protein\_kinase\_related\_to\_rat\_erk2\_  
 z29481cds\_624-792:in\_reversesequence,\_898-1186,mrna\_for\_3-  
 hydroxyanthranilic\_acid\_dioxygenase

## Metagene 154

d00408\_1373-1921,fetal\_liver\_cytochrome\_p-450\_(p-  
 450\_hfla),\_complete\_cds,fetal\_liver\_cytochrome\_p-45  
 d13638\_5003-5557,mrna\_for\_kiaa0013\_gene,\_complete\_cds  
 hg2320-ht2416\_at\_hg2320-ht2416\_integrin,\_betasubunit

m24351\_cds2\_at\_m24351\_m24351,not\_in\_gb\_record,\_pthlh\_gene\_(parathyroid\_hormone-like\_protein\_a)\_extra  
 m73489\_3312-3660,heat-stable\_enterotoxin\_receptor\_mrna,\_complete\_cds\_  
 u73330exon\_13-77,pac\_85d2,\_complete\_sequence/gb=u73330\_/ntype=dna\_/annot=exon  
 x95425cds\_2672-3061:in\_reversesequence,\_3810-3857,mrna\_for\_ehk-  
 1\_receptor\_tyrosine\_kinase\_

Metagene 53

k01160mrna\_1077-1232,ii\_histocompatibility\_antigen\_dc-alpha\_chain\_mrna\_  
 m26041\_1273-1405,mhc\_ii\_dq\_alpha\_mrna,\_complete\_cds\_  
 m63379mrna\_1190-1646,trpm-2\_protein\_gene\_  
 u38810\_2191-2659,mab-21\_cell\_fate-  
 determining\_protein\_homolog\_(cagrl)\_mrna,\_complete\_cds\_

Metagene 33

hg1728-ht1734\_at\_hg1728-ht1734\_non-  
 specific\_cross\_reacting\_antigen,\_altsplice\_form\_2\_  
 j04046mrna\_1559-2089,calmodulin\_mrna,\_complete\_cds\_  
 s77835\_88-380,\_il-2=interleukin-  
 2\_[human,brain,mrna,\_418\_nt]/gb=s77835\_/ntype=rna\_  
 s83362mrna\_10-109,\_differentiation-  
 stimulating\_factor/leukemia\_inhibitory\_factor\_receptor\_{5'\_region  
 u65581\_958-1420,ribosomal\_protein\_l3-like\_mrna,\_complete\_cds.  
 x58234mrna\_31-253,mrna\_for\_anti-lectin\_antibody\_epitope\_(clone\_p36/8-5)

Metagene 184

d13720\_3754-4319,mrna\_for\_lyk,\_complete\_cds  
 d30715mrna#3\_3-198,\_alternative\_splicing;\_type-2\_mrna\_from\_pap\_(pancreatitis-  
 associated\_protein)\_gene  
 l39061mrna\_1198-1654,transcription\_factor\_sl1\_mrna,\_partial\_cds\_  
 m34276cds\_2066-2228:in\_reversesequence,\_213-354,plasminogen\_gene  
 u09178\_3355-3898,dihydropyrimidine\_dehydrogenase\_mrna,\_complete\_cds  
 u37707\_2429-2969,dlg3\_mrna,\_complete\_cds\_  
 u38291mrna\_9685-10027,microtubule-  
 associated\_protein\_1a\_(map1a)\_genomic\_sequence  
 u66578cds\_598-1036:in\_reversesequence,\_1277,putative\_g\_protein-  
 coupled\_receptor\_(gpr23)\_gene,\_comple  
 u69263\_474-1002,matrilin-2\_precursor\_mrna,\_partial\_cds\_  
 u79667\_3199-3522,alpha1a-voltage-  
 dependent\_calcium\_channel\_mrna,\_splice\_form\_bi-1-v2-ggcag,\_partial\_  
 u87223\_4830-5196,contactin\_associated\_protein\_(caspr)\_mrna,\_complete\_cds\_  
 x01388cds\_14-272:in\_reversesequence,\_349-529,mrna\_for\_pre-apolipoprotein\_ciii\_  
 x66358cds#1\_633-1041,mrna\_kkialre\_for\_serine/threonine\_protein\_kinase  
 x75346cds\_788-1157:in\_reversesequence,\_1205-  
 1305,mrna\_for\_map\_kinase\_activated\_protein\_kinase\_

Metagene 419

d13264\_1681-  
 2167,mrna\_for\_macrophage\_scavenger\_receptor\_type\_i,\_3'\_untranslated\_region\_  
 d38122\_1307-1829,mrna\_for\_fas\_ligand,\_complete\_cds\_  
 hg1686-ht4572\_s\_at\_hg1686-  
 ht4572\_transcription\_factor\_e4tf1,\_respiratory,\_gammasubunit,\_altsplice\_4\_  
 u25029\_1010-1556,glucocorticoid\_receptor\_alpha\_mrna,\_variant\_3'\_utr  
 u34844exon\_40-259,mercurial-insensitive\_water-  
 channel\_gene,\_5'\_region\_and\_partial\_exon/gb=u34844\_/nt  
 u52191\_4854-5396,smcy\_(h-y)\_mrna,\_complete\_cds\_

Metagene 331

ac002045mrna#2\_625-908,\_a-589h1.1\_fromchromosomebac\_clone\_cit987-ska-  
 589h1\_~complete\_genomic\_sequenc  
 d10523\_3533-4079,mrna\_for\_2-oxoglutarate\_dehydrogenase,\_complete\_cds\_  
 d31840\_3679-4148,drpla\_mrna\_for\_orf,\_complete\_cds  
 d50912\_2685-3183,mrna\_for\_kiaa0122\_gene,\_partial\_cds\_  
 d80008\_2695-3205,mrna\_for\_kiaa0186\_gene,\_complete\_cds  
 d86963\_4563-5097,mrna\_for\_kiaa0208\_gene,\_complete\_cds  
 d87078\_4798-5296,mrna\_for\_kiaa0235\_gene,\_partial\_cds\_  
 hg1612-ht1612\_at\_hg1612-ht1612\_macmarcks\_  
 hg2525-ht2621\_at\_hg2525-ht2621\_helix-loop-helix\_protein\_delta\_max,\_altsplice\_1\_  
 hg3635-ht3845\_f\_at\_hg3635-ht3845\_zinc\_finger\_protein,\_kruppel-like\_  
 l07648\_1955-2321,mxi1\_mrna,\_complete\_cds\_  
 l76702mrna\_2447-3005,b56-delta\_mrna,\_complete\_cds\_  
 m13452\_1927-2435,lamin\_a\_mrna,\_3'\_end  
 m91670\_301-787,ubiquitin\_carrier\_protein\_(e2-epf)\_mrna,\_complete\_cds\_  
 s49592\_1868-2425,\_transcription\_factor\_e2f\_like\_protein\_[human,\_mrna,\_2492\_nt]  
 u09820\_5579-6058,helicase\_ii\_(rad541)\_mrna,\_complete\_cds.  
 u22963\_752-1238,i\_histocompatibility\_antigen-like\_protein\_mrna,\_complete\_cds.  
 u34044\_1143-1647,selenium\_donor\_protein\_(seld)\_mrna,\_complete\_cds  
 u37012\_3868-  
 4372,cleavage\_and\_polyadenylation\_specificity\_factor\_mrna,\_complete\_cds  
 u52426\_3469-3997,gok\_(gok)\_mrna,\_complete\_cds  
 u54778\_1131-1671,14-3-3\_epsilon\_mrna,\_complete\_cds\_  
 u57342\_967-  
 1459,myelodysplasia/myeloid\_leukemia\_factor(mlf2)\_mrna,\_complete\_cds\_  
 u72761\_2753-3233,karyopherin\_betamrna,\_complete\_cds/gb=u72761\_/ntype=rna  
 u81984\_2277-2739,endothelial\_pas\_domain\_protein(epas1)\_mrna,\_complete\_cds\_  
 all\_x06323\_1105-  
 1520,mrl3\_mrna\_for\_ribosomal\_protein\_l3\_homologue\_(mrl3\_=mammalian\_ribosome\_l  
 3\_)\_  
 x71428mrna\_1284-1788,fus\_mrna  
 x75755mrna#1\_1337-1471,pr264\_gene\_  
 all\_x76717\_3-268,mt-11\_mrna  
 all\_x83928\_456-919,mrna\_for\_transcription\_factor\_tfiid\_subunit\_tafii28\_  
 all\_x90824\_828-1337,mrna\_for\_usf2a\_&\_usf2b,\_clone\_p9dh\_  
 x97160mrna\_2016-  
 2532,\_tfe3\_transcription\_factor\_gene\_extracted\_fromtfe3\_gene,\_exons\_1,2,3\_(and\_  
 joine  
 y07595cds\_948-  
 1344:in\_reversesequence,\_1501,mrna\_for\_52\_kd\_subunit\_of\_transcription\_factor\_tf  
 iih

y13247\_3077-3581,fb19\_mrna  
 y13620\_5732-6182,mrna\_for\_bcl9\_gene/gb=y13620\_/ntype=rna  
 z37166cds\_1006-1252:in\_reversesequence,\_1432-  
 1570,bat1\_mrna\_for\_nuclear\_rna\_helicase\_(dead\_family)

Metagene 295

u78551\_838-1396,gallbladder\_mucin\_muc5b\_mrna,\_partial\_cds\_

Metagene 183

105628\_4400-4969,multidrug\_resistance-  
 associated\_protein\_(mrp)\_mrna,\_complete\_cds  
 107541\_950-1436,replication\_factor\_38-kda\_subunit\_mrna,\_complete\_cds  
 u28413\_1440-  
 1926,cockayne\_syndrome\_complementation\_group\_a\_csa\_protein\_(csa)\_mrna,\_complete  
 \_cds

Metagene 20

af008937\_508-916,syntaxin-16c\_mrna,\_complete\_cds/gb=af008937\_/ntype=rna\_  
 d90282\_4830-5136,carbaryl\_phosphate\_synthetase\_i\_(ec\_6.3.4.16)\_mrna  
 hg2846-ht2983\_at\_hg2846-ht2983\_dihydrofolate\_reductase,\_altsplice\_6  
 l19161\_1001-1385,translation\_initiation\_factor\_eif-  
 2\_gamma\_subunit\_mrna,\_complete\_cds  
 l24804\_223-721,(p23)\_mrna,\_complete\_cds  
 l36463\_2081-2627,ras\_inhibitor\_(rin1)\_mrna,\_complete\_cds  
 l77701mrna\_43-337,cox17\_mrna,\_complete\_cds  
 m90356cds\_222-618:in\_reversesequence,\_1194-  
 1281,btf3\_protein\_homologue\_gene,\_complete\_cds\_  
 u34301mrna\_2-  
 35,nonmuscle\_myosin\_heavy\_chain\_iib\_gene,\_promoter\_region\_and\_exon/gb=u34301\_/n  
 type=dna  
 u47025\_3462-3994,fetal\_brain\_glycogen\_phosphorylase\_b\_mrna,\_complete\_cds\_  
 u55936\_367-757,snap-23\_mrna,\_complete\_cds  
 u70322\_2456-3014,transportin\_(trn)\_mrna,\_complete\_cds  
 x68836cds\_653-1139,mrna\_for\_s-adenosylmethionine\_synthetase  
 z18859mrna\_933-  
 1461,cone\_transducin\_alpha\_subunit\_gene\_extracted\_fromgene\_for\_cone\_transducin\_  
 alpha\_

Metagene 383

l11005\_4386-4878,aldehyde\_oxidase\_(haox)\_mrna,\_complete\_cds  
 u81262\_2433-2877,lerk-5\_(lerk-5)\_mrna,\_complete\_cds  
 all\_x89426\_1465-1958,mrna\_for\_esm-1\_protein

Metagene 339



d42045\_3927-4419,mrna\_for\_kiaa0086\_gene,\_complete\_cds  
 all\_m86933\_669-  
 706,amelogenin\_(amely)\_mrna,\_complete\_cds,amelogenin\_(amely)\_mrna,\_complete\_cds  
 m96980\_2034-2598,myelin\_transcription\_factor(mtf1)\_mrna,\_3'\_end  
 all\_x16282\_710-1185,mrna\_for\_zinc\_finger\_protein\_(clone\_647)\_  
 x89960cds\_21-327:in\_reversesequence,\_458-  
 698,mrna\_for\_mitochondrial\_capsule\_selenoprotein

Metagene 300

d15050\_4757-5231,mrna\_for\_transcription\_factor\_areb6,\_complete\_cds\_  
 hg3748-ht4018\_at\_hg3748-ht4018\_basic\_transcription\_factor,\_44\_kda\_subunit  
 s82472cds\_3-  
 73,\_beta\_#name?\_polymerase\_beta\_{exon\_alpha\_to\_exon\_vii\_region}\_[human,\_genomic  
 ,\_124\_nt,

Metagene 291

af006609\_5-189,rgs3\_mrna,\_5'\_utr/gb=af006609\_/ntype=rna\_  
 d38491\_298-808,mrna\_for\_kiaa0117\_gene,\_partial\_cds\_  
 d50924\_3807-4083,mrna\_for\_kiaa0134\_gene,\_complete\_cds  
 m86826\_1501-2023,igf\_binding\_protein\_complex\_acid-  
 labile\_subunit\_a\_mrna,\_complete\_cds  
 m97252\_5809-6271,kallmann\_syndrome\_(kal)\_mrna,\_complete\_cds\_  
 u27768\_235-709,rgp4\_mrna,\_complete\_cds\_  
 u51127\_1706-2084,interferon\_regulatory\_factor(humirf5)\_mrna,\_complete\_cds\_  
 u62961\_2749-3241,succinyl\_coa:3-  
 oxoacid\_coa\_transferase\_precursor\_(oxct)\_mrna,\_complete\_cds

Metagene 215

d67029\_4839-5355,sec141\_mrna,\_complete\_cds\_  
 m61916\_5027-5582,laminin\_b1\_chain\_mrna,\_complete\_cds\_  
 m69225mrna\_8371-8845,bullous\_pemphigoid\_antigen\_(bpag1)\_mrna,\_complete\_cds\_  
 u10550\_1591-2107,gem\_gtpase\_(gem)\_mrna,\_complete\_cds\_  
 u50928\_4486-  
 4858,autosomal\_dominant\_polycystic\_kidney\_disease\_type\_ii\_(pkd2)\_mrna,\_complete  
 \_cds  
 u73936\_5049-5523,jagged(hj1)\_mrna,\_complete\_cds\_  
 u97105\_4818-5364,n2a3\_mrna,\_complete\_cds  
 x05908cds\_814-1012:in\_reversesequence,\_1110-1338,mrna\_for\_lipocortin  
 all\_x81895\_791-1350,genx-5624\_mrna,\_3'\_utr/gb=x81895\_/ntype=rna

Metagene 109

hg1327-ht1327\_s\_at\_hg1327-ht1327\_statherin\_  
 hg2723-ht2819\_at\_hg2723-ht2819\_proto-oncogene\_n-cym

hg3971-ht4241\_at\_hg3971-ht4241\_transcription\_factor  
 hg4332-ht4602\_at\_hg4332-ht4602\_zinc\_finger\_protein\_znfpt1  
 107949\_1619-2075,gnrh\_receptor\_mrna,\_complete\_cds\_  
 m11722\_1473-2037,terminal\_transferase\_mrna,\_complete\_cds\_  
 m13143\_1762-  
 2224,\_nucleotide\_sequence\_of\_the\_cdna\_insert\_of\_lambda\_pk129\_coding\_forplasma\_p  
 rekallikr  
 m83363\_4104-4614,plasma\_membrane\_calcium-  
 pumping\_atpase\_(pmca4)\_mrna,\_complete\_cds\_  
 s69369\_779-  
 1115,\_pax3a=transcription\_factor\_[human,\_adult\_cerebellum,\_mrna,\_1248\_nt]  
 s69965\_171-597,\_beta-synuclein\_[human,\_brain,\_mrna,\_730\_nt]\_  
 u83117\_1201-1477,sentrin\_mrna,\_complete\_cds  
 all\_x64594\_1290-1855,mrna\_for\_50\_kda\_erythrocyte\_plasma\_membrane\_glycoprotein

## Metagene 36

hg2538-ht2634\_at\_hg2538-ht2634\_heterogeneous\_nuclear\_ribonucleoprotein\_c\_  
 u43653\_2816-3155,obese\_protein\_(ob)\_mrna,\_complete\_cds\_  
 v00532mrna\_387-911,\_ifna\_gene\_(interferon\_alpha-  
 i)\_extracted\_fromgene\_for\_leukocyte\_(alpha)\_interfer  
 all\_x46632\_2953-3206,hspde4c1\_gene\_for\_3'\_,5'-  
 cyclic\_amp\_phosphodiesterase,hspde4c1\_gene\_for\_3'\_,5'

## Metagene 290

d13540\_1948-2500,mrna\_for\_protein-tyrosine\_phosphatase\_  
 s83325\_1796-2275,\_aspartyl(asparaginy1)beta-  
 hydroxylase\_[human,\_hepatoblastoma\_cell\_line\_hepg2,\_mrna  
 all\_x53296\_1099-1657,mrna\_for\_irap\_  
 all\_x95237\_1357-1868,mrna\_for\_cysteine-rich\_secretory\_protein-1

## Metagene 487

s76067cds\_405-759,\_cng2=cyclic\_nucleotide-  
 gated\_cation\_channel\_[human,\_peripheral\_leucocytes,\_genomi  
 u13021\_844-1392,positive\_regulator\_of\_programmed\_cell\_death\_ich-11\_(ich-  
 1)\_mrna,\_complete\_cds  
 u72508\_757-1105,b7\_mrna,\_complete\_cds  
 x83490exon\_3-34:in\_reversesequence,\_389,mrna\_for\_fas/apo-1\_(clone\_pcrtm11-  
 fasdelta(3,4))/gb=x83490\_  
 z31690cds\_838-1129:in\_reversesequence,\_1226-  
 1445,(hepg2)\_lal\_mrna\_for\_lyosomal\_acid\_lipase\_

## Metagene 481

175847\_1808-2330,zinc\_finger\_protein\_45\_(znf45)\_mrna,\_complete\_cds\_  
 176465\_1929-2493,nad+  
 dependenthydroxyprostaglandin\_dehydrogenase\_(pgdh)\_mrna,\_complete\_cds\_

m28585\_329-839,leukocyte\_interferon-alpha\_mrna,\_complete\_cds,\_clone\_pifn105  
 u50196\_1238-1760,adenosine\_kinase\_mrna,\_complete\_cds\_  
 u92458\_3747-4269,metabotropic\_glutamate\_receptormrna,\_complete\_cds

Metagene 355

all\_x85750\_1935-  
 2500,mrna\_for\_transcript\_associated\_with\_monocyte\_to\_macrophage\_differentiation  
 y09306cds\_308-812,mrna\_for\_protein\_kinase,\_dyrk6,\_partial/gb=y09306\_/ntype=rna\_

Metagene 289

all\_d29992\_987-1132,mrna\_for\_placental\_protein(pp5),\_complete\_cds\_  
 m86849\_1747-2179,connexin\_26\_(gjb2)\_mrna\_  
 all\_m96132\_32-66,mhc\_ii\_hla-dr-beta-1\*09012\_(hla-drb1\*09012)\_gene,\_3'\_end\_cds

Metagene 236

m11321mrna\_1193-1703,group-specific\_component\_vitamin\_d-  
 binding\_protein\_mrna,\_complete\_cds\_  
 m58509cds#1\_1114-1441:in\_reversesequence,\_4757-  
 4867,\_fdxr\_gene\_(adrenodoxin\_reductase)\_extracted\_fro  
 s57153\_2388-  
 2878,\_rbp1=retinoblastoma\_binding\_proteinisoform\_i\_{alternatively\_spliced}\_[hum  
 an,\_mrna\_  
 s79854\_1585-  
 1963,\_typeiodothyronine\_deiodinase=selenoenzyme\_[human,\_placenta,\_mrna,\_2066\_nt  
 l\_  
 u34360\_3316-3832,lymphoid\_nuclear\_protein\_(laf-4)\_mrna,\_complete\_cds\_  
 all\_v01515\_5300-5550,gene\_encoding\_preproglucagonglucagon\_is\_a\_29-  
 amino\_acid\_pancreatic\_hormone\_whic

Metagene 139

hg4518-ht4921\_r\_at\_hg4518-ht4921\_transcription\_factor\_btf3\_homolog\_  
 s81083mrna\_3078-3438,\_<beta>-  
 add\_gene\_extracted\_from\_beta\_#name?\_beta\_subunit\_63\_kda\_isoform/membran  
 all\_x86019\_2045-2574,mrna\_for\_prpl-2\_protein\_

Metagene 72

j02986exon#3\_1617-  
 1983,\_fgf4\_gene\_(transforming\_protein)\_extracted\_fromtransforming\_protein\_(hst)  
 \_ge  
 m22489\_1036-1504,bone\_morphogenetic\_protein\_2a\_(bmp-2a)\_mrna\_  
 u63289\_1548-2010,rna-binding\_protein\_cug-bp/hnab50\_(nab50)\_mrna,\_complete\_cds

## Metagene 396

d14043\_1834-2362,mrna\_for\_mgc-24,\_complete\_cds\_  
 d26067\_2680-3166,mrna\_for\_kiaa0033\_gene,\_partial\_cds\_  
 d29805\_3485-3995,mrna\_for\_beta-1,4-galactosyltransferase,\_complete\_cds\_  
 d29963mrna\_885-1443,sfa-  
 l\_(a\_member\_of\_transmembranesuperfamily)\_mrna,\_complete\_cds\_  
 d30655\_1263-1809,mrna\_for\_eukaryotic\_initiation\_factor\_4a11  
 d43636\_3576-4080,mrna\_for\_kiaa0096\_gene,\_partial\_cds\_  
 d50919\_3864-4404,mrna\_for\_kiaa0129\_gene,\_complete\_cds\_  
 d50926\_3626-4124,mrna\_for\_kiaa0136\_gene,\_partial\_cds\_  
 d87446\_5583-6135,mrna\_for\_kiaa0257\_gene,\_partial\_cds\_  
 d87685\_5584-5920,mrna\_for\_kiaa0244\_gene,\_partial\_cds\_  
 j04058\_767-1217,electron\_transfer\_flavoprotein\_alpha-subunit\_mrna,\_complete\_cds\_  
 l14837\_7335-7839,tight\_junction\_(zonula\_occludens)\_protein\_zo-  
 1\_mrna,\_complete\_cds\_  
 l19872\_4756-5059,ah-receptor\_mrna,\_complete\_cds\_  
 l40027mrna\_1586-2132,glycogen\_synthase\_kinase\_mrna,\_complete\_cds\_  
 l40392mrna\_1818-2280,(clone\_sl64)\_mrna,\_3'\_end\_of\_cds\_  
 l48513mrna\_941-1445,paraoxonase(pon2)\_mrna,\_complete\_cds\_  
 m20867\_2463-2986,glutamate\_dehydrogenase\_(gdh)\_mrna,\_complete\_cds\_  
 m29204mrna#1\_2236-2782,dna-binding\_factor\_mrna,\_complete\_cds\_  
 m31013mrna\_4587-5091,nonmuscle\_myosin\_heavy\_chain\_(nmhc)\_mrna,\_3'\_end  
 m62831mrna\_1210-1750,transcription\_factor\_etr101\_mrna,\_complete\_cds\_  
 m65217\_1840-2278,heat\_shock\_factor(hsf2)\_mrna,\_complete\_cds\_  
 m77142\_1629-2193,polyadenylate\_binding\_protein\_(tia-1)\_mrna,\_complete\_cds\_  
 m96954\_806-1313,nucleolysin\_tiar\_mrna,\_complete\_cds\_  
 s72008\_1731-2229,\_hcdc10=cdc10\_homolog\_[human,\_fetal\_lung,\_mrna,\_2314\_nt]\_  
 s80562\_1042-1582,\_acidic\_calponin\_[human,\_kidney,\_mrna,\_1607\_nt]  
 u11313mrna\_2104-2587,sterol\_carrier\_protein-x/sterol\_carrier\_protein-2\_(scp-  
 x/scp-2)\_gene,\_promoter\_  
 u14588\_3012-3570,paxillin\_mrna,\_complete\_cds\_  
 u23942\_2811-3129,lanosterol\_14-  
 demethylase\_cytochrome\_p450\_(cyp51)\_mrna,\_complete\_cds\_  
 u31383\_755-1151,g\_protein\_gamma-10\_subunit\_mrna,\_complete\_cds\_  
 u35113\_2039-2555,metastasis-associated\_mta1\_mrna,\_complete\_cds\_  
 u43077\_964-1510,cdc37\_homolog\_mrna,\_complete\_cds\_  
 u53209\_968-1436,transformer-2\_alpha\_(htra-2\_alpha)\_mrna,\_complete\_cds\_  
 u61167\_3488-4028,sh3\_domain-containing\_protein\_sh3p18\_mrna,\_complete\_cds\_  
 u79267\_987-1437,clone\_23840\_mrna,\_partial\_cds\_  
 u90909\_944-1412,clone\_23722\_mrna\_sequence  
 x04654cds\_1467-1819:in\_reversesequence,\_2524-2634,mrna\_for\_u1\_rna-  
 associated\_70k\_protein\_  
 all\_x72727\_2460-2794,tunp\_mrna\_for\_transformation\_upregulated\_nuclear\_protein  
 all\_x76061\_4282-4793,p130\_mrna\_for\_130k\_protein  
 x80230mrna\_1187-1697,mrna\_(clone\_c-2k)\_mrna\_for\_serine/threonine\_protein\_kinase  
 all\_x87838\_2803-3320,mrna\_for\_beta-catenin\_  
 all\_x98172\_2240-2754,mrna\_for\_mach-alpha-1\_protein\_  
 all\_z15115\_2781-3346,top2\_mrna\_for\_dna\_topoisomerase\_ii\_(partial)  
 all\_z24725\_2759-3210,mitogen\_inducible\_gene\_mig-2,\_complete\_cds\_

## Metagene 351

d38503\_915-  
 1455,pms8\_mrna\_(yeast\_mismatch\_repair\_gene\_pms1\_homologue),\_partial\_cds\_(c-  
 terminal\_regio  
 hg3313-ht3490\_at\_hg3313-ht3490\_thyroid\_hormone\_receptor,\_beta-2  
 hg3996-ht4266\_at\_hg3996-ht4266\_cpg-enriched\_dna,\_clone\_s21\_

Metagene 152

hg3115-ht3291\_at\_hg3115-ht3291\_golli-mbp\_  
 l02950\_673-1177,mu-crystallin\_mrna,\_complete\_cds\_  
 all\_m10950\_57-304,alpha-fetoprotein\_(afp)\_gene  
 m64572\_3431-3923,protein\_tyrosine\_phosphatase\_mrna,\_complete\_cds\_  
 s68134\_500-665,\_crem=cyclic\_amp-  
 responsive\_element\_modulator\_beta\_isoform\_[human,\_mrna,\_1030\_nt]  
 u41898\_73-505,sodium\_cotransporter\_rkst1\_mrna,\_partial\_cds/gb=u41898\_/ntype=rna  
 u50708\_946-1384,branched\_chain\_alpha-  
 ketoacid\_dehydrogenase\_e1\_beta\_subunit\_mrna,\_complete\_cds\_

Metagene 420

d14838\_915-1317,mrna\_for\_fgf-9,\_complete\_cds\_  
 d38548\_4682-5210,mrna\_for\_kiaa0076\_gene,\_complete\_cds\_  
 d63851\_3157-3643,mrna\_for\_unc-18\_homologue,\_complete\_cds\_  
 d87073\_5307-5847,mrna\_for\_kiaa0236\_gene,\_complete\_cds\_  
 hg1728-ht1734\_s\_at\_hg1728-ht1734\_non-  
 specific\_cross\_reacting\_antigen,\_altsplice\_form\_2\_  
 m28827\_620-1112,thymocyte\_antigen\_cd1c\_mrna,\_complete\_cds\_  
 m92449\_668-1190,ltr\_mrna,\_3'\_end\_of\_coding\_region\_and\_3'\_flank\_  
 u02388\_2097-2337,cytochrome\_p450\_4f2\_(cyp4f2)\_mrna,\_complete\_cds\_  
 u59632\_2578-  
 3138,h5\_mrna,\_partial\_cds,\_and\_platelet\_glycoprotein\_ib\_beta\_chain\_mrna,\_comple  
 te\_cds  
 u72517\_413-  
 953,alternatively\_spliced\_variant\_c7f\_(c3f)\_mrna,\_partial\_3'\_utr/gb=u72517\_/nty  
 pe=rna\_

Metagene 219

d38462exon\_57-  
 549,gene\_for\_a1\_chain\_of\_type\_xix\_collagen,\_exon\_+3'\_/gb=d38462\_/ntype=dna\_/ann  
 ot=exon  
 l20433\_3738-3780,octamer\_binding\_transcription\_factor(otf1)\_mrna,\_complete\_cds  
 z68204cds\_43-373,mrna\_for\_succinyl\_coa\_synthetase/gb=z68204\_/ntype=rna\_

Metagene 15

l29306\_723-  
 1116,tryptophan\_hydroxylase\_(tph)\_mrna,\_complete\_cds/gb=l29306\_/ntype=rna

all\_m14159\_1264-1482, t-cell\_receptor\_beta-chain\_j2.1\_gene\_extracted\_fromt-cell\_receptor\_germline\_be  
 m20566mrna\_2745-3180, interleukinreceptor\_mrna, \_complete\_cds\_  
 s69232\_1584-1992, \_electron\_transfer\_flavoprotein-ubiquinone\_oxidoreductase\_[human, \_fetal\_liver, \_mrna  
 u09851\_44-254, zinc\_finger\_protein\_(znf148)\_mrna, \_partial\_cds\_  
 y07512\_3211-3715, mrna\_for\_type\_i\_beta\_cgmp-dependent\_protein\_kinase\_(ec\_2.7.1.37)  
 all\_z80779\_563-822, h2b/g\_gene

Metagene 11

hg2662-ht2758\_at\_hg2662-ht2758\_homeotic\_protein\_emx1\_  
 l09753\_1377-1827, cd30\_ligand\_mrna, \_complete\_cds\_  
 s71018\_282-798, \_cyclophilin\_c\_[human, \_kidney, \_mrna, \_883\_nt]\_  
 s76473\_2563-3079, \_trkb\_[human, \_brain, \_mrna, \_3194\_nt]

Metagene 133

all\_d00726\_1842-2413, mrna\_for\_ferrochelatase\_(ec\_4.99.1.1)\_  
 d16217\_1904-2414, mrna\_for\_calpastatin, \_complete\_cds\_  
 d63390\_600-1164, mrna\_for\_acetylhydrolase\_ib\_beta-subunit, \_complete\_cds\_  
 d87464\_2481-2961, mrna\_for\_kiaa0274\_gene, \_complete\_cds\_  
 hg2850-ht4814\_s\_at\_hg2850-ht4814\_biliary\_glycoprotein, \_altsplce\_5, \_a  
 hg3578-ht3781\_at\_hg3578-ht3781\_autoimmune\_antigen, \_thyroid\_disease-related\_antigen\_  
 hg417-ht417\_s\_at\_hg417-ht417\_cathepsin\_b\_  
 hg4234-ht4504\_at\_hg4234-ht4504\_methylenetetrahydrofolate\_reductase\_  
 hg4660-ht5073\_at\_hg4660-ht5073\_microtubule-associated\_protein\_1b\_  
 hg945-ht945\_s\_at\_hg945-ht945\_nucleic\_acid-binding\_protein  
 j05213\_430-958, sialoprotein\_mrna, \_complete\_cds\_  
 l07033\_967-1507, hydroxymethylglutaryl-coa\_lyase\_mrna, \_complete\_cds\_  
 l38486mrna\_1162-1720, microfibril-associated\_glycoprotein(mfap4)\_mrna, \_3'\_end\_of\_cds\_  
 m71243mrna\_25-  
 38: not\_in\_gb\_record, glycophorin\_sta\_(type\_a)\_exonsand\_4, \_partial/gb=m71243\_/nty  
 pe=dna\_  
 m76424gene\_6565-7070, carbonic\_anhydrase\_vii\_(ca\_vii)\_gene  
 u01824\_1402-1912, glutamate/aspartate\_transporter\_ii\_mrna, \_complete\_cds\_  
 u07000cds#4\_558-810: in\_reversesequence, \_97660-  
 97876, \_bcr\_gene\_(unknown)\_extracted\_frombreakpoint\_clu  
 u13044\_1429-1945, nuclear\_respiratory\_factor-2\_subunit\_alpha\_mrna, \_complete\_cds\_  
 u19948\_1058-1616, protein\_disulfide\_isomerase\_(pdip)\_mrna, \_complete\_cds\_  
 u27831cds\_1110-1578: in\_reversesequence, \_1602-1680, striatum-enriched\_phosphatase\_(step)\_mrna, \_partial  
 u44059\_429-909, thyrotroph\_embryonic\_factor\_(tef)\_mrna, \_complete\_cds  
 u49441\_258-  
 648, mitochondrial\_trifunctional\_protein\_beta\_subunit\_mrna, \_partial\_cds/gb=u4944  
 1\_/ntype=r  
 u51205\_333-873, cop9\_homolog\_(hcop9)\_mrna, \_complete\_cds\_  
 u59057\_226-754, beta-a4\_crystallin\_(cryba4)\_mrna, \_complete\_cds\_  
 u59736\_2496-2772, transcription\_factor\_(nfatc.b)\_mrna, \_complete\_cds\_  
 u63455mrna\_4412-4868, sulfonylurea\_receptor\_(surl)\_gene\_

u67988\_1623-2163,guanylate\_kinase\_associated\_protein\_(gkap)\_mrna,\_complete\_cds\_  
u86358\_296-818,chemokine\_(teck)\_mrna,\_complete\_cds/gb=u86358\_/ntype=rna  
u90918\_1794-2094,clone\_23654\_mrna\_sequence\_  
u96769mrna\_1266-1746,chondroadherin\_gene,\_5'\_flanking\_region\_and\_  
u96781mrna#1\_2433-2961,\_atp2a1\_gene\_(ca2+\_atpase\_of\_fast-  
twitch\_skeletal\_muscle\_sarcolemmal\_reticulum)  
x65633cds\_585-870:in\_reversesequence,\_1568-1766,acth-  
r\_gene\_for\_adrenocorticotrophic\_hormone\_receptor  
x66114mrna\_564-1074,gene\_for\_2-oxoglutarate\_carrier\_protein\_  
all\_x77197\_2631-3166,mrna\_for\_chloride\_channel\_  
x83973cds\_2262-2538:in\_reversesequence,\_2738-2822,mrna\_for\_ttf-i  
x91117mrna\_1655-2033,hg\_net\_gene\_exon\_1\_  
x92521cds\_1127-1484:in\_reversesequence,\_1618-1768,mrna\_for\_mmp-19\_protein\_  
x93996mrna\_2570-3113,mrna\_for\_afx\_protein\_  
x95406exon#1-2\_12-17:not\_in\_gb\_record,cyclin\_e\_gene.  
y07847exon#3\_36-582,mrna\_for\_rrp22\_protein\_  
z71389mrna\_85-295,mrna\_for\_skin-antimicrobial-peptide(sap1).

Metagene 61

m31166mrna\_1286-1784,tumor\_necrosis\_factor-inducible\_(tsg-  
14)\_mrna,\_complete\_cds\_  
u60415\_2126-2570,bhlh-pas\_protein\_jap3\_mrna,\_complete\_cds  
u70981\_749-1283,interleukin-13\_receptor\_mrna,\_complete\_cds\_  
z83803\_7-259,mrna\_for\_axonemal\_dynein\_heavy\_chain\_(partial,\_id\_hdhc4)

Metagene 463

hg2709-ht2805\_at\_hg2709-ht2805\_serine/threonine\_kinase\_  
hg3137-ht3313\_at\_hg3137-ht3313\_zinc\_finger\_protein\_znf81\_  
hg4052-ht4322\_at\_hg4052-ht4322\_glutamate\_ionotropic\_receptor  
m13666\_800-992,c-myb\_mrna,\_3'\_end  
m15656cds\_712-1066:in\_reversesequence,\_3992-4082,aldolase\_b\_(aldob)\_gene  
m54995\_108-603,connective\_tissue\_activation\_peptide\_iii\_mrna,\_complete\_cds\_  
s69790\_962-1412,brush-  
1=tumor\_suppressor\_{3'\_region}\_[human,breast\_epithelium,\_mrna\_partial,\_1485\_  
all\_x53065\_85-462,spr2-1\_gene\_for\_small\_proline\_rich\_protein\_(exon\_2)  
y10571cds\_696-978:in\_reversesequence,\_1002-1194,mrna\_for\_ding\_gene  
all\_y11897\_19-320,brx\_gene\_3'\_utr/gb=y11897\_/ntype=rna\_  
z75330cds\_3384-3714:in\_reversesequence,\_4156-4312,mrna\_for\_nuclear\_protein\_sa-  
1.

Metagene 414

d86640\_2374-2902,mrna\_for\_stac,\_complete\_cds\_  
hg2157-ht2227\_at\_hg2157-ht2227\_mucin\_4,\_tracheobronchial\_  
j03507\_3421-3865,complement\_protein\_component\_c7\_mrna,\_complete\_cds  
all\_l15296\_3031-3082,clone\_hrcnc2b\_retinal\_rod\_cyclic\_nucleotide-  
gated\_cation\_channel\_gene,\_complete  
l41390exon#1\_244-395,corebeta-1,6-n-  
acetylglucosaminyltransferase\_(coregnt)\_gene,\_exon/gb=l41390\_/nt

m59820mrna\_2435-2975,granulocyte\_colony-  
 stimulating\_factor\_receptor\_(csf3r)\_mrna,\_complete\_cds\_  
 m77481mrna\_1021-1566,antigen\_(mage-1)\_gene,\_complete\_cds\_  
 m82962mrna\_2313-2835,n-benzoyl-l-tyrosyl-p-amino-  
 benzoic\_acid\_hydrolase\_alpha\_subunit\_(pph\_alpha)\_mr  
 m87284\_2479-2923,69\_kda\_2'\_5'\_oligoadenylate\_synthetase\_(p69\_2-  
 5a\_synthetase)\_mrna,\_complete\_cds\_  
 u05291\_1363-1849,fibromodulin\_mrna,\_partial\_cds\_  
 u29589exon\_2948-  
 3488,m3\_muscarinic\_acetylcholine\_receptor\_(chrn3)\_gene,\_complete\_cds\_  
 u43672\_2939-3443,putative\_transmembrane\_receptor\_il-1rrp\_mrna,\_complete\_cds\_  
 u71601\_960-1422,zinc\_finger\_protein\_zfp47\_(zf47)\_mrna,\_partial\_cds\_  
 x06482cds\_60-405:in\_reversesequence,\_884-887,theta\_1-globin\_gene  
 all\_x14975\_7566-8337,cd1\_r2\_gene\_for\_mhc-related\_antigen\_  
 x55989mrna\_169-354,ecrp\_gene\_for\_eosinophil\_cationic\_related\_protein  
 y10512mrna\_14-452,mrna\_for\_cd282\_protein/gb=y10512\_/ntype=rna

Metagene 113

110102mrna#1\_392-794,sex-determining\_region\_y\_(sry)\_gene,\_complete\_cds\_  
 l34081mrna\_1055-1601,bile\_acid\_coa:\_amino\_acid\_n-  
 acyltransferase\_mrna,\_complete\_cds\_  
 m34353\_6763-7342,transmembrane\_tyrosine-  
 specific\_protein\_kinase\_(ros1)\_mrna,\_complete\_cds\_  
 m61156\_1122-1308,activator\_protein\_2b\_(ap-2b)\_mrna,\_complete\_cds\_  
 m95767\_1065-1563,di-n-acetylchitobiase\_mrna,\_complete\_cds\_  
 all\_x02956\_1039-1253,interferon\_alpha\_gene\_ifn-alpha\_5\_  
 all\_x07994\_5703-6244,mrna\_for\_lactase-phlorizin\_hydrolase\_lph\_(ec\_3.2.1.23-62)\_  
 x68994exon\_4-55,creb\_gene,\_exon\_y  
 all\_x78686\_706-1121,ena-78\_mrna  
 all\_x95239\_863-1362,mrna\_for\_cysteine-rich\_secretory\_protein-2/type\_i  
 y10508mrna\_370-660,mrna\_for\_cd190\_protein/gb=y10508\_/ntype=rna\_

Metagene 106

hg2007-ht2056\_s\_at\_hg2007-ht2056\_proto-oncogene\_sno,\_altsplice\_n\_

Metagene 319

d42072\_2020-2542,mrna\_for\_nf1\_n-isoform-exon11,\_complete\_cds\_  
 hg3998-ht4268\_at\_hg3998-ht4268\_1-glycerol-3-phosphate:nad+\_oxidoreductase  
 m28170\_1894-1987,cell\_surface\_protein\_cd19\_(cd19)\_gene,\_complete\_cds\_  
 m62843\_906-  
 1404,brain\_protein\_recognized\_by\_the\_sera\_of\_patients\_with\_paraneoplastic\_senso  
 ry\_neurono  
 s67247\_365-  
 821,\_smooth\_muscle\_myosin\_heavy\_chain\_isoform\_smemb\_[human,\_umbilical\_cord,\_fet  
 al\_aorta,\_  
 u08006exon#1\_78-567,complementalpha\_subunit\_(c8a)\_gene  
 u09411\_1794-2343,zinc\_finger\_protein\_znf132\_mrna,\_complete\_cds\_  
 u40343\_657-1119,cdk\_inhibitor\_p19ink4d\_mrna,\_complete\_cds\_



u52827\_1022-1508,cri-du-chat\_region\_mrna,\_clone\_nibb11\_  
u66052mrna\_7-271,clone\_w2-6\_mrna\_from\_chromosome\_x/gb=u66052\_/ntype=rna  
x07173cds\_2503-2803:in\_reversesequence,\_2956-  
3028,mrna\_for\_second\_protein\_of\_inter-alpha-trypsin\_inh  
x16316cds\_2109-2355:in\_reversesequence,\_2483-2693,mrna\_for\_vav\_oncogene\_  
x63578mrna\_31-535,gene\_for\_parvalbumin

## Metagene 170

109230\_933-1460,c-c\_chemokine\_receptor\_type(c-c\_ckr-1)\_mrna,\_complete\_cds\_  
147276\_383-934,(cell\_line\_h1-60)\_alpha\_topoisomerase\_truncated-  
form\_mrna,\_3'\_utr/gb=147276\_/ntype=rn  
m13150mrna\_776-1337,mas\_proto-oncogene\_mrna,\_complete\_cds  
m20137mrna\_400-820,interleukin(il-3)\_mrna,\_complete\_cds,\_clone\_pcd-sr-alpha\_  
u33202\_104-354,mdm2-d\_(mdm2)\_mrna,\_complete\_cds/gb=u33202\_/ntype=rna\_  
all\_x66894\_3881-4417,facc\_mrna\_from\_complementation\_group\_c\_(fa(c))  
all\_y08263\_1373-1902,mrna\_for\_aad14\_protein,\_partial\_  
all\_y09980\_16580-17121,hoxd3\_gene\_

## Metagene 75

hg1227-ht1227\_s\_at\_hg1227-ht1227\_collagen,\_type\_ii,\_alpha\_1  
all\_j00116\_4597-4806,alpha-1(ii)\_collagen\_gene\_col2a1,\_partial\_cds\_  
m60299exon\_73-163,alpha-  
1\_collagen\_type\_ii\_gene,\_exons\_1,and/gb=m60299\_/ntype=dna\_/annot=exon  
u14550\_1319-1877,sialyltransferase\_sthm\_(sthm)\_mrna,\_complete\_cds  
u22322\_2205-2587,nuclear\_tyrosine\_protein\_kinase\_rak\_mrna,\_complete\_cds  
all\_x57830\_2409-3016,serotonin\_5-ht2\_receptor\_mrna\_

## Metagene 223

all\_m60749\_829-1061,histone\_h4\_(h4)\_gene,\_complete\_cds\_  
u24577\_1182-1512,ldl-phospholipase\_a2\_mrna,\_complete\_cds\_

## Metagene 116

d63412\_1299-1713,mrna\_for\_aquaporin,\_complete\_cds  
hg2981-ht3938\_s\_at\_hg2981-ht3938\_epican,\_altsplice\_12  
u61849\_4650-5040,neuronal\_pentraxin(nptx1)\_mrna,\_complete\_cds\_

## Metagene 332

137362\_1009-1579,(clone\_d2-  
115)\_kappa\_opioid\_receptor\_(oprk1)\_mrna,\_complete\_cds  
all\_m28879\_3325-4444,granzyme\_b\_(ctla-1)\_gene,\_complete\_cds  
u34070cds\_744-1053:in\_reversesequence,\_1731-  
1763,ccat/enhancer\_binding\_protein\_alpha\_gene,\_complete

u57592\_3563-4043,jumonji\_putative\_protein\_(jumonji)\_mrna,\_complete\_cds\_  
u93867\_1248-  
1764,rna\_polymerase\_iii\_subunit\_(rpc62)\_mrna,\_complete\_cds/gb=u93867\_/ntype=rna  
all\_z28339\_2084-2649,mrna\_for\_delta\_4-3-oxosteroidbeta-reductase

Metagene 196

d37984\_1856-2314,mrna\_for\_dna\_helicase\_q1,\_partial\_cds\_  
l22214\_2335-2857,adenosine\_a1\_receptor\_(adoral)\_mrna\_exons\_1-6,\_complete\_cds\_  
u17743\_699-1221,jnk\_activating\_kinase\_(jnkkl1)\_mrna,\_complete\_cds\_  
u21051mrna#1\_2326-2647,g\_protein-coupled\_receptor\_(gpr4)\_gene,\_complete\_cds\_  
u45975\_882-1434,phosphatidylinositol\_(4,5)bisphosphate\_5-  
phosphatase\_homolog\_mrna,\_partial\_cds\_  
u50743\_13-439,na,k-atpase\_gamma\_subunit\_mrna,\_complete\_cds\_

Metagene 150

d17390\_2313-2829,mrna\_for\_mdc\_protein  
d49410exon\_48-534,gene\_for\_interleukinreceptor\_alpha\_subunit  
hg3063-ht3224\_at\_hg3063-ht3224\_major\_histocompatibility\_complex,\_i\_  
hg3355-ht3532\_at\_hg3355-ht3532\_peroxisome\_proliferator\_activated\_receptor  
hg4417-ht4687\_f\_at\_hg4417-ht4687\_homeotic\_protein\_hpx-2  
l11931\_1454-  
1644,cytosolic\_serine\_hydroxymethyltransferase\_(shmt)\_mrna,\_complete\_cds\_  
m21056cds\_193-403:in\_reversesequence,\_165-345,pancreatic\_phospholipase\_a-  
2\_(pla-2)\_gene\_  
m76231\_292-790,sepiapterin\_reductase\_mrna,\_complete\_cds  
m81379\_1126-1546,alpha-3\_type\_iv\_collagen\_(col4a3)\_mrna,\_3'\_end  
m86383\_1007-  
1527,nicotinic\_acetylcholine\_receptor\_alphasubunit\_mrna,\_complete\_cds\_  
m86407\_2299-2833,alpha\_actinin(actn3)\_mrna,\_complete\_cds\_  
m95678\_3990-4494,phospholipase\_c-beta-2\_mrna,\_complete\_cds  
u06643\_71-463,keratinocyte\_lectin(hkl-14)\_mrna,\_complete\_cds.  
u16127\_3025-3589,glutamate/kainate\_receptor\_subunit\_(eaa5)\_mrna,\_complete\_cds  
u43142\_1456-  
1972,vascular\_endothelial\_growth\_factor\_related\_protein\_vrp\_mrna,\_complete\_cds\_  
u59913\_1640-2168,chromosomemad\_homolog\_smad5\_mrna,\_complete\_cds\_  
u62437\_1943-  
2393,nicotinic\_acetylcholine\_receptor\_beta2\_subunit\_precursor,\_mrna,\_complete\_c  
ds  
u71300\_1307-  
1703,srna\_activating\_protein\_complex\_50kd\_subunit\_(snap50)\_mrna,\_complete\_cds\_  
all\_x15217\_2292-2875,sno\_oncogene\_mrna\_for\_snoa\_protein,\_ski-related\_  
all\_x54741\_2389-2918,cypxib2\_gene\_for\_aldosterone\_synthase\_  
x60592mrna\_415-973,cdw40\_mrna\_for\_nerve\_growth\_factor\_receptor-related\_b-  
lymphocyte\_activation\_molec  
x60655mrna\_990-1474,evx1\_mrna  
x62891mrna\_57-390,mutant\_coseg\_gene\_for\_vasopressin-neurophysin\_precursor  
x91257\_1281-1797,mrna\_for\_seryl-trna\_synthetase  
x92475\_905-1295,mrna\_for\_itba1\_protein\_  
x95191cds\_707-848,mrna\_for\_delta-sarcoglycan/gb=x95191\_/ntype=rna  
all\_y11215\_971-1446,mrna\_for\_skap55\_protein/gb=y11215\_/ntype=rna  
z22865cds\_164-578:in\_reversesequence,\_620,dermatopontin\_mrna,\_complete\_cds

reverse\_z49155\_27087-  
27346,dna\_from\_cosmid\_183d3,\_huntington's\_disease\_region,\_chromosome\_4p16.3\_

Metagene 263

ab003698\_2634-3138,mrna\_for\_cdc7-related\_kinase,\_complete\_cds  
m77140\_91-409,pro-galanin\_mrna,\_3'\_end\_  
m98447mrna\_2256-2670,keratinocyte\_transglutaminase\_gene,\_complete\_cds\_  
u23752\_1679-1919,sox-11\_mrna,\_complete\_cds

Metagene 282

aj001421cds\_117-567:in\_reversesequence,\_585-  
600,mrna\_for\_rer1\_protein/gb=aj001421\_/ntype=rna\_  
d86981\_5936-6410,mrna\_for\_kiaa0228\_gene,\_partial\_cds\_  
142452mrna\_1100-  
1520,pyruvate\_dehydrogenase\_kinase\_isoenzyme(pdk3)\_mrna,\_complete\_cds  
m22632mrna\_1744-  
2284,mitochondrial\_aspartate\_aminotransferase\_mrna,\_complete\_cds\_  
m87503\_1085-1535,ifn-responsive\_transcription\_factor\_subunit\_mrna,\_complete\_cds\_  
u01923\_1649-2090,btk\_region\_clone\_ftp-3\_mrna\_  
u02081\_1642-  
2026,guanine\_nucleotide\_regulatory\_protein\_(net1)\_mrna,\_complete\_cds\_  
u04285utr#1\_689-  
1148,lysosomal\_acid\_lipase,\_cholesteryl\_ester\_hydrolase\_(lipa)\_gene  
u16799\_865-1419,na,k-atpase\_beta-1\_subunit\_mrna,\_complete\_cds  
u40038\_1236-1425,gtp-binding\_protein\_alpha\_q\_subunit\_(gnaq)\_mrna,\_complete\_cds\_  
u53445\_2442-  
2928,ovarian\_cancer\_downregulated\_myosin\_heavy\_chain\_homolog\_(doc1)\_mrna,\_compl  
ete\_cds\_  
u58046\_4637-5176,p167\_mrna,\_complete\_cds\_  
u76421\_4572-4962,dsrna\_adenosine\_deaminase\_drada2b\_(drada2b)\_mrna,\_complete\_cds\_  
u77718\_2100-2592,desmosome\_associated\_protein\_pinin\_mrna,\_complete\_cds\_  
u81006\_1886-2348,p76\_mrna,\_complete\_cds  
u89505\_1087-1537,h1ark\_mrna,\_complete\_cds  
u94586\_145-445,nadh:ubiquinone\_oxidoreductase\_mlrq\_subunit\_mrna,\_complete\_cds  
all\_x01060\_4427-4986,mrna\_for\_transferrin\_receptor\_  
all\_x13916\_14416-14876,mrna\_for\_ldl-receptor\_related\_protein\_  
x53586mrna\_4766-  
5306,\_integrin\_alpha(or\_alpha\_e)\_protein\_gene\_extracted\_frommrna\_for\_integrin\_a  
lpha\_  
all\_x68560\_2909-3480,spr-2\_mrna\_for\_gt\_box\_binding\_protein\_  
x69978cds\_3218-3494:in\_reversesequence,\_3769-3781,mrna\_for\_xp-g\_factor  
all\_x71490\_1059-1552,mrna\_for\_vacuolar\_proton\_atpase,\_subunit\_d  
all\_x72790\_30-1461,endogenous\_retrovirus\_mrna\_for\_orf/gb=x72790\_/ntype=rna\_  
x77909cds\_888-1122:in\_reversesequence,\_1202-1406,ikbl\_mrna  
x82676\_3333-3873,mrna\_for\_tyrosine\_phosphatase\_  
all\_y00757\_629-1134,mrna\_for\_polypeptide\_7b2\_  
all\_z34975\_2303-2862,ldlc\_mrna\_  
z49989cds\_779-1079:in\_reversesequence,\_1540,mrna\_for\_smoothelin\_

Metagene 85

d38553\_2125-2665,mrna\_for\_kiaa0074\_gene,\_partial\_cds\_  
d78367\_1372-1810,mrna\_for\_k12\_keratin,\_complete\_cds\_  
j03133\_2096-2612,transcription\_factor\_sp1\_mrna,\_3'\_end\_  
106895\_503-  
977,antagonizer\_of\_myc\_transcriptional\_activity\_(mad)\_mrna,\_complete\_cds\_  
l41816mrna\_891-1389,cam\_kinase\_i\_mrna,\_complete\_cds\_  
s78085\_719-1187,\_pdcd2=programmed\_cell\_death-  
2/rp8\_homolog\_[human,\_fetal\_lung,\_mrna,\_1282\_nt]\_  
all\_u66083\_2217-  
2758,contig\_of\_two\_cosmids\_from\_llnl\_x\_chromosome\_library\_(u83f1,\_u109h10),\_inc  
ludin  
u89916\_375-879,putative\_osp\_like\_protein\_mrna,\_partial\_cds  
all\_x62048\_1820-2343,wee1\_hu\_gene

Metagene 385

m32402mrna\_1851-2253,placental\_protein\_(pp11)\_mrna,\_complete\_cds\_  
m93107\_978-1278,heart\_(r)-3-hydroxybutyrate\_dehydrogenase\_mrna,\_3'\_end

Metagene 465

af015913\_1437-1947,skblhs\_mrna,\_complete\_cds/gb=af015913/\_ntype=rna\_  
d11428\_1253-1757,mrna\_for\_pmp-22(pas-ii/sr13/gas-  
3)\_of\_peripheral\_myelin,\_complete\_cds\_  
d16294\_1019-1523,mrna\_for\_mitochondrial\_3-oxoacyl-coa\_thiolase,\_complete\_cds\_  
d21063\_2853-3303,mrna\_for\_kiaa0030\_gene,\_partial\_cds\_  
d38524\_2673-3213,mrna\_for\_5'-nucleotidase\_  
d63476\_4587-4953,mrna\_for\_kiaa0142\_gene,\_complete\_cds\_  
hg1827-ht1856\_s\_at\_hg1827-  
ht1856\_cytochrome\_p450,\_subfamily\_iic,\_altsplice\_form\_2  
hg2981-ht3127\_s\_at\_hg2981-ht3127\_epican,\_altsplice\_11  
hg3521-ht3715\_at\_hg3521-ht3715\_ras-related\_protein\_rap1b\_  
j05682\_1023-1575,subunit\_c\_of\_v-atpase\_(vat\_c)\_mrna,\_3'\_end  
l28997\_443-953,arll\_mrna,\_complete\_cds  
l31801\_2229-2535,monocarboxylate\_transporter(slc16a1)\_mrna,\_complete\_cds\_  
m25753mrna\_1103-1427,cyclin\_b\_mrna,\_3'\_end\_  
all\_m27161\_6940-7265,mhc\_i\_cd8\_alpha-chain\_(leu-2/t8)\_gene,\_complete\_cds\_  
m67468\_3244-3720,fragile\_x\_mental\_retardationfmr-  
1\_gene,\_3'\_end,\_clones\_bc72\_and\_bc22\_  
m74524\_1190-1658,hhr6a\_(yeast\_radhomologue)\_mrna,\_complete\_cds  
m90656\_2044-2590,gamma-glutamylcysteine\_synthetase\_(gcs)\_mrna,\_complete\_cds  
u00001\_2019-2547,homologue\_of\_spombe\_nuc2+\_and\_anidulans\_bima  
u01833\_690-1164,nucleotide-binding\_protein\_mrna,\_complete\_cds  
u09564\_3725-4205,serine\_kinase\_mrna,\_complete\_cds  
u15128cds\_1011-1299:in\_reversesequence,\_2065-2233,beta-1,2-n-  
acetylglucosaminyltransferase\_ii\_(mgat2  
u17714\_2774-  
3068:not\_in\_gb\_record,putative\_tumor\_suppressor\_(snc6)\_mrna,\_complete\_cds\_  
u27460\_1582-1798,uridine\_diphosphoglucose\_pyrophosphorylase\_mrna,\_complete\_cds\_  
u39318\_159-  
675,e2\_ubiquitin\_conjugating\_enzyme\_ubch5c\_(ubch5c)\_mrna,\_complete\_cds

u61145\_2035-2509,enhancer\_of\_zeste\_homolog(ezh2)\_mrna,\_complete\_cds\_  
 u61232\_1407-1869,tubulin-folding\_cofactor\_e\_mrna,\_complete\_cds\_  
 u69141\_1311-1719,glutaryl-coa\_dehydrogenase\_mrna,\_complete\_cds\_  
 u72263\_2410-  
 2931,multiple\_exostoses\_type\_ii\_protein\_ext2.i\_mrna,\_complete\_cds/gb=u72263\_/nt  
 type=rna\_  
 u88047\_1567-1969,dna\_binding\_protein\_homolog\_(drx)\_mrna,\_partial\_cds\_  
 all\_x02160\_4717-4976,mrna\_for\_insulin\_receptor\_precursor\_  
 all\_x54993\_1096-1685,tfiid\_mrna  
 all\_x56807\_2617-3194,dsc2\_mrna\_for\_desmocollins\_type\_2a\_and\_2b\_  
 x59244mrna\_2391-2967,znf43\_mrna  
 x61100mrna\_1983-  
 2445,\_75\_kda\_subunit\_nadh\_dehydrogenase\_precursor\_gene\_extracted\_frommrna\_for\_m  
 itoch  
 all\_x63468\_2398-2915,mrna\_for\_transcription\_factor\_tfiie\_alpha\_  
 all\_x64229\_888-1393,dek\_mrna\_  
 x65867cds#1\_1157-1409:in\_reversesequence,\_1447-  
 1639,mrna\_for\_adenylosuccinate\_lyase\_  
 all\_x79201\_2342-2775,mrna\_for\_syt  
 x85753\_1268-1646,mrna\_for\_cdk8\_protein\_kinase  
 y00971mrna\_1891-  
 2419,mrna\_for\_phosphoriobosyl\_pyrophosphate\_synthetase\_subunit\_ii\_(ec\_2.7.6.1)\_  
 y09943cds\_117-452:in\_reversesequence,\_561-602,mrna\_for\_ngf-inducible\_pc3\_anti-  
 proliferative\_protein\_

Metagene 411

d17570\_565-1083,mrna\_for\_zona-pellucida-binding\_protein\_(sp38),\_complete\_cds.  
 d49394\_1619-2123,mrna\_for\_serotonin\_5-ht3\_receptor,\_complete\_cds\_  
 hg2358-ht4858\_s\_at\_hg2358-ht4858\_proto-oncogene\_ets-1,\_altsplice\_2\_  
 l39833\_2587-3097,(clone\_hkvbeta3)\_k+\_channel\_beta\_subunit\_mrna,\_complete\_cds  
 m13577mrna\_1550-2096,myelin\_basic\_protein\_(mbp)\_mrna,\_complete\_cds\_  
 m14113mrna\_8440-8986,coagulation\_factor\_viii:c\_mrna,\_complete\_cds  
 all\_m33987\_2226-2701,carbonic\_anhydrase\_i\_(cai)\_mrna,\_complete\_cds\_  
 m35296\_3284-3758,tyrosine\_kinase\_arg\_gene\_mrna\_  
 m64934\_1917-2397,kell\_blood\_group\_protein\_mrna\_  
 all\_s71129\_3-426,\_acetylcholinesterase\_{i4-  
 e5\_doman}\_[human,\_tumor\_cell\_lines,\_genomic,\_847\_nt]\_  
 s78234\_2755-3259,\_nuc2\_homolog\_[human,\_fibroblasts,\_mrna,\_3320\_nt]  
 u00238\_3024-3552,glutamine\_prpp\_amidotransferase\_(gpat)\_mrna\_complete\_cds  
 u00943\_1017-1203,clone\_a9a2brb2\_(cac)n/(gtg)n\_repeat-containing\_mrna\_  
 u03397\_787-1358,receptor\_protein\_4-1bb\_mrna,\_complete\_cds  
 u15460\_322-844,bzip\_protein\_b-atf\_mrna,\_complete\_cds\_  
 u27326\_1666-  
 2123,alpha\_(1,3/1,4)\_fucosyltransferase\_(fut3)\_mrna,\_major\_transcript\_i,\_comple  
 te\_cds  
 u31875\_979-1399,hep27\_protein\_mrna,\_complete\_cds.  
 u40846\_1964-2399,alpha-n-acetylglucosaminidase\_(nag)\_mrna,\_complete\_cds  
 u51477\_2883-3444,diacylglycerol\_kinase\_zeta\_mrna,\_complete\_cds\_  
 u62317mrna#6\_1634-  
 2156,\_hypothetical\_protein\_384d8gene\_extracted\_from\_chromosome\_22q13\_bac\_clone\_  
 cit  
 u71364\_1097-1553,serine\_proteinase\_inhibitor\_(p19)\_mrna,\_complete\_cds

all\_u73167\_4971-  
 35099, h\_luca14.2a\_gene\_extracted\_fromcosmid\_luca14, h\_luca14.2a\_gene\_extracted  
 \_from  
 u79274\_883-1381, clone\_23733\_mrna, complete\_cds.  
 v00574cds\_225-538:in\_reversesequence, 3330-  
 3468, germ\_line\_gene\_homologous\_to\_bladder\_carcinoma\_oncog  
 all\_x17622\_3693-4210, hbk2\_mrna\_for\_potassium\_channel\_protein\_  
 x51688mrna\_1054-1438, mrna\_for\_cyclin\_a\_  
 all\_x62515\_13260-13708, mrna\_for\_basement\_membrane\_heparan\_sulfate\_proteoglycan\_  
 x70040cds\_3944-4130:in\_reversesequence, 4236-4470, ron\_mrna\_for\_tyrosine\_kinase\_  
 x85781exon\_2-551, nos2\_gene, exon\_27\_/gb=x85781\_/ntype=dna\_/annot=exon  
 y10055cds\_2802-3096:in\_reversesequence, 3310-3532, mrna\_for\_phosphoinositide\_3-  
 kinase\_

## Metagene 326

l10035\_162-666:in\_reversesequence, 684-690, crystallin\_beta-  
 b2\_mrna, complete\_cds  
 m16594\_790-904, glutathione\_s-transferase\_ha\_subunit(gst)\_mrna, complete\_cds\_  
 u81523\_1378-1870, endometrial\_bleeding\_associated\_factor\_mrna, complete\_cds.  
 all\_y10375\_1179-1706, mrna\_for\_sirp-alpha1

## Metagene 237

d17427\_3421-3506, mrna\_for\_desmocollin\_type\_4\_  
 d25278\_2024-2510, mrna\_for\_kiaa0036\_gene, complete\_cds  
 d26528\_1017-1515, mrna\_for\_rna\_helicase, complete\_cds\_  
 d32202\_2017-2263, mrna\_for\_alpha\_1c\_adrenergic\_receptor\_isoform\_2, complete\_cds\_  
 d43768\_663-1197, numan\_mrna\_for\_scm-1(single\_cysteine\_motif-1), complete\_cds\_  
 all\_d49742\_2413-2984, mrna\_for\_hgf\_activator\_like\_protein, complete\_cds\_  
 d49817\_1233-1725, mrna\_for\_fructose\_6-phosphate, 2-kinase/fructose\_2,6-  
 bisphosphatase, complete\_cds  
 d49950\_495-918, liver\_mrna\_for\_interferon-  
 gamma\_inducing\_factor(igif), complete\_cds\_  
 d64158\_415-  
 668: not\_in\_gb\_record, mrna\_for\_atp\_binding\_protein\_associated\_with\_cell\_differen-  
 tiation, p  
 d82061\_357-876, b-cell\_mrna\_for\_a\_member\_of\_the\_short-  
 chain\_alcohol\_dehydrogenase\_family, partial\_cds  
 d82343\_474-960, mrna\_for\_amy, complete\_cds  
 d88270exon#2\_89-293:in\_reversesequence, 18899-  
 19103, (lambda)\_dna\_for\_immunoglobulin\_light\_chain  
 hg1804-ht1829\_at\_hg1804-ht1829\_ornithine\_aminotransferase-like  
 hg2367-ht2463\_s\_at\_hg2367-ht2463\_trithorax\_homolog\_hrx\_  
 hg2416-ht2512\_at\_hg2416-ht2512\_gal\_beta\_1,3(4)glcnac\_alpha2,3-sialyltransferase  
 hg2562-ht2658\_s\_at\_hg2562-ht2658\_a-myb\_  
 hg2689-ht2785\_at\_hg2689-ht2785\_mucin\_5b, tracheobronchial  
 hg3364-ht3541\_at\_hg3364-ht3541\_ribosomal\_protein\_l37\_  
 hg4102-ht4372\_at\_hg4102-ht4372\_n-ethylmaleimide-sensitive\_factor\_  
 hg4115-ht4385\_at\_hg4115-ht4385\_olfactory\_receptor\_or17-210\_  
 hg4333-ht4603\_at\_hg4333-ht4603\_zinc\_finger\_protein\_znfpt7  
 hg961-ht961\_at\_hg961-ht961\_guanine\_nucleotide\_exchange\_factor\_  
 j00073exon#2\_132-255: not\_in\_gb\_record, alpha-cardiac\_actin\_gene, 5'\_flank\_and

j00306cds\_40-304:in\_reversesequence, \_1168-2537, somatostatin\_i\_gene\_and\_flanks\_  
l40371mrna\_661-1075, thyroid\_receptor\_interactor\_(trip4)\_mrna, \_3'\_end\_of\_cds\_  
l42354mrna\_25-409, (clone\_48es4)\_mrna\_fragment/gb=l42354\_/ntype=rna  
l42451mrna\_947-  
1397, pyruvate\_dehydrogenase\_kinase\_isoenzyme(pdk2)\_mrna, \_complete\_cds\_  
l77559mrna\_55-403, dgs-b\_partial\_mrna/gb=l77559\_/ntype=rna\_  
m12963mrna\_871-  
985, i\_alcohol\_dehydrogenase\_(adh1)\_alpha\_subunit\_mrna, \_complete\_cds\_  
m14091mrna\_1209-1731, thyroxine-binding\_globulin\_mrna, \_complete\_cds\_  
m14123cds#2\_830-1280, \_pol\_fromendogenous\_retrovirus\_herv-  
k10/gb=m14123\_/ntype=dna\_/annot=cds, \_pol\_fr  
m14123cds#3\_13-175, \_pol\_fromendogenous\_retrovirus\_herv-  
k10/gb=m14123\_/ntype=dna\_/annot=cds, \_pol\_from  
m25629\_270-846, kallikrein\_mrna, \_complete\_cds, \_clone\_clone\_phkk25\_  
m25809\_1358-1817, endomembrane\_proton\_pump\_subunit\_mrna, \_complete\_cds\_  
m26958\_46-235, parathyroid\_hormone-  
related\_protein\_(pthrp)\_mrna, \_5'\_flank, \_clone\_pbrf52/gb=m26958\_/nt  
m29194cds\_1090-1408:in\_reversesequence, \_175-223, triglyceride\_lipase\_gene  
m29994exon#1\_2-80, alpha-i\_spectrin\_gene, \_exon/gb=m29994\_/ntype=dna\_/annot=exon\_  
m31241\_s\_at\_m31241\_m31241, not\_in\_gb\_record, complement\_receptor\_(cr1)\_gene\_  
m60721mrna\_1630-2182, homeobox\_gene, \_complete\_cds\_  
m62982\_1795-2299, arachidonate\_12-lipoxygenase\_mrna, \_complete\_cds\_  
m63603\_1052-1574, phospholamban\_mrna, \_complete\_cds\_  
m63928\_645-1161, t\_cell\_activation\_antigen\_(cd27)\_mrna, \_complete\_cds\_  
m74093\_1283-1685, cyclin\_mrna\_  
m83664\_1098-1416, mhc\_ii\_lymphocyte\_antigen\_(hla-  
dp)\_beta\_chain\_mrna, \_complete\_cds\_  
m89914\_8414-8952, neurofibromin\_(nf1)\_gene, \_complete\_cds\_  
m93283\_898-1438, pancreatic\_lipase\_related\_protein(plrp1)\_mrna, \_complete\_cds\_  
m99438\_1768-2332, transducin-like\_enhancer\_protein\_(tle3)\_mrna, \_complete\_cds\_  
s69115\_250-808, granulocyte\_colony-  
stimulating\_factor\_induced\_gene\_[human, \_cml\_patient, \_bone\_marrow\_  
s76756\_510-954, \_4r-map2=microtubule-  
associated\_protein4r\_isoform\_[human, \_brain, \_mrna\_partial, \_1012\_n  
u00944\_1121-1619, clone\_a9a2brb6\_(cac)n/(gtg)n\_repeat-containing\_mrna\_  
u04806\_247-787, flt3/flk2\_ligand\_mrna, \_complete\_cds.  
u09367\_1942-2449, zinc\_finger\_protein\_znf136  
u20230exon\_7-  
127, guanyl\_cyclase\_c\_gene, \_partial\_cds/gb=u20230\_/ntype=dna\_/annot=exon\_  
u23430exon\_172-496:in\_reversesequence, \_793-  
994, cholecystokinin\_type\_a\_receptor\_(cck-a)\_gene  
u33052\_2643-3212, lipid-activated, \_protein\_kinase\_prk2\_mrna, \_complete\_cds\_  
u34038\_880-1390, proteinase-activated\_receptor-2\_mrna, \_complete\_cds\_  
u37143\_1256-1832, cytochrome\_p450\_monooxygenase\_cyp2j2\_mrna, \_complete\_cds\_  
all\_u37219\_2132-2583, cyclophilin-like\_protein\_cyp-60\_mrna, \_complete\_cds\_  
u40223cds\_660-  
1068:in\_reversesequence, \_1548, uridine\_nucleotide\_receptor\_(unr)\_gene, \_complete\_  
cds  
u47011mrna#1\_581-791:in\_reversesequence, \_751-  
961, \_fgf8\_gene\_(fibroblast\_growth\_factorprecursor)\_extr  
u48707\_123-597, protein\_phosphatase-1\_inhibitor\_mrna, \_complete\_cds\_  
u50527\_1493-1891, brca2\_region, \_mrna\_sequence\_cg018\_  
u59286\_49-439, beta-r1\_mrna, \_partial\_cds/gb=u59286\_/ntype=rna\_  
u59321\_1625-1967, dead-box\_protein\_p72\_(p72)\_mrna, \_complete\_cds\_  
u60519\_2965-3499, apoptotic\_cysteine\_protease\_mch4\_(mch4)\_mrna, \_complete\_cds\_  
u66048mrna\_2400-2838, clone\_161455-2-3\_b\_cell\_expressed\_mrna\_from\_chromosome\_x  
u66088\_1895-2369, sodium\_iodide\_symporter\_mrna, \_complete\_cds

u71088\_1325-1586,map\_kinase\_kinase\_mek5c\_mrna,\_complete\_cds  
 u75272\_743-1283,gastriecin\_mrna,\_complete\_cds  
 u75276\_2760-3225,tfiib\_related\_factor\_hbrf\_(hbrf)\_mrna,\_complete\_cds.  
 u79115\_337-886,death\_adaptor\_molecule\_raidd\_(raidd)\_mrna,\_complete\_cds.  
 u79253\_734-1100,clone\_23893\_mrna,\_complete\_cds.  
 u90306\_13-175,iroquois-class\_homeodomain\_protein\_irx-  
 4\_mrna,\_partial\_cds/gb=u90306\_/ntype=rna  
 u96629mrna#1\_1142-  
 1658,\_2a8.2\_gene\_(unknown\_protein\_cit987sk\_2a8\_1)\_extracted\_fromchromosomebac\_c  
 lon  
 all\_x00588\_5021-5514,mrna\_for\_precursor\_of\_epidermal\_growth\_factor\_receptor  
 x02612mrna#3\_656-1184,gene\_for\_cytochrome\_p(1)-450\_  
 all\_x03663\_3391-3824,mrna\_for\_c-fms\_proto-oncogene\_  
 x17254cds\_911-1211:in\_reversesequence,\_1335-  
 1449,mrna\_for\_the\_transcription\_factor\_eryf1  
 x54673cds\_1493-1775:in\_reversesequence,\_2015-  
 2135,gat1\_mrna\_for\_gaba\_transporter  
 all\_x65873\_3040-3551,mrna\_for\_kinesin\_(heavy\_chain)  
 x65977cds\_118-268:in\_reversesequence,\_325-499,mrna\_for\_corticostatin\_hp-  
 4\_precursor\_  
 all\_x74301\_4170-4479,mrna\_for\_mhc\_ii\_transactivator  
 all\_x78416\_369-921,alpha-s1-casein\_mrna  
 all\_x80878\_4120-4349,r\_kappa\_b\_mrna  
 all\_x82895\_2890-3425,mrna\_for\_dlg2\_  
 x95190cds\_1574-1958:in\_reversesequence,\_2170,mrna\_for\_branched\_chain\_acyl-  
 coa\_oxidase\_  
 x97302mrna\_40-235,mrna\_for\_ptg-1\_protein/gb=x97302\_/ntype=rna  
 x99393cds\_292-552:in\_reversesequence,\_655-787,cmkbr5\_gene,\_non-  
 functional\_mutant  
 y11999cds\_31-358,mrna\_for\_inositol\_1,4,5-trisphosphate\_3-  
 kinase/gb=y11999\_/ntype=rna\_  
 z29090cds\_2967-3183:in\_reversesequence,\_3201-  
 3393,mrna\_for\_phosphatidylinositol\_3-kinase  
 z69923cds\_1572-1818:in\_reversesequence,\_6905-  
 7019,dna\_sequence\_from\_cosmid\_l219f9,\_huntington's\_dise  
 z84483cds\_1166-  
 1676,dna\_sequence\_from\_pac\_46h23,\_brca2\_gene\_region\_chromosome\_13q12-  
 13\_contains\_klot

Metagene 218

d89377\_1587-2148,mrna\_for\_msx-2,\_complete\_cds,mrna\_for\_msx-2,\_complete\_cds  
 l01042\_2723-  
 3209,hiv1\_tata\_element\_modulatory\_factor\_mrna\_sequence\_from\_chromosome\_3\_  
 l02932\_1331-1829,peroxisome\_proliferator\_activated\_receptor\_mrna,\_complete\_cds\_  
 l40636\_3438-  
 3822,(clone\_fbk\_iii\_16)\_protein\_tyrosine\_kinase\_(net\_ptk)\_mrna,\_complete\_cds  
 l77571mrna\_1738-2218,dgs-a\_mrna,\_3'\_end\_  
 m13207exon#2-4\_6-288:in\_reversesequence,\_2583:not\_in\_gb\_record,granulocyte-  
 macrophage\_colony-stimula  
 all\_m19159\_3664-4193,placental\_heat-stable\_alkaline\_phosphatase\_(plap-  
 1)\_gene,\_complete\_cds  
 m20681mrna#2\_3326-3842,glucose\_transporter-like\_protein-  
 iii\_(glut3),\_complete\_cds



m21934\_at\_m21934\_m21934,not\_in\_gb\_record,rearranged\_and\_truncated\_ig\_gamma\_heavy\_chain\_disease\_(riv)  
 m22005cds\_49-367,interleukingene,\_clone\_pattacil-2c/2tt,\_complete\_cds,\_clone\_pattacil-2c/2tt/gb=m220  
 m28210\_356-686,gtp-binding\_protein\_(rab3a)\_mrna,\_complete\_cds\_  
 m30894\_1015-1513,t-cell\_receptor\_ti\_rearranged\_gamma-chain\_mrna\_v-j-c\_region,\_complete\_cds\_  
 m62800mrna\_1350-1827,52-kd\_ss-a/ro\_autoantigen\_mrna,\_complete\_cds\_u28833\_1571-  
 2075,down\_syndrome\_critical\_region\_protein\_(dscr1)\_mrna,\_complete\_cds  
 u47292exon\_120-564,spasmolytic\_polypeptide\_(sp)\_gene,\_5'\_region\_and  
 u64675\_1439-1853,sperm\_membrane\_protein\_bs-63\_mrna,\_complete\_cds\_  
 u66838\_1138-1594,cyclin\_a1\_mrna,\_complete\_cds  
 u67614\_at\_u67614\_u67614,not\_in\_gb\_record,sinusoidal\_reduced\_glutathione\_transporter-associated\_prote  
 all\_x54457\_2328-2416,mrna\_for\_bile-salt-stimulated\_lipase\_(bssl)\_(ec\_3.1.1.3)  
 all\_x59656\_1286-1827,crk-like\_gene\_crkl  
 all\_x76342\_1484-2019,adh7\_mrna\_  
 all\_x78926\_1271-1812,hzf3\_mrna\_for\_zinc\_finger\_protein\_  
 x79568cds\_1038-1314:in\_reversesequence,\_1399-1627,bdp1\_mrna\_for\_protein-tyrosine-phosphatase\_  
 all\_y00787\_1314-1469,mrna\_for\_mdncf\_(monocyte-derived\_neutrophil\_chemotactic\_factor)\_  
 all\_z29074\_1968-2269,mrna\_for\_cytokeratin\_9

## Metagene 377

d49488\_640-1138,mrna\_for\_alpha-tocopherol\_transfer\_protein,\_complete\_cds\_  
 l34363cds\_3540-3847:in\_reversesequence,\_4791-4896,x-linked\_nuclear\_protein\_(xnp)\_gene,\_complete\_cds\_  
 l39064mrna\_3922-4348,interleukinreceptor\_(il9r)\_gene,\_complete\_cds  
 m20218exon\_15-249:not\_in\_gb\_record,coagulation\_factor\_xi\_gene\_  
 m26665\_267-  
 484,histatin(his2)\_mrna,\_complete\_cds,histatin(his2)\_mrna,\_complete\_cds  
 m59499mrna#1\_3549-3891,lipoprotein-associated\_coagulation\_inhibitor\_(laci)\_gene  
 m61176\_1093-1549,brain-derived\_neurotrophic\_factor\_(bdnf)\_mrna,\_complete\_cds\_  
 u02632\_2711-3047,calcium-activated\_potassium\_channel\_mrna,\_partial\_cds\_  
 u27193\_1872-2346,protein-tyrosine\_phosphatase\_mrna,\_complete\_cds\_

## Metagene 96

hg2668-ht2764\_at\_hg2668-ht2764\_bradykinin\_receptor\_  
 u58032\_1007-  
 l322,myotubularin\_related\_protein(mtmr1)\_gene,\_partial\_cds/gb=u58032\_/ntype=dna\_/annot=c  
 u89012\_2087-2639,dentin\_matrix\_acidic\_phosphoprotein(dmp1)\_mrna,\_complete\_cds

## Metagene 63

d55638\_227-659,b-cell\_pabl\_(pseudoautosomal\_boundary-like\_sequence)\_mrna,\_clone\_bc4/gb=d55638\_/ntype

d78261\_1293-  
1433,icsat\_transcription\_factor\_mrna,\_partial\_cds,\_similar\_to\_mouse\_pip/lsirf\_(  
\_irf-4)\_s  
hg1437-ht1437\_s\_at\_hg1437-ht1437\_proto-oncogene\_trk  
hg2825-ht2949\_at\_hg2825-ht2949\_ret\_transforming\_gene\_  
hg3570-ht3773\_at\_hg3570-ht3773\_protein\_phosphatase\_inhibitor\_homolog\_  
hg668-ht4793\_at\_hg668-ht4793\_t-cell\_factor\_1,\_a/b/c,\_altsplice\_1,\_a  
j04430mrna\_794-1350,tartrate-resistant\_acid\_phosphatase\_typemrna,\_complete\_cds  
108187\_551-1079,cytokine\_receptor\_(ebi3)\_mrna,\_complete\_cds  
134059\_2447-3017,cadherin-4\_mrna,\_complete\_cds  
m37984mrna\_97-  
589,slow\_twitch\_skeletal\_muscle/cardiac\_muscle\_troponin\_c\_gene,\_complete\_cds  
m57506mrna\_25-481,\_scyal\_gene\_(secreted\_protein\_i-  
309)\_extracted\_fromsecreted\_protein\_(i-309)\_gene,\_  
m74089\_1911-2271,tb1\_gene\_mrna,\_3'\_end\_  
s77094\_1075-  
1621,\_nicotinic\_acetylcholine\_receptor\_alpha\_subunit|achr\_alpha\_subunit\_[human,  
\_thymic\_c  
s80050mrna\_653-1133,\_udp-n-acetylglucosamine:\_alpha-6-d-mannoside\_beta-1,6-n-  
acetylglucosaminyltrans  
s82185\_419-905,\_brag-1=brain-related\_apoptosis\_gene/bcl-2\_homolog\_[human,\_mg-  
107\_glioma,\_mrna\_partia  
u00928\_611-1151,clone\_ce29\_4.1\_(cac)n/(gtg)n\_repeat-containing\_mrna  
u09412\_1619-2045,zinc\_finger\_protein\_znf134\_mrna,\_complete\_cds\_  
u11878\_4-169,interleukin-  
8\_receptor\_type\_b\_(il8rb)\_mrna,\_splice\_variant\_il8rb10,\_partial\_cds/gb=u118  
u12775exon\_156-342:not\_in\_gb\_record,agouti\_gene  
u13022\_1572-2124,negative\_regulator\_of\_programmed\_cell\_death\_ich-1s\_(ich-  
1)\_mrna,\_complete\_cds\_  
u15306\_3076-3466,cysteine-rich\_sequence-specific\_dna-  
binding\_protein\_nfx1\_mrna,\_complete\_cds\_  
u18259\_6077-6647,clone\_ciita-8\_mhc\_ii\_transactivator\_ciita\_mrna,\_complete\_cds  
u22178\_3-  
321,prostatic\_secretory\_protein\_57\_mrna,\_complete\_cds/gb=u22178/\_ntype=rna  
u28488\_1344-1847,putative\_g\_protein-coupled\_receptor\_(az3b)\_mrna,\_complete\_cds\_  
u34877\_511-997,biliverdin-ixalpha\_reductase\_mrna,\_complete\_cds\_  
u43959\_758-815,betaadducin\_mrna,\_alternatively\_spliced\_partial\_cds  
u77129\_2447-2975,spsl/ste20\_homolog\_khs1\_mrna,\_complete\_cds  
u79247\_1157-1559,clone\_23599\_mrna\_sequence\_  
u83115\_6327-6753,non-lens\_beta\_gamma-  
crystallin\_like\_protein\_(aim1)\_mrna,\_partial\_cds  
u85430\_3114-3279,transcription\_factor\_nfatx4\_mrna,\_complete\_cds  
x04327mrna\_1084-1564,erythrocyte\_2,3-bisphosphoglycerate\_mutase\_mrna\_ec\_2.7.5.4  
all\_x13255\_2280-2725,mrna\_for\_dopamine\_beta-hydroxylase\_type\_a\_(ec\_1.14.17.1)  
x15393mrna\_19-541,motilin\_gene\_exon(and\_joined\_cds)  
x59711cds\_626-998:in\_reversesequence,\_1244-1280,mrna\_for\_caat-  
box\_dna\_binding\_protein\_subunit\_a\_  
x67337\_2825-3365,hpbrii-4\_mrna\_  
all\_x69636\_1268-1951,mrna\_sequence\_(15q11-13)  
all\_x78933\_1420-1970,hzf10\_mrna\_for\_zinc\_finger\_protein  
x83441mrna\_2724-3102,mrna\_for\_dna\_ligase\_iv  
all\_x90568\_81371-81864,mrna\_for\_titin\_protein\_(clone\_hh1-hh54)\_  
all\_x91868\_915-1378,mrna\_for\_six1\_protein  
all\_x96754\_846-1051,gene\_encoding\_kappa\_light\_chain\_constant\_region  
x98206mrna\_55-277:in\_reversesequence,\_307,mrna\_for\_uv-  
b\_repressed\_sequence,\_hur/gb=x98206/\_ntype=rna

## Metagene 77

u12767\_4598-  
 4922,mitogen\_induced\_nuclear\_orphan\_receptor\_(minor)\_mrna,\_complete\_cds  
 u79298\_928-1312,clone\_23803\_mrna,\_partial\_cds  
 x58987mrna\_1801-2299,mrna\_for\_d-1\_dopamine\_receptor  
 all\_x97671\_31-566,mrna\_for\_erythropoietin\_receptor\_

## Metagene 380

m27281\_642-1116,vascular\_permeability\_factor\_mrna,\_complete\_cds  
 m75110\_814-1312,h,k-atpase\_beta\_subunit\_mrna,\_complete\_cds\_  
 m99487\_2039-2555,prostate-specific\_membrane\_antigen\_(psm)\_mrna,\_complete\_cds\_  
 u73704\_1248-1764,48\_kda\_fkbp-associated\_protein\_fap48\_mrna,\_complete\_cds

## Metagene 229

m27160mrna\_1441-1879,tyrosinase\_(tyr)\_mrna,\_complete\_cds\_  
 m64590\_3317-3737,glycine\_decarboxylase\_mrna,\_complete\_cds  
 u26712\_2910-3318,cb1-b\_truncated\_formlacking\_leucine\_zipper\_mrna,\_complete\_cds

## Metagene 345

d00632\_1032-  
 1470,plasma\_(extracellular)\_mrna\_for\_glutathione\_peroxidase,\_complete\_cds  
 d38145\_1418-1952,mrna\_for\_prostacyclin\_synthase,\_complete\_cds  
 s77812\_148-  
 211,\_flt=vascular\_endothelial\_growth\_factor\_receptor/vegf\_receptor/cell\_surface  
 \_tyrosine\_  
 u05861exon\_50-243:not\_in\_gb\_record,hepatic\_dihydrodiol\_dehydrogenase\_gene\_

## Metagene 327

hg4167-ht4437\_at\_hg4167-ht4437\_nuclear\_factor\_1,\_a\_type  
 hg855-ht855\_s\_at\_hg855-ht855\_dna\_excision\_repair\_protein\_ercc6\_  
 j05037\_918-1368,serine\_dehydratase\_mrna,\_complete\_cds  
 j05401\_1158-  
 1554,sarcomeric\_mitochondrial\_creatine\_kinase\_(mtck)\_gene,\_complete\_cds  
 146353mrna\_6579-7077,high-mobility\_group\_phosphoprotein\_(hmg1-c)\_gene,\_exons\_3-  
 jan  
 u10886\_4762-5068,density\_enhanced\_phosphatase-1\_mrna,\_complete\_cds\_  
 u22233\_1659-2166,methylthioadenosine\_phosphorylase\_(mtap)\_mrna,\_complete\_cds\_  
 all\_x03350\_1973-2514,mrna\_for\_alcohol\_dehydrogenase\_beta-1-subunit\_(adh1-  
 2\_allele)\_  
 z94753exon\_92-444:in\_fullsequence,\_1246-  
 1265,dna\_sequence\_from\_pac\_465g10\_on\_chromosome\_x\_contains\_m

## Metagene 187

l08835mrna#1\_3166-  
 3367,\_dm\_kinase\_gene\_(myotonic\_dystrophy\_kinase)\_extracted\_frommyotonic\_dystrop  
 hy\_  
 all\_m19311\_876-  
 1059,calmodulin\_mrna,\_complete\_cds,calmodulin\_mrna,\_complete\_cds\_  
 u53506\_1344-1836,type\_ii\_iodothyronine\_deiodinase\_mrna,\_complete\_cds.

## Metagene 490

af005775\_275-755,caspase-  
 like\_apoptosis\_regulatory\_protein(clarp)\_mrna,\_alternatively\_spliced,\_compl  
 l35269exon\_1602-2040,zinc\_finger\_protein\_35\_(znf35)\_gene  
 u32499\_848-929,d3\_dopamine\_receptor\_mrna,\_complete\_cds.  
 u78107\_667-1105,gamma\_snap\_mrna,\_complete\_cds  
 u85946\_2030-2288,brain\_secretory\_protein\_hsec10p\_(hsec10)\_mrna,\_complete\_cds\_

## Metagene 484

ab003177\_604-1096,mrna\_for\_proteasome\_subunit\_p27,\_complete\_cds  
 hg3187-ht3366\_s\_at\_hg3187-ht3366\_tyrosine\_phosphatase\_1,\_non-  
 receptor,\_altsplce\_3\_  
 hg3546-ht3744\_s\_at\_hg3546-ht3744\_pre-  
 mrna\_splicing\_factor\_sf2p33,\_altsplce\_form\_1\_  
 m19650\_1446-1700,2'\_,3'\_-cyclic\_nucleotide\_3'\_'-  
 phosphodiesterase\_mrna,\_complete\_cds  
 s62904\_2130-  
 2523,\_thiopurine\_methyltransferase\_[human,t84\_colon\_carcinoma\_cell,\_mrna,\_2742  
 \_nt]\_  
 u47007\_1818-2250,transcriptional\_repressor\_(nab1)\_nab1\_mrna,\_complete\_cds  
 u51004\_166-508,putative\_protein\_kinase\_c\_inhibitor\_(pkci-1)\_mrna,\_complete\_cds\_  
 u90304\_1272-1782,iroquois-class\_homeodomain\_protein\_irx-2a\_mrna,\_complete\_cds  
 z93784cds\_702-  
 1008:in\_reversesequence,\_58791:not\_in\_gb\_record,dna\_sequence\_from\_pac\_398c22\_on  
 \_chromo

## Metagene 480

d38500\_574-  
 958,pms6\_mrna\_(yeast\_mismatch\_repair\_gene\_pms1\_homologue),\_partial\_cds\_(c-  
 terminal\_region  
 hg1751-ht1768\_s\_at\_hg1751-ht1768\_chorionic\_somatototropin\_hormone\_cs-5  
 hg1783-ht1803\_s\_at\_hg1783-ht1803\_islet\_amyloid\_polypeptide\_  
 hg4116-ht4386\_s\_at\_hg4116-ht4386\_olfactory\_receptor\_or17-219\_  
 l14813\_856-1147,carboxyl\_ester\_lipase\_like\_protein\_(cell)\_mrna,\_complete\_cds\_  
 l76703mrna\_2687-3245,b56epsilon\_mrna,\_complete\_cds  
 m26856cds\_1126-1456:in\_reversesequence,\_3467-3600,21-  
 hydroxylase\_b\_gene,\_complete\_cds\_

all\_m60746\_531-844,histone\_h3.1\_(h1f3)\_gene,\_complete\_cds  
s52028\_582-1141,\_cystathionine\_gamma-lyase\_{clone\_hcl-  
1}\_[human,\_liver,\_mrna,\_1194\_nt]  
s68271\_891-1191,\_crem=cyclic\_amp-  
responsive\_element\_modulator\_[human,\_mrna,\_1431\_nt]  
u03886\_2214-2730,gs2\_mrna,\_complete\_cds  
u10685exon#2\_992-1142:in\_reversesequence,\_3043-3271,mage-  
10\_antigen\_(mage10)\_gene,\_complete\_cds\_  
u47050\_2888-3296,putative\_calcium\_influx\_channel\_(htrp3)\_mrna,\_complete\_cds  
u49114\_2196-2700,prohormone\_convertaseprecursor\_(pc5)\_mrna,\_partial\_cds\_  
u58522\_1608-2124,huntingtin\_interacting\_protein\_(hip2)\_mrna,\_complete\_cds  
u66036\_732-1236,sulfotransferase\_mrna,\_complete\_cds  
u74382\_1317-1900,telomeric\_repeat\_dna-binding\_protein\_(pin2)\_mrna,\_complete\_cds  
u84573\_2882-3422,lysyl\_hydroxylase\_isoform(plod2)\_mrna,\_complete\_cds\_  
u87593\_f\_at\_u87593\_u87593,\_4040\_in\_u87593\_31-  
568,endogenous\_retrovirus\_clone\_pl.8\_polymerase\_mrna,\_p  
all\_x16546\_724-1319,dna\_for\_eosinophil\_derived\_neurotoxin  
x17576cds\_802-1078:in\_reversesequence,\_1233-  
1389,melanoma\_mrna\_for\_nck\_protein,\_showing\_homology\_to\_  
all\_z22970\_4355-4674,mrna\_for\_m130\_antigen\_cytoplasmic\_variant\_2\_

Metagene 477

ab000897\_43-373,mrna\_for\_cadherin\_fib3,\_partial\_cds/gb=ab000897\_/ntype=rna  
hg3033-ht3194\_at\_hg3033-ht3194\_spliceosomal\_protein\_sap\_62\_  
hg3426-ht3610\_s\_at\_hg3426-ht3610\_zinc\_finger\_protein\_hzf-16,\_kruppel-  
like,\_altsplice\_1\_  
l24559\_1634-2078,dna\_polymerase\_alpha\_mrna,\_complete\_cds  
u07139\_2039-2459,voltage-gated\_calcium\_channel\_beta\_subunit\_mrna,\_complete\_cds\_  
u36500\_2741-3209,lymphoid-specific\_sp100\_homolog\_(lysp100-b)\_mrna,\_complete\_cds  
u46767\_288-768,monocyte\_chemoattractant\_protein-4\_precursor\_(mcp-  
4)\_mrna,\_complete\_cds\_  
all\_u60269\_13-524,endogenous\_retrovirus\_herv-  
k(hml6)\_proviral\_clone\_hml6.17\_putative\_polymerase\_and\_  
x76223exon\_2-540,mal\_gene\_exon\_4.  
x89267exon#10\_225-  
312,dna\_for\_uroporphyrinogen\_decarboxylase\_gene/gb=x89267\_/ntype=dna\_/annot=exo  
n\_  
x90978\_1187-1751,mrna\_for\_an\_acute\_myeloid\_leukaemia\_protein\_(1793bp)

Metagene 467

d38502\_850-  
1120,pms4\_mrna\_(yeast\_mismatch\_repair\_gene\_pms1\_homologue),\_partial\_cds\_(c-  
terminal\_regio  
d84145\_458-980,ws-3\_mrna,\_complete\_cds\_  
hg1828-ht1857\_at\_hg1828-ht1857\_nexin,\_glia-derived\_  
hg3513-ht3707\_at\_hg3513-ht3707\_myosin,\_heavy\_polypeptide,\_light\_meromyosin\_  
hg3954-ht4224\_s\_at\_hg3954-ht4224\_landsteiner-  
wiener\_blood\_group\_glycoprotein\_(lw)  
hg4114-ht4384\_at\_hg4114-ht4384\_olfactory\_receptor\_or17-209\_  
reverse\_j04742\_384-607:in\_j04742cds\_49-  
110,autonomous\_replicating\_sequence\_h1\_(arsh1)\_

103785\_72-582,regulatory\_myosin\_light\_chain\_(myl5)\_mrna,\_complete\_cds  
 all\_126336\_2691-3220,heat\_shock\_protein\_hspa2\_gene,\_complete\_cds\_  
 135253\_972-1047,p38\_mitogen\_activated\_protein\_(map)\_kinase\_mrna,\_complete\_cds  
 140388mrna\_195-  
 675,thyroid\_receptor\_interactor\_(trip15)\_mrna,\_5'\_end\_of\_cds/gb=140388\_/ntype=r  
 na  
 all\_m21388\_2-95,unproductively\_rearranged\_ig\_mu-chain\_mrna\_v-  
 region\_(vd),\_5'\_end,\_clone\_mu-3a1a.,unp  
 m21984\_441-951,(clone\_pwhnt16)\_skeletal\_muscle\_troponin\_t\_mrna,\_complete\_cds  
 m31523\_4155-4353,transcription\_factor\_(e2a)\_mrna,\_complete\_cds\_  
 m33653\_467-965,(clones\_ht-[125,133])\_alpha-  
 2\_type\_iv\_collagen\_(col4a2)\_mrna,\_complete\_cds  
 m62840mrna\_1755-2175,acyloxyacyl\_hydrolase\_mrna,\_complete\_cds  
 m65134mrna\_3588-4102,complement\_component\_c5\_mrna,\_3'\_end  
 m90391\_1736-2866,putative\_il-16\_protein\_precursor,\_mrna,\_complete\_cds  
 s66427\_4218-4764,\_rbp1=retinoblastoma\_binding\_protein[human,\_nalm-6\_pre-  
 b\_cell\_leukemia,\_mrna,\_4834\_  
 s70609\_1781-  
 2339,\_glycine\_transporter\_type\_1b\_[human,\_substantia\_nigra,\_mrna,\_2364\_nt]  
 s81264\_50-243,\_hs-tbx2=t-box\_gene\_{t-  
 box\_region}\_[human,\_fetal\_kidney,\_mrna\_partial,\_283\_nt]/gb=s812  
 u03486cds\_625-1045:in\_reversesequence,\_1121-1211,connexin40\_gene,\_complete\_cds  
 u06632\_2039-2579,p80-coilin\_mrna,\_complete\_cds\_  
 u16997\_1218-1764,orphan\_receptor\_ror\_gamma\_mrna,\_complete\_cds  
 u19487\_1843-2329,prostaglandin\_e2\_receptor\_mrna,\_complete\_cds  
 u21936\_2630-3038,peptide\_transporter\_(hpept1)\_mrna,\_complete\_cds\_  
 u27459\_2534-  
 2984,origin\_recognition\_complex\_protein homolog\_horc21\_mrna,\_complete\_cds  
 u43318\_1805-  
 2291,putative\_transmembrane\_receptor\_(frizzled\_5)\_mrna,\_complete\_cds\_  
 u51010exon\_17-222,nicotinamide\_n-  
 methyltransferase\_gene,\_exonand\_5'\_flanking\_region/gb=u51010\_/ntype  
 u59289\_3350-3824,h-cadherin\_mrna,\_complete\_cds\_  
 u61374\_1265-  
 1715,novel\_protein\_with\_short\_consensus\_repeats\_of\_six\_cysteines\_mrna,\_complete  
 \_cds  
 u61836mrna\_540-  
 972,putative\_cyclin\_g1\_interacting\_protein\_mrna,\_partial\_sequence\_  
 u62317mrna#7\_2016-  
 2532,\_hypothetical\_protein\_384d8gene\_extracted\_from\_chromosome\_22q13\_bac\_clone\_  
 cit  
 u66617\_2252-  
 2786,swi/snf\_complex\_60\_kda\_subunit\_(baf60a)\_mrna,\_alternatively\_spliced,\_compl  
 ete\_cds\_  
 u78027mrna#4\_1964-2372,\_l44l\_gene\_(l44-  
 like\_ribosomal\_protein)\_extracted\_frombruton\_tyrosine\_kinase\_  
 u82256\_1325-1823,arginase\_type\_ii\_mrna,\_complete\_cds\_  
 u82303\_25-313,unknown\_protein\_mrna,\_partial\_cds/gb=u82303\_/ntype=rna\_  
 u95020\_1276-1786,voltage-dependent\_calcium\_channel\_beta-  
 4\_subunit\_mrna,\_complete\_cds.  
 x04898mrna\_49-445,gene\_for\_apolipoprotein\_aII\_  
 all\_x52056\_778-1304,mrna\_for\_spi-1\_proto-oncogene  
 x59770mrna\_685-1213,il-1r2\_mrna\_for\_type\_ii\_interleukin-  
 1\_receptor,(cell\_line\_cb23)\_  
 x61177mrna\_1495-1933,hsil5r2\_gene\_for\_interleukin-5\_receptor\_type\_2  
 x79780cds\_94-622:in\_reversesequence,\_646,ypt3\_mrna  
 all\_z35085\_1960-2506,mrna\_for\_unknown\_antigen

z47055cds\_437-  
968,partial\_cdna\_sequence,\_farnesyl\_pyrophosphate\_synthetase\_like-  
4/gb=z47055\_/ntype=d

Metagene 459

d21853\_1111-1543,mrna\_for\_kiaa0111\_gene,\_complete\_cds  
d79986\_4973-5513,mrna\_for\_kiaa0164\_gene,\_complete\_cds  
d87077\_5465-5975,mrna\_for\_kiaa0240\_gene,\_partial\_cds\_  
hg3076-ht3238\_s\_at\_hg3076-  
ht3238\_heterogeneous\_nuclear\_ribonucleoprotein\_k,\_altsplice\_1  
hg3514-ht3708\_at\_hg3514-ht3708\_tropomyosin\_tm30nm,\_cytoskeletal  
hg4322-ht4592\_at\_hg4322-ht4592\_tubulin,\_beta\_  
j02621mrna\_653-1214,non-histone\_chromosomal\_protein\_hmg-14\_mrna,\_complete\_cds  
j04029\_1450-  
2007,keratintype\_i\_intermediate\_filament\_(krt10)\_mrna,\_complete\_cds\_  
j04152mrna\_1181-1648,\_mls1\_gene\_extracted\_fromgastrointestinal\_tumor-  
associated\_antigen\_ga733-1\_prot  
l37368\_1849-2359,(clone\_e5.1)\_rna-binding\_protein\_mrna,\_complete\_cds\_  
l40397mrna\_979-1267,(clone\_s3li125)\_mrna,\_3'\_end\_of\_cds\_  
l42379mrna\_2645-3155,bone-derived\_growth\_factor\_(bpgf-1)\_mrna,\_complete\_cds\_  
m16342mrna#2\_1287-  
1581,nuclear\_ribonucleoprotein\_particle\_(hnrbp)\_c\_protein\_mrna,\_complete\_cds\_  
m19311mrna\_520-  
1052,calmodulin\_mrna,\_complete\_cds,calmodulin\_mrna,\_complete\_cds\_  
m23379\_3723-4179,gtpase-activating\_protein\_ras\_p21\_(rasa)\_mrna,\_complete\_cds\_  
u00947\_1301-1347,clone\_c4e\_3.2\_(cac)n/(gtg)n\_repeat-containing\_mrna  
u06631\_3269-3779,(h326)\_mrna,\_complete\_cds\_  
u20998\_973-1417,signal\_recognition\_particle\_subunit(srp9)\_mrna,\_complete\_cds\_  
u35048\_1159-1675,tsc-22\_protein\_mrna,\_complete\_cds\_  
u35451\_1643-2027,heterochromatin\_protein\_p25\_mrna,\_complete\_cds\_  
u57877\_766-1144,integral\_membrane\_protein\_cii-  
3\_mrna,\_nuclear\_gene\_encoding\_mitochondrial\_protein,\_c  
u77948\_2714-3236,bruton\_tyrosine\_kinase-associated\_protein-  
135\_mrna,\_complete\_cds  
u79282\_1087-1651,clone\_23801\_mrna\_sequence\_  
u90549\_1452-1932,non-histone\_chromosomal\_protein\_(nhc)\_mrna,\_complete\_cds  
u90551\_1071-1623,histone\_2a-like\_protein\_(h2a/1)\_mrna,\_complete\_cds  
u95740mrna#1\_5316-  
5856,\_362g6.1\_gene\_(unknown\_protein\_cit987sk\_362g6\_1)\_extracted\_fromchromosome\_  
16p  
x01703exon#4\_929-1151,gene\_for\_alpha-tubulin\_(b\_alpha\_1)\_  
x15729cds\_1538-1820:in\_reversesequence,\_2069-2215,mrna\_for\_nuclear\_p68\_protein  
x59405exon#12\_1560-2040,\_h.sapiens,\_gene\_for\_membrane\_cofactor\_protein  
all\_x63753\_5116-5621,son-a\_mrna  
all\_x68194\_1513-2090,h-sp1\_mrna  
all\_x72841\_1378-1937,ief\_7442\_mrna\_  
all\_x74104\_650-1059,mrna\_for\_trap\_beta\_subunit\_  
all\_x75304\_9705-10252,giantin\_mrna\_  
x81003mrna\_1032-1560,hcg\_v\_mrna  
all\_x81198\_3084-3673,mrna\_(clone\_p5)\_for\_archain\_  
all\_x81625\_3058-3617,mrna\_for\_cl1\_protein  
all\_x84908\_3722-3975,mrna\_for\_phosphorylase-kinase,\_beta\_subunit\_  
all\_x86098\_2367-2704,mrna\_for\_bs69\_protein\_  
all\_x95648\_1063-1658,mrna\_for\_eif-2b\_alpha\_subunit\_

all\_z72499\_3157-3740,mrna\_for\_herpesvirus\_associated\_ubiquitin-specific\_protease\_(hausp).

Metagene 446

d17391\_2957-3497,mrna\_for\_alpha\_4(iv)\_collagen,\_c-terminal\_  
hg4582-ht4987\_at\_hg4582-ht4987\_glucocorticoid\_receptor,\_beta\_  
l04569\_8323-8890,(clone\_hht-1)\_l-type\_voltage-  
dependent\_calcium\_channel\_a1\_subunit\_(hht)\_mrna,\_compl  
m37815mrna#1\_1079-1589,\_cd28\_gene\_(glycoprotein\_cd28)\_extracted\_fromt-  
cell\_membrane\_glycoprotein\_cd2  
z49995mrna\_2014-2590,mrna\_(non-coding;\_clone\_h2a)

Metagene 435

d14874\_908-1406,mrna\_for\_adrenomedullin,\_complete\_cds  
d50857\_5954-6440,dock180\_protein\_mrna,\_complete\_cds  
hg1428-ht1428\_s\_at\_hg1428-ht1428\_globin,\_beta  
hg2815-ht2931\_s\_at\_hg2815-  
ht2931\_myosin,\_light\_chain,\_alkali,\_smooth\_muscle,\_non-muscle,\_altsplice\_2  
hg3523-ht4899\_s\_at\_hg3523-ht4899\_proto-oncogene\_c-myc,\_altsplice\_3,\_orf\_114  
l09235\_1323-1845,vacuolar\_atpase\_(isoform\_va68)\_mrna,\_complete\_cds\_  
l10838\_79-499,sr\_protein\_family,\_pre-  
mrna\_splicing\_factor\_(srp20)\_mrna,\_complete\_cds  
l42601cds\_1334-1665:in\_reversesequence,\_247-  
470,keratinisoform\_k6c\_(krt6c)\_gene\_  
m81637\_1078-1603,grancalcin\_mrna,\_complete\_cds\_  
s82297\_3-391,\_beta\_2-microglobulin\_{11bp\_deleted\_between\_nucleotides\_98-  
99}\_[human,\_colon\_cancer\_cel  
u07158\_641-1169,syntaxin\_mrna,\_complete\_cds  
u37518\_1162-1390,tnf-related\_apoptosis\_inducing\_ligand\_trail\_mrna,\_complete\_cds  
u43083\_1408-1582,g\_alpha-q\_(gaq)\_mrna,\_complete\_cds  
u84569\_647-1217,yf5\_mrna,\_complete\_cds\_  
u91327mrna\_156-654,chromosome\_12p15\_bac\_clone\_cit987sk-  
99d8\_complete\_sequence/gb=u91327\_/ntype=dna\_  
x03689cds\_17-255,mrna\_fragment\_for\_elongation\_factor\_tu\_(n-  
terminus)/gb=x03689\_/ntype=rna  
x89399\_s\_at\_x89399\_x89399,not\_in\_gb\_record,mrna\_for\_ins(1,3,4,5)p4-  
binding\_protein  
x95073\_657-1119,mrna\_for\_translin\_associated\_protein\_x\_

Metagene 404

d87009cds#5\_1325-1565:in\_fullsequence,\_35519-  
35735,\_5'\_oy11.1\_gene\_extracted\_from(lambda)\_dna\_for\_im  
m68895mrna\_858-1278,alcohol\_dehydrogenasegene,\_complete\_cds  
x54489mrna\_660-1034,gene\_for\_melanoma\_growth\_stimulatory\_activity\_(mgsa)  
all\_x68242\_408-889,mrna\_for\_hin-1

Metagene 338



d50370\_2047-2581,mrna\_for\_nucleosome\_assembly\_protein,\_complete\_cds  
 l43576\_709-1009,(clone\_est02946)\_mrna\_  
 m36118\_491-828,cytotoxin\_serine\_protease-c\_mrna,\_complete\_cds  
 s81419\_25-  
 349,\_dystrophin,\_dystrophin\_{purkinje\_promoter,\_alternatively\_spliced}\_[human,\_  
 cortical\_br  
 u04735\_1728-  
 2184,microsomal\_stress\_70\_protein\_atpase\_core\_(stch)\_mrna,\_complete\_cds  
 u45255mrna\_1576-1952,paired-box\_protein\_pax2\_(pax2)\_gene\_  
 u58331\_762-1041,placental\_delta\_sarcoglycan\_mrna,\_complete\_cds\_  
 u63139\_5305-5779,rad50\_(rad50)\_mrna,\_complete\_cds  
 x92110mrna\_714-1242,mrna\_for\_hcgviii\_protein\_  
 z47553mrna\_1761-2247,mrna\_for\_flavin-containing\_monooxygenase(fmo5)\_

Metagene 316

hg172-ht3924\_at\_hg172-ht3924\_spermidine/spermine\_n1-  
 acetyltransferase,\_altsplice\_2\_  
 s79267\_2828-3398,\_cd4\_receptor\_{exonsand\_2}\_[human,\_t-  
 lymphocyte,\_mrna,\_3429\_nt]\_  
 u10868\_2267-2765,aldehyde\_dehydrogenase\_aldh7\_mrna,\_complete\_cds\_  
 u31449\_773-1337,intestinal\_and\_liver\_tetraspan\_membrane\_protein\_(il-  
 tmp)\_mrna,\_complete\_cds  
 u57911\_1693-2203,fetal\_brain\_(239fb)\_mrna,\_from\_the\_wagr\_region,\_complete\_cds  
 u67934cds\_375-501:in\_reversesequence,\_549-  
 765,44.9\_kda\_protein\_c18b11\_homolog\_gene,\_partial\_cds  
 x58022mrna\_803-1223,mrna\_for\_corticotropin-  
 releasing\_factor\_binding\_protein\_(crf-bp)\_

Metagene 299

s75881\_234-719,\_a-myb=dna-binding\_transactivator\_{3'\_region}\_[human,\_ccrf-  
 cem\_t-leukemia\_line,\_mrna\_  
 z21707cds\_552-912:in\_reversesequence,\_954-984,pl8\_mrna

Metagene 298

d64110\_615-1161,mrna\_for\_tob\_family,\_complete\_cds  
 hg2564-ht2660\_s\_at\_hg2564-ht2660\_gamma-  
 aminobutyric\_acid\_(gaba)\_a\_receptor,\_alpha\_subunit  
 j04056\_746-1118,carbonyl\_reductase\_mrna,\_complete\_cds  
 m64174\_3012-3468,protein-tyrosine\_kinase\_(jak1)\_mrna,\_complete\_cds\_  
 u82319\_470-980,clone\_ydd19\_mrna\_sequence\_  
 x67594cds\_507-909:in\_reversesequence,\_1119-1221,mrna\_for\_msh\_receptor\_

Metagene 296

m69177\_1992-2436,monoamine\_oxidase\_b\_(maob)\_mrna,\_complete\_cds\_  
 m94151\_3127-3631,cadherin-associated\_protein-related\_(cap-r)\_mrna,\_complete\_cds\_  
 u01102exon#1-3\_4-  
 109:not\_in\_gb\_record,lung\_clara\_cellskda\_secretory\_protein\_(cc10)\_gene,\_satelli  
 te\_a  
 u49835\_832-1361,ykl-39\_precursor\_mrna,\_complete\_cds  
 u88898\_561-757,endogenous\_retroviral\_h\_protease/integrase-  
 derived\_orf1\_mrna,\_complete\_cds,\_and\_putat

Metagene 277

ac000066cds\_2985-3237:in\_reversesequence,\_48519-  
 48663,bac\_clone\_rg293f11\_from\_7q21-7q22\_  
 af000560\_1220-1697,ttf-i\_interacting\_peptidemrna,\_partial\_cds.  
 d86958\_6175-6430,mrna\_for\_kiaa0203\_gene,\_complete\_cds  
 hg3369-ht3546\_at\_hg3369-ht3546\_potassium\_channel,\_voltage-gated,\_isk-  
 related\_family,\_member\_1  
 l43575mrna\_1021-1106,(clone\_48a8)\_mrna  
 m15841\_492-945,u2\_small\_nuclear\_rna-associated\_b''\_antigen\_mrna,\_complete\_cds  
 m27878\_2656-3172,dna\_binding\_protein\_(hpf2)\_mrna,\_complete\_cds\_  
 m31516mrna\_1492-2002,decay-accelerating\_factor\_mrna,\_complete\_cds  
 m34309\_4410-4836,epidermal\_growth\_factor\_receptor\_(her3)\_mrna,\_complete\_cds  
 m99436\_1808-2246,transducin-like\_enhancer\_protein\_(tle2)\_mrna,\_complete\_cds  
 u18242\_761-  
 1265,calcium\_modulating\_cyclophilin\_ligand\_(camlg)\_mrna,\_complete\_cds\_  
 u51334\_1840-2068,putative\_rna\_binding\_protein\_(rbp56)\_mrna,\_complete\_cds\_  
 u60205\_1192-1726,methyl\_sterol\_oxidase\_(erg25)\_mrna,\_complete\_cds  
 u65928\_711-1125,jun\_activation\_domain\_binding\_protein\_mrna,\_complete\_cds\_  
 u82279\_1505-2069,immunoglobulin-like\_transcriptmrna,\_complete\_cds\_  
 u91521\_2098-2470,peroxin(hspex12)\_mrna,\_complete\_cds.  
 all\_x79353\_1624-2189,xap-4\_mrna\_for\_gdp-dissociation\_inhibitor\_  
 all\_x80754\_1279-1862,mrna\_for\_gtp-binding\_protein  
 x81851cds\_26-326,\_hsapiens\_il-4\_gene\_splice\_variant/gb=x81851/\_ntype=rna  
 all\_x83543\_7066-7427,apxl\_mrna\_  
 x90999cds\_390-726:in\_reversesequence,\_828-942,mrna\_for\_glyoxalase\_ii  
 all\_x99584\_197-630,mrna\_for\_smt3a\_protein  
 all\_y00291\_2443-2888,hap\_mrna\_encoding\_a\_dna-binding\_hormone\_receptor  
 all\_y07566\_951-1066,mrna\_for\_rit\_protein\_

Metagene 270

d45917\_634-1120,mrna\_for\_timp-3,\_partial\_cds\_(c-terminus\_region)\_  
 d83174\_1524-1896,mrna\_for\_collagen\_binding\_protein\_2,\_complete\_cds\_  
 d86479\_2250-2814,mrna\_for\_aebp1\_gene,\_complete\_cds\_  
 d87258\_1489-1999,cancellous\_bone\_osteoblast\_mrna\_for\_serin\_protease\_with\_igf-  
 binding\_motif,\_complete  
 hg2197-ht2267\_s\_at\_hg2197-ht2267\_collage,\_type\_vii,\_alpha\_1  
 hg3543-ht3739\_at\_hg3543-ht3739\_insulin-like\_growth\_factor\_  
 hg987-ht987\_at\_hg987-ht987\_mac25\_  
 j02611mrna\_208-766,apolipoprotein\_d\_mrna,\_complete\_cds\_  
 j03040\_1508-2000,sparc/osteonectin\_mrna,\_complete\_cds  
 j03278\_5029-5485,platelet-  
 derived\_growth\_factor\_(pdgf)\_receptor\_mrna,\_complete\_cds\_

132137\_1910-2309,germline\_oligomeric\_matrix\_protein\_(comp)\_mrna,\_complete\_cds  
 136033\_2929-3343,pre-  
 b\_cell\_stimulating\_factor\_homologue\_(sdf1b)\_mrna,\_complete\_cds  
 m11718\_716-1274,alpha-2\_type\_v\_collagen\_gene,\_3'\_end\_  
 m16279mrna\_757-1153,mic2\_mrna,\_complete\_cds  
 m25269\_1791-2211,tyrosine\_kinase\_(elk1)\_oncogene\_mrna,\_complete\_cds\_  
 m55593mrna#1\_2600-2936,collagenase\_type\_iv\_(clg4)\_gene\_  
 m85289\_14032-14302,heparan\_sulfate\_proteoglycan\_(hspg2)\_mrna,\_complete\_cds\_  
 m96233exon#8\_114-  
 467,glutathione\_transferase\_mu\_number(gstm4)\_gene,\_complete\_cds  
 all\_u14394\_4004-4533,tissue\_inhibitor\_of\_metalloproteinases-  
 3\_mrna,\_complete\_cds\_  
 u16306\_10722-11142,chondroitin\_sulfate\_proteoglycan\_versican\_v0\_splice-  
 variant\_precursor\_peptide\_mrn  
 u24389cds\_1495-1696:in\_reversesequence,\_207-339:not\_in\_gb\_record,lysyl\_oxidase-  
 like\_protein\_gene\_  
 u60115\_1863-2211,skeletal\_muscle\_lim-protein\_slim1\_mrna,\_complete\_cds  
 u77846mrna\_979-  
 1356,elastin\_gene,\_partial\_cds\_and\_partial\_3'\_utr,elastin\_gene,\_partial\_cds\_and  
 \_parti  
 all\_x15880\_1690-2273,mrna\_for\_collagen\_vi\_alpha-1\_c-terminal\_globular\_domain\_  
 x15882cds\_984-1230:in\_reversesequence,\_1272-1554,mrna\_for\_collagen\_vi\_alpha-  
 2\_c-terminal\_globular\_do  
 x79683cds\_4908-5361:in\_reversesequence,\_5594-5620,lamb2\_mrna\_for\_beta2\_laminin  
 x86693mrna\_2171-2675,mrna\_for\_hevin\_like\_protein\_  
 z48199exon#4\_1510-2026,syndecan-1\_gene\_(exons\_2-5)\_  
 z49269exon#1-3\_76-199:not\_in\_gb\_record,gene\_for\_chemokine\_hcc-1\_

## Metagene 265

d84110\_1113-1515,mrna\_for\_werner\_syndrome-1/type\_4,\_complete\_cds\_  
 d86982\_5824-6286,mrna\_for\_kiaa0229\_gene,\_partial\_cds\_  
 hg4518-ht4921\_at\_hg4518-ht4921\_transcription\_factor\_btf3\_homolog\_  
 x04085mrna\_1684-  
 2236,gene\_for\_catalase\_(ec\_1.11.1.6)\_5'\_flank\_and\_exonmapping\_to\_chromosome\_11,  
 \_band  
 x67098exon#8\_40-454,rts\_alpha\_mrna\_containing\_four\_open\_reading\_frames\_

## Metagene 247

d86983\_5131-5485,mrna\_for\_kiaa0230\_gene,\_partial\_cds\_  
 hg142-ht142\_at\_hg142-ht142\_modulator\_recognition\_factor\_  
 hg3995-ht4265\_at\_hg3995-ht4265\_cpg-enriched\_dna,\_clone\_s19\_  
 j04599\_1078-  
 1630,hpgi\_mrna\_encoding\_bone\_small\_proteoglycan\_i\_(biglycan),\_complete\_cds\_  
 j05243\_7216-7732,nonerythroid\_alpha-spectrin\_(sptan1)\_mrna,\_complete\_cds\_  
 106139\_3573-4083,receptor\_protein-tyrosine\_kinase\_(tek)\_mrna,\_complete\_cds\_  
 141143\_1635-  
 2085,expressed\_pseudo\_tcta\_mrna\_at\_t(1;3)\_translocation\_site,\_complete\_cds  
 m13194mrna\_586-  
 1006,excision\_repair\_protein\_(erccl1)\_mrna,\_complete\_cds,\_clone\_pcde\_  
 m25079\_163-230,sickle\_cell\_beta-globin\_mrna,\_complete\_cds  
 m57609mrna\_4490-5012,dna-binding\_protein\_(gli3)\_mrna,\_complete\_cds\_

x15306mrna\_3269-3707,nf-h\_gene,\_exon(and\_joined\_cds)\_  
 x75546cds\_626-926:in\_reversesequence,\_1204,mrna\_for\_fibromodulin  
 z83799\_15-239,mrna\_for\_axonemal\_dynein\_heavy\_chain\_(partial,\_id\_hdhc1).  
 all\_z84721\_30317-  
 34635,dna\_sequence\_from\_cosmid\_gg1\_from\_a\_contig\_from\_the\_tip\_of\_the\_short\_arm  
 of\_c

Metagene 243

m60974\_731-1304,growth\_arrest\_and\_dna-damage-  
 inducible\_protein\_(gadd45)\_mrna,\_complete\_cds\_  
 all\_x14894\_826-1385,mrna\_for\_myogenic\_factor\_myf-5\_

Metagene 242

d10704\_1969-2365,mrna\_for\_choline\_kinase\_  
 d13413mrna\_578-617,mrna\_for\_tumor-  
 associated\_120\_kda\_nuclear\_protein\_p120,\_partial\_cds(carboxyl\_term  
 d13900\_748-1234,mrna\_for\_mitochondrial\_short-chain\_enoyl-  
 coa\_hydratase,\_complete\_cds\_  
 d64108\_1595-2079,mrna\_for\_dmc1\_homologue,\_complete\_cds\_  
 hg3999-ht4269\_at\_hg3999-ht4269\_retinoic\_acid\_receptor,\_beta,\_isoform\_1\_  
 j03071cds#3\_151-604:in\_reversesequence,\_14327-28953,\_growth\_hormone\_gh-  
 1\_gene\_extracted\_fromgrowth\_h  
 l13042exon#2-3\_11-216:not\_in\_gb\_record,calbindin\_d-9k\_gene,\_5'\_end\_cds\_  
 l14778\_1665-2225,calmodulin-  
 dependent\_protein\_phosphatase\_catalytic\_subunit\_(ppp3ca)\_mrna,\_complete\_  
 l37043mrna\_742-1294,casein\_kinase\_i\_epsilon\_mrna,\_complete\_cds\_  
 l46720cds\_2231-2557:in\_reversesequence,\_2650-2828,autotaxin-t\_(atx-  
 t)\_gene,\_complete\_cds\_  
 all\_m55420\_605-897:in\_m55420cds\_109-140,ige\_chain,\_lastexons\_  
 m63904mrna\_1519-2029,g-alphaprotein\_mrna,\_complete\_cds\_  
 m65066\_1903-2323,camp-dependent\_protein\_kinase\_regulatory\_subunit\_ri-  
 beta\_mrna,\_3'\_end\_  
 m75099\_25-493,rapamycin\_and\_fk506-binding\_protein,\_complete\_cds\_  
 m87338\_1120-1660,replication\_factor\_40-kda\_subunit\_(a1)\_mrna,\_complete\_cds\_  
 s68616\_4005-4491,\_na+/h+\_exchanger\_nhe-1\_isoform\_[human,\_heart,\_mrna,\_4516\_nt]  
 u20530\_47-593,bone\_phosphoprotein\_spp-  
 24\_precursor\_mrna,\_complete\_cds/gb=u20530\_/ntype=rna\_  
 u22398\_1030-1468,cdk-inhibitor\_p57kip2\_(kip2)\_mrna,\_complete\_cds\_  
 u33839\_at\_u33839\_u33839,not\_in\_gb\_record,potassium\_channel\_mrna,\_complete\_cds/g  
 b=u33839\_/ntype=rna\_  
 u61262\_4667-5195,neogenin\_mrna,\_complete\_cds\_  
 u66619\_1165-1699,swi/snf\_complex\_60\_kda\_subunit\_(baf60c)\_mrna,\_complete\_cds\_  
 u82313\_133-439,unknown\_protein\_mrna,\_partial\_cds/gb=u82313\_/ntype=rna\_  
 x69391cds\_395-821,mrna\_for\_ribosomal\_protein\_l6  
 all\_x82693\_134-681,mrna\_for\_e48\_antigen

Metagene 241

d83735\_1551-2085,adult\_heart\_mrna\_for\_neutral\_calponin,\_complete\_cds\_

j04182\_1914-2394,lysosomal\_membrane\_glycoprotein-1\_(lamp1)\_mrna,\_complete\_cds\_  
 all\_108895\_3518-4059,mads/mef2-  
 family\_transcription\_factor\_(mef2c)\_mrna,\_complete\_cds\_  
 m19267\_1476-1600,tropomyosin\_mrna,\_complete\_cds  
 all\_m19481\_278-651:in\_m19481cds\_818-921,follistatin\_gene  
 m21574mrna\_5807-6293,platelet-  
 derived\_growth\_factor\_receptor\_alpha\_(pdgfra)\_mrna,\_complete\_cds\_  
 m74719\_1971-2475,sef2-1b\_protein\_(sef2-1b)\_mrna,\_complete\_cds  
 m95787\_494-1004,22kda\_smooth\_muscle\_protein\_(sm22)\_mrna,\_complete\_cds  
 s57132\_3108-  
 3615,\_coll16a1=type\_xvi\_collagen\_alphachain\_[human,\_placenta,\_mrna\_partial,\_3720  
 \_nt]  
 s73591\_2169-2649,\_brain-expressed\_hhcpa78\_homolog\_[human,\_hl-  
 60\_acute\_promyelocytic\_leukemia\_cells,\_  
 u26710\_3398-3878,cbl-b\_mrna,\_complete\_cds  
 u44975\_791-1301,dna-binding\_protein\_cpbbp\_(cpbbp)\_mrna,\_partial\_cds  
 u53446\_2680-3220,mitogen-responsive\_phosphoprotein\_doc-2\_mrna,\_complete\_cds  
 u82532\_231-753,gdi-dissociation\_inhibitor\_rhogdigamma\_mrna,\_complete\_cds  
 u90913\_659-1157,clone\_23665\_mrna\_sequence  
 all\_x13839\_768-1300,mrna\_for\_vascular\_smooth\_muscle\_alpha-actin  
 all\_x86809\_1916-2367,mrna\_for\_major\_astrocytic\_phosphoprotein\_pea-15\_  
 y12670mrna\_531-1011,ob-rgrp\_gene/gb=y12670\_/ntype=rna  
 all\_z24727\_1355-1569,tropomyosin\_isoform\_mrna,\_complete\_cds  
 z26248cds\_178-  
 640:in\_reversesequence,\_1512,mrna\_for\_eosinophil\_granule\_major\_basic\_protein  
 all\_z48923\_3300-3835,mrna\_for\_bmpr-ii

Metagene 240

hg491-ht491\_at\_hg491-ht491\_fc\_receptor\_iib3\_for\_igg,\_low\_affinity  
 m73720mrna\_1032-1584,mast\_cell\_carboxypeptidase\_a\_(mc-cpa)\_gene  
 m82919\_1201-1579,gamma\_amino\_butyric\_acid\_(gabaa)\_receptor\_beta-  
 3\_subunit\_mrna,\_complete\_cds\_  
 u27109\_3633-4155,prepromultimerin\_mrna,\_complete\_cds\_

Metagene 203

d50582cds\_954-1128:in\_reversesequence,\_1367-  
 1535,gene\_for\_inward\_rectifier\_k\_channel,\_complete\_cds\_  
 hg2365-ht2461\_at\_hg2365-ht2461\_glyceraldehyde-3-phosphate\_dehydrogenase  
 hg4188-ht4458\_at\_hg4188-ht4458\_n-methyl-d-  
 aspartate\_receptor\_subunit,\_splice\_variant\_hnr1n\_  
 j00146\_388-718,dihydrofolate\_reductase\_pseudogene\_(psi-hd1)  
 l23808\_1297-1717,metalloproteinase\_(hme)\_mrna,\_complete\_cds  
 l27071\_1963-2527,tyrosine\_kinase\_(txk)\_mrna,\_complete\_cds  
 l37378mrna\_3182-3680,guanylyl\_cyclase\_(retgc-2)\_mrna,\_complete\_cds  
 l40380mrna\_285-795,thyroid\_receptor\_interactor\_(trip11)\_mrna,\_3'\_end\_of\_cds\_  
 all\_l48728\_380-  
 657:not\_in\_gb\_record,\_tcrbv10s1\_gene\_extracted\_fromt\_cell\_receptor\_beta\_(tcrbv1  
 0s1)\_g  
 m18079cds\_85-343:in\_reversesequence,\_4158-  
 4278,\_human,\_intestinal\_fatty\_acid\_binding\_protein\_gene,\_c  
 m23234mrna\_3313-3865,membrane\_glycoprotein\_p\_(mdr3)\_mrna,\_complete\_cds\_

m29386mrna\_200-701, prolactin\_mrna, \_3'\_end  
 m94633exon\_1275-  
 1611, recombination\_acitivating\_protein\_(rag2)\_gene, \_last\_exon/gb=m94633/\_ntype=  
 dna\_  
 s77763\_1132-  
 1624, \_nuclear\_factor\_erythroidisoform\_f=basic\_leucine\_zipper\_protein\_{alternati  
 vely\_spli  
 all\_u07807\_3319-4740:in\_u07807cds\_13-  
 110, metallothionein\_iv\_(mtiv)\_gene, \_complete\_cds\_  
 u10687exon#10\_1056-1412, mage-4a\_antigen\_(mage4a)\_gene, \_complete\_cds\_  
 u11690\_3665-4241, faciogenital\_dysplasia\_(fgd1)\_mrna, \_complete\_cds\_  
 u13948\_3283-3787, zinc\_finger/leucine\_zipper\_protein\_(af10)\_mrna, \_complete\_cds\_  
 u19345\_2258-2756, arl\_protein\_(ar)\_mrna, \_complete\_cds\_  
 u26174\_499-991, pre-granzymemrna, \_complete\_cds\_  
 u33017\_1248-  
 1680, signaling\_lymphocytic\_activation\_molecule\_(slam)\_mrna, \_complete\_cds\_  
 u35459\_629-1109, bomapin\_mrna, \_complete\_cds/gb=u35459/\_ntype=rna  
 u52521\_753-1131, arfaptin\_1, \_putative\_target\_protein\_of\_adp-  
 ribosylation\_factor, \_mrna, \_complete\_cds\_  
 u72671\_2390-2930, telencephalin\_precursor\_mrna, \_complete\_cds\_  
 u96115\_162-594, ww\_domain-  
 containing\_protein\_wwp3\_mrna, \_partial\_cds/gb=u96115/\_ntype=rna\_  
 x12453mrna\_993-1539, mrna\_for\_retinal\_s-antigen\_(48\_kda\_protein)  
 all\_x12530\_1083-1415, mrna\_for\_b\_lymphocyte\_antigen\_cd20\_(b1, \_bp35)\_  
 x17648cds#2\_1069-1177:in\_reversesequence, \_1341-1605, mrna\_for\_granulocyte-  
 macrophage\_colony-stimulati  
 all\_x17651\_829-1412, myf-4\_mrna\_for\_myogenic\_determination\_factor\_  
 all\_x52520\_2414-2673, mrna\_for\_tyrosine\_aminotransferase\_(tat)\_(ec\_2.6.1.5)\_  
 x54131mrna\_5534-6026, htp\_beta\_mrna\_for\_protein\_tyrosine\_phosphatase\_beta  
 x57303cds\_1488-1866:in\_reversesequence, \_2022-2028, rec11\_mrna  
 x61615cds\_2830-3160:in\_reversesequence, \_3482-  
 3548, mrna\_for\_leukemia\_inhibitory\_factor\_(lif)\_receptor  
 x65550exon#15\_2051-  
 2549, mki67a\_mrna\_(long\_type)\_for\_antigen\_of\_monoclonal\_antibody\_ki-67\_  
 all\_y10032\_1065-1588, mrna\_for\_putative\_serine/threonine\_protein\_kinase\_  
 all\_z29067\_1423-1802, nek3\_mrna\_for\_protein\_kinase  
 z30425cds\_649-1009:in\_reversesequence, \_1299-  
 1311, mrna\_for\_orphan\_nuclear\_hormone\_receptor.  
 z35491mrna\_797-1253, mrna\_for\_novel\_glucocorticoid\_receptor-associated\_protein

Metagene 199

ac002086cds\_1686-1974:in\_reversesequence, \_98485, pac\_clone\_dj525n14\_from\_xq23  
 k03218cds\_1068-1587:in\_reversesequence, \_197-230, c-src-1\_proto-oncogene  
 l17418exon\_3-  
 229:not\_in\_gb\_record, \_complement\_receptorgene\_extracted\_fromcomplement\_receptor  
 \_type(al  
 l26953\_2282-2846, chromosomal\_protein\_mrna, \_complete\_cds\_  
 u96136\_4729-5233, delta-catenin\_mrna, \_complete\_cds\_

Metagene 194

l36642mrna\_3940-4474,receptor\_protein-  
 tyrosine\_kinase\_(hek11)\_mrna,\_complete\_cds  
 l78833cds#3\_363-645:in\_fullsequence,\_17171-  
 17279,\_brca1\_gene\_extracted\_frombrca1,\_rho7\_and\_vati\_gene  
 m81886\_2390-2861,glutamate\_receptor\_type(hbgr1)\_mrna,\_complete\_cds  
 all\_u17579\_1465-1982,\_growth\_hormone-  
 releasing\_hormone\_receptor\_form\_b\_gene\_extracted\_fromgrowth\_hor

Metagene 193

d78334\_496-1018,mrna\_for\_ankyrin\_motif,\_complete\_cds\_  
 u59228\_407-797,ectodermal\_dysplasia\_protein\_(eda)\_mrna,\_complete\_cds\_  
 x07384cds\_2933-3269:in\_reversesequence,\_3377-3527,mrna\_for\_gli\_protein  
 all\_x73608\_2895-3478,mrna\_for\_testican\_

Metagene 189

af000562\_43-427,uropalakin\_ii\_mrna,\_partial\_cds  
 d63134mrna\_73-439,mrna\_for\_ets-like\_30\_kda\_protein/gb=d63134\_/ntype=rna  
 all\_j00220\_1704-1849,ig\_germline\_h-chain\_g-e-a\_region\_a:\_gamma-  
 3\_5'\_flank,ig\_germline\_h-chain\_g-e-a\_  
 all\_j05253\_8895-9496,interstitial\_retinol-  
 binding\_protein\_(irbp)\_gene,\_complete\_cds  
 l37792mrna\_1565-2015,syntaxin\_1a\_mrna,\_complete\_cds  
 all\_m23533\_3030-3556,alphaadrenergic\_receptor\_gene,\_complete\_cds  
 m29610\_179-  
 451,glycophorin\_e\_mrna,\_complete\_cds,glycophorin\_e\_mrna,\_complete\_cds  
 u13706\_3-63,elav-like\_neuronal\_proteinisoform\_hel-n2\_(hel-  
 n1)\_mrna,\_partial\_cds/gb=u13706\_/ntype=rna  
 u14383\_958-1372,mucin\_(muc8)\_mrna,\_partial\_cds\_  
 u20536\_935-1428,cysteine\_protease\_mch2\_isoform\_alpha\_(mch2)\_mrna,\_complete\_cds\_  
 u33921\_578-1046,\_hsu33921cdna\_  
 u50535\_1856-2270,brca2\_region,\_mrna\_sequence\_cg006\_  
 u58970\_1284-  
 1824,putative\_outer\_mitochondrial\_membrane\_34\_kda\_translocase\_htom34\_mrna,\_comp  
 lete\_cds  
 u66406\_2835-3255,putative\_eph-related\_ptk\_receptor\_ligand\_lerk-  
 8\_(eplg8)\_mrna,\_complete\_cds  
 u90065\_615-1178,potassium\_channel\_kcno1\_mrna,\_complete\_cds\_  
 v00551mrna\_366-878,\_messenger\_rna\_forleukocyte\_(alpha)\_interferon  
 all\_x05345\_1772-1953,mrna\_for\_histidyl-trna\_synthetase\_(hrs)\_  
 x14448mrna\_1017-1299:in\_reversesequence,\_11301-11319,gla\_gene\_for\_alpha-d-  
 galactosidase\_a\_(ec\_3.2.1.  
 x86012cds\_61-319:in\_fullsequence,\_6603-  
 6795,dna\_sequence\_from\_intron\_22\_of\_the\_factor\_viii\_gene,\_xq2  
 all\_y00477\_5141-  
 5216,bone\_marrow\_serine\_protease\_gene\_(medullasin)\_(leukocyte\_neutrophil\_elasta  
 se\_ge

Metagene 173

m24736\_3222-3785,endothelial\_leukocyte\_adhesion\_molecule(elam-  
1)\_mrna,\_complete\_cds\_  
y07565cds\_307-614:in\_reversesequence,\_833-1024,mrna\_for\_rin\_protein\_

Metagene 167

hg4704-ht5146\_at\_hg4704-ht5146\_glial\_growth\_factor  
m19301mrna\_944-1448,branched-chain\_alpha-  
keto\_acid\_dehydrogenase\_(e2)\_mrna,\_complete\_cds\_  
m95610\_1971-2493,alphatype\_ix\_collagen\_(col9a2)\_mrna,\_partial\_cds\_  
u65437mrna\_7-307,homeodomain-containing\_protein\_(hanf)\_gene,\_partial\_cds

Metagene 161

ab006781\_528-1007,mrna\_for\_galectin-4,\_complete\_cds/gb=ab006781/\_ntype=rna  
af007111\_1609-2017,mdm2-like\_p53-binding\_protein\_(mdmx)\_mrna,\_complete\_cds  
d49357\_958-1438,mrna\_for\_s-adenosylmethionine\_synthetase,\_complete\_cds\_  
d86984\_5659-6139,mrna\_for\_kiaa0231\_gene,\_partial\_cds\_  
hg2261-ht2351\_s\_at\_hg2261-ht2351\_antigen,\_prostate\_specific,\_altsplce\_form\_2  
hg3527-ht3721\_f\_at\_hg3527-ht3721\_luteinizing\_hormone,\_beta\_subunit\_  
hg3994-ht4264\_at\_hg3994-ht4264\_cpg-enriched\_dna,\_clone\_s16\_  
hg4058-ht4328\_at\_hg4058-ht4328\_oncogene\_aml1-evi-1,\_fusion\_activated\_  
hg4533-ht4938\_at\_hg4533-ht4938\_kallistatin,\_protease\_inhibitor\_4\_  
j04739mrna\_1212-  
1650,bactericidal\_permeability\_increasing\_protein\_(bpi)\_mrna,\_complete\_cds\_  
l15309\_2444-2960,zinc\_finger\_protein\_(znf141)\_mrna,\_complete\_cds\_  
l17075\_1130-1607,tgf-b\_superfamily\_receptor\_type\_i\_mrna,\_complete\_cds  
l24774\_272-757,delta3,\_delta2-coa-isomerase\_mrna,\_3'\_end  
l42583cds\_1334-1665:in\_reversesequence,\_305-  
528,keratinisoform\_k6a\_(krt6a)\_gene\_  
all\_m24900\_1501-  
2054,triiodothyronine\_recptor\_(thra1,\_ear1),\_and\_ear2\_genes,\_lastexons\_each\_  
m27093\_2049-2509,nuclear-encoded\_mitochondrial\_branched\_chain\_alpha-  
keto\_acid\_dehydrogenase\_transacy  
m36067mrna\_2602-3040,dna\_ligase\_i\_mrna,\_complete\_cds\_  
m73077\_2770-3178,glucocorticoid\_receptor\_repression\_factor(grf-  
1)\_mrna,\_complete\_cds  
m94055\_5925-6285,voltage-gated\_sodium\_channel\_mrna,\_complete\_cds\_  
all\_u17894\_870-1231,alpha(1,2)fucosyltransferase\_(fut2)\_gene,\_complete\_cds\_  
u38545\_3056-3578,arf-activated\_phosphatidylcholine-  
specific\_phospholipase\_dla\_(hp1d1)\_mrna,\_complete  
u45448\_2014-2535,p2x1\_receptor\_mrna,\_complete\_cds  
u68727\_2868-3414,homeobox-containing\_protein\_mrna,\_complete\_cds  
u90550\_2991-3513,butyrophilin\_(btf2)\_mrna,\_complete\_cds  
x76029cds\_141-453:in\_reversesequence,\_636-756,mrna\_for\_neuromedin\_u\_  
all\_x99226\_4853-5412,mrna\_for\_faa\_protein

Metagene 158

m92843\_1144-1583,zinc\_finger\_transcriptional\_regulator\_mrna,\_complete\_cds  
u62015\_1475-1841,cyr61\_mrna,\_complete\_cds\_



v01512mrna#2\_1533-2061,cellular\_oncogene\_c-fos\_(complete\_sequence)  
 all\_x51345\_1604-1744,jun-b\_mrna\_for\_jun-b\_protein  
 all\_x52541\_2549-3102,mrna\_for\_early\_growth\_response\_protein(hegr1)  
 all\_x68277\_1459-1952,cl\_100\_mrna\_for\_protein\_tyrosine\_phosphatase  
 all\_x75918\_2858-3417,mrna\_for\_not

Metagene 146

x12556mrna\_3159-3483,mrna\_for\_dbl\_proto-oncogene\_  
 all\_x52011\_699-1144,myf6\_gene\_encoding\_a\_muscle\_determination\_factor\_

Metagene 141

u19180\_535-925,b\_melanoma\_antigen\_(bage)\_mrna,\_complete\_cds  
 u30828\_1078-1630,splicing\_factor\_srp55-2\_(srp55)\_mrna,\_complete\_cds  
 u51269\_3408-3900,armadillo\_repeat\_protein\_mrna,\_complete\_cds\_

Metagene 137

af005037\_574-  
 1030,secretory\_carrier\_membrane\_protein\_(scamp1)\_mrna,\_complete\_cds/gb=af005037  
 \_/ntype=  
 d87449\_5359-5785,mrna\_for\_kiaa0260\_gene,\_partial\_cds\_  
 100972\_2064-2202,cystathionine-beta-synthase\_(cbs)\_mrna  
 149218exon\_4-  
 91,retinoblastoma\_susceptibility\_protein\_(rb1)\_e413kbp\_deletion\_mutant\_(resulti  
 ng\_in\_pr  
 m88163\_3059-  
 3581,global\_transcription\_activator\_homologous\_sequence\_mrna,\_complete\_cds\_  
 u79296\_1366-1876,dihydrolipoamide\_acetyl\_transferase\_mrna,\_partial\_cds.

Metagene 129

108010exon#6\_94-211:not\_in\_gb\_record,reg\_gene\_homologue,\_complete\_cds  
 132831exon\_463-1036,g\_protein-coupled\_receptor\_(gpr3)\_gene,\_complete\_cds  
 m19888\_58-580,small\_proline\_rich\_protein\_(spri)\_mrna,\_clone\_128  
 m19989\_cds1\_at\_m19989\_m19989,not\_in\_gb\_record,platelet-  
 derived\_growth\_factor\_(pdgfa)\_a\_chain\_gene,pl  
 all\_m59216\_1586-2163:in\_m59216cds\_1091,gamma-aminobutyric\_acid-a\_(gaba-  
 a)\_receptor\_beta-1\_subunit\_  
 u58681cds\_807-1116:in\_reversesequence,\_1191-  
 1434:not\_in\_gb\_record,neurogenic\_basic-helix-loop-helix\_  
 all\_x63337\_548-1101,hb2a\_gene\_for\_high\_sulfur\_keratin  
 z29572cds\_52-322:in\_reversesequence,\_95-605,antisense\_mrna\_for\_bcma\_peptide  
 z48511exon#4\_572-1148,xg\_mrna\_(clone\_pep11)

Metagene 88

d13640\_4563-5091,mrna\_for\_kiaa0015\_gene,\_complete\_cds  
 hg2414-ht2510\_s\_at\_hg2414-ht2510\_prostaglandin\_receptor\_ep1\_subtype  
 hg3236-ht3413\_f\_at\_hg3236-ht3413\_neurofibromatosis\_tumor\_suppressor  
 hg3342-ht3519\_s\_at\_hg3342-ht3519\_id1\_  
 j03801\_911-1418,lysozyme\_mrna,\_complete\_cds\_with\_an\_alu\_repeat\_in\_the\_3'\_flank\_  
 all\_100389\_1196-1792,cytochrome\_p-450gene\_  
 m11058mrna\_2351-2879,3-hydroxy-3-  
 methylglutaryl\_coenzyme\_a\_reductase\_mrna,\_complete\_cds  
 m19045\_907-1414,lysozyme\_mrna,\_complete\_cds  
 all\_m31551\_576-1134,urokinase\_inhibitor\_(pai-2)\_gene\_  
 m31667\_f\_at\_m31667\_m31667\_4040\_in\_all\_m31667\_1679-  
 2265,cytochrome\_p450\_(cyp1a2)\_gene\_  
 u32576mrna\_19-535,apolipoprotein\_apoc-iv\_(apoc4)\_gene,\_complete\_cds\_  
 u33267\_1613-2081,glycine\_receptor\_beta\_subunit\_(glrb)\_mrna,\_complete\_cds\_  
 u50361\_16-319,calcium,\_calmodulin-  
 dependent\_protein\_kinase\_ii\_delta\_mrna,\_partial\_cds/gb=u50361\_/nty  
 u60269cds#2\_171-429,endogenous\_retrovirus\_herv-  
 k(hml6)\_proviral\_clone\_hml6.17\_putative\_polymerase\_an  
 u72507mrna\_855-1341,40871\_mrna\_partial\_sequence  
 x14008mrna\_926-1433,lysozyme\_gene\_(ec\_3.2.1.17)\_  
 all\_x51417\_1050-1651,mrna\_for\_steroid\_hormone\_receptor\_herr2\_  
 y10207mrna\_61-475,mrna\_for\_cd171\_protein/gb=y10207\_/ntype=rna

Metagene 83

d90224\_2791-3319,mrna\_for\_glycoprotein\_34\_(gp34)\_  
 hg415-ht415\_at\_hg415-ht415\_lectin\_galactoside-binding,\_soluble,\_2\_  
 k03204mrna\_582-1130,prb1\_locus\_salivary\_proline-  
 rich\_protein\_mrna,\_clone\_cp3,\_complete\_cds\_  
 m14758mrna#1\_4264-4561,p-glycoprotein\_(mdr1)\_mrna,\_complete\_cds\_  
 m36653\_1448-1663,2-oct\_factor\_mrna,\_complete\_cds\_  
 m64231mrna\_1264-1624,spermidine\_synthase\_gene,\_complete\_cds\_  
 m64358exon\_16-189,rhom-3\_gene,\_exon/gb=m64358\_/ntype=dna\_/annot=exon\_  
 all\_u67368\_952-1411,multiple\_exostosis(ext2)\_gene\_  
 all\_x16105\_1077-1226,mrna\_for\_rd\_protein,\_rna-binding  
 x58255mrna\_2472-2862,flg-2\_gene\_for\_fibroblast\_growth\_factor\_receptor  
 all\_x67235\_1087-1595,mrna\_for\_proline\_rich\_homeobox\_(prh)\_protein  
 y10209mrna\_79-331,mrna\_for\_cd301\_protein/gb=y10209\_/ntype=rna  
 all\_z70723\_1812-2239,mrna\_for\_serum\_arylalkylphosphatase

Metagene 65

d29642\_2294-2582,mrna\_for\_kiaa0053\_gene,\_complete\_cds  
 hg1155-ht4822\_at\_hg1155-ht4822\_colony-  
 stimulating\_factor\_1,\_macrophage,\_altsplice\_3  
 hg1996-ht2044\_at\_hg1996-ht2044\_guanine\_nucleotide-binding\_protein\_rap2,\_ras-  
 oncogene\_related\_  
 hg243-ht243\_s\_at\_hg243-ht243\_lowe\_oculocerebrorenal\_syndrome\_protein\_  
 hg2797-ht2905\_at\_hg2797-ht2905\_clathrin,\_light\_polypeptide\_altsplice\_1  
 hg4011-ht4804\_s\_at\_hg4011-ht4804\_dystrophin-  
 associated\_glycoprotein,\_50\_kda,\_altsplice\_2\_  
 hg4757-ht5207\_s\_at\_hg4757-ht5207\_oncogene\_mll-af4,\_fusion\_activated

j00268gene\_270-1415,insulin\_gene\_  
 l78440mrna\_2089-2509,stat4\_mrna,\_complete\_cds\_  
 m10321mrna\_5749-6321,von\_willebrand\_factor\_mrna,\_3'\_end  
 m34455\_1427-1889,interferon-gamma-inducible\_indoleamine\_2,3-  
 dioxygenase\_(ido)\_mrna,\_complete\_cds\_  
 m61827mrna\_1289-1850,leukosialin\_(cd43)\_gene,\_complete\_cds  
 m74542\_1131-1611,aldehyde\_dehydrogenase\_type\_iii\_(aldhiii)\_mrna,\_complete\_cds  
 all\_u24683\_219-474,anti-b\_cell\_autoantibody\_igm\_heavy\_chain\_variable\_v-d-  
 j\_region\_(vh4)\_gene,\_clone\_  
 u34587\_1545-2061,corticotropin-releasing\_factor\_receptormrna,\_complete\_cds  
 u48861\_1914-  
 2430,betanicotinic\_acetylcholine\_receptor\_subunit\_mrna,\_complete\_cds  
 u51096\_1240-1720,homeobox\_protein\_cdx2\_mrna,\_complete\_cds  
 all\_u58675\_25626-39844,\_orl7-  
 228\_gene\_extracted\_fromolfactory\_receptor\_gene\_cluster\_on\_chromosome\_17  
 u64315\_2269-2832,dna\_repair\_endonuclease\_subunit\_(xpf)\_mrna,\_complete\_cds  
 u81600\_368-734,paired-like\_homeodomain\_protein\_prx-2\_mrna,\_partial\_cds.  
 u82010mrna\_2432-  
 2930,\_homo\_sapiensheme\_a:\_farnesyltransferase\_(cox10)\_gene\_promoter\_region\_and  
 x58399mrna\_491-903,l2-  
 9\_transcript\_of\_unrearranged\_immunoglobulin\_v(h)5\_pseudogene.  
 x60003mrna\_543-965,delta\_creb\_mrna\_for\_camp-  
 responsive\_element\_(cre)\_binding\_protein\_  
 all\_x63359\_2216-2781,ugt2bio\_mrna\_for\_udp\_glucuronosyltransferase  
 x68985cds\_482-656,mrna\_for\_hepatic\_leukemia\_factor\_  
 x72882cds\_19-103:in\_reversesequence,\_144-186,14a6ck\_dna\_sequence  
 x74764cds\_2202-2538:in\_reversesequence,\_2903-  
 3041,mrna\_for\_receptor\_protein\_tyrosine\_kinase\_  
 x75342cds\_1407-1767:in\_reversesequence,\_2095-2239,shb\_mrna  
 all\_x84213\_1094-1357,bak\_mrna\_for\_bcl-2\_homologue  
 x89416cds\_1386-1440:in\_reversesequence,\_1533-  
 1932,mrna\_for\_protein\_phosphatase\_5\_  
 x91911cds\_321-711:in\_reversesequence,\_912-950,mrna\_for\_rtvpl-1\_protein\_  
 x97267mrna\_321-861,lpap\_gene  
 all\_x98085\_4149-4642,mrna\_for\_tenascin-r\_  
 all\_x99664\_723-1276,mrna\_for\_protein\_containing\_sh3\_domain,\_sh3gl3\_  
 all\_y00796\_4559-5109,mrna\_for\_leukocyte-associated\_molecule-  
 1\_alpha\_subunit\_(lfa-1\_alpha\_subunit)  
 y08409cds\_4-385:in\_reversesequence,\_431,spot14\_gene\_  
 y08639cds\_837-1353:in\_reversesequence,\_1953-  
 2001,mrna\_for\_transcription\_factor\_rzrbeta  
 y09216\_214-736,mrna\_for\_protein\_kinase,\_dyrk2  
 all\_z11697\_1190-1701,mrna\_for\_hb15  
 z23115cds\_197-677:in\_reversesequence,\_817-835,bcl-xl\_mrna\_  
 z67743cds\_1792-2320:in\_reversesequence,\_2350,mrna\_for\_clc-  
 7\_chloride\_channel\_protein

Metagene 57

all\_l41913\_305-  
 502,retinoblastoma\_susceptibility\_protein\_(rb1)\_gene,\_exon\_26,\_bases\_174145-  
 174668\_in  
 all\_x75958\_1683-2170,trkb\_mrna\_for\_protein-tyrosine\_kinase\_

Metagene 41

hg2441-ht2537\_s\_at\_hg2441-ht2537\_retinoblastoma\_protein,\_mutated\_  
 m16282cds\_25-133:in\_reversesequence,\_283-  
 469,fragile\_x\_locus\_m2c\_containing\_an\_unidentified\_open\_rea  
 all\_m17254\_1366-1889,erg2\_gene\_encoding\_erg2\_protein,\_complete\_cds\_  
 u84540mrna\_1083-1341,dystrobrevin\_isoform\_dtn-  
 3\_(dtn)\_gene,\_exon\_11b\_and\_complete\_cds/gb=u84540\_/nty  
 y10202mrna\_169-529,mrna\_for\_cd207\_protein/gb=y10202\_/ntype=rna\_

## Metagene 37

j04076mrna\_2171-2651,early\_growth\_responseprotein\_(egr2)\_mrna,\_complete\_cds\_  
 m31659mrna\_1130-  
 1640,gt\_mitochondrial\_solute\_carrier\_protein\_homologue\_mrna,\_complete\_cds  
 all\_x95677\_1773-2368,mrna\_for\_argbpib\_protein/gb=x95677\_/ntype=rna\_

## Metagene 29

d78014\_4608-4998,mrna\_for\_dihydropyrimidinase\_related\_protein-3,\_complete\_cds  
 hg2614-ht2710\_at\_hg2614-ht2710\_collagen,\_type\_viii,\_alpha\_1  
 m61906\_2813-3326,p13-kinase\_associated\_p85\_mrna\_sequence\_  
 u29953mrna\_1150-1468,pigment\_epithelium-derived\_factor\_gene,\_complete\_cds\_  
 u40572\_1105-1627,beta2-syntrophin\_(snt\_b2)\_mrna,\_complete\_cds  
 u79294\_831-1371,clone\_23748\_mrna,\_complete\_cds.  
 x15525mrna\_1670-  
 2084,lysosomal\_acid\_phosphatase\_gene\_(ec\_3.1.3.2)\_exon(and\_joined\_cds)\_  
 all\_x68742\_2942-3423,mrna\_for\_integrin,\_alpha\_subunit  
 x96719cds\_86-398:in\_reversesequence,\_674-710,mrna\_for\_aicl\_(activation-  
 induced\_c-type\_lectin)\_

## Metagene 25

af001294\_285-735,ipl\_(ipl)\_mrna,\_complete\_cds.  
 d16227\_589-943,mrna\_for\_bdp-  
 1\_protein\_(a\_member\_of\_the\_recoverin\_family),\_complete\_cds\_  
 d50930\_4876-5368,mrna\_for\_kiaa0140\_gene,\_complete\_cds  
 d78012\_2289-2793,mrna\_for\_dihydropyrimidinase\_related\_protein-1,\_complete\_cds  
 d79985\_3997-4393,mrna\_for\_kiaa0163\_gene,\_complete\_cds  
 d90359\_5384-5912,ccg1\_mrna\_  
 hg2566-ht4792\_r\_at\_hg2566-ht4792\_microtubule-  
 associated\_protein\_tau,\_altsplice\_3,\_exon\_8\_  
 j03930exon#11\_638-  
 1118,intestinal\_alkaline\_phosphatase\_(alpi)\_gene,\_complete\_cds\_  
 j04469exon#9\_11-  
 173:not\_in\_gb\_record,mitochondrial\_creatine\_kinase\_(ckmt)\_gene,\_complete\_cds  
 j05249\_941-1409,replication\_protein\_a\_32-kda\_subunit\_mrna,\_complete\_cds  
 l14856cds\_746-1100:in\_reversesequence,\_1324-  
 1393,somatostatin\_receptor\_gene,\_complete\_cds\_  
 l18983mrna\_3114-3588,tyrosine\_phosphatase\_(ia-2/ptp)\_mrna,\_complete\_cds\_

l27479\_797-1307,x123\_mrna,\_3'\_end  
 l47345\_2141-2609,elongin\_a\_mrna,\_complete\_cds\_  
 m36430\_321-753,transducin\_beta-1\_subunit\_mrna,\_3'\_end  
 m57732mrna\_2643-  
 3165,hepatic\_nuclear\_factor(tcf1)\_mrna,\_complete\_cds,\_clones\_hcl10,\_hcl12,\_hcl1  
 7,\_an  
 reverse\_m81780\_4000-4487:in\_m81780cds#3\_175-  
 296,\_smpd1\_gene\_(acid\_sphingomyelinase)\_extracted\_fromac  
 m88468\_1378-1906,mevalonate\_kinase\_mrna,\_complete\_cds\_  
 u01147mrna\_4659-  
 5211,guanine\_nucleotide\_regulatory\_protein\_(abr)\_mrna,\_complete\_cds  
 u09584\_1382-1835,pl6\_protein\_(pl6)\_mrna,\_complete\_cds  
 u47742\_7360-  
 7810,monocytic\_leukaemia\_zinc\_finger\_protein\_(moz)\_mrna,\_complete\_cds  
 u47928\_2047-2491,protein\_a\_alternatively\_spliced\_form(a-2)\_mrna,\_complete\_cds\_  
 u53786\_6024-6432:not\_in\_gb\_record,envoplakin\_(evpl)\_mrna,\_complete\_cds

## Metagene 7

j00207mrna#2\_661-1075,\_ifna\_gene\_(interferon\_alpha-  
 a)\_extracted\_fromleukocyte\_interferon\_(leif)\_alph  
 j05016mrna\_2252-  
 2824,(clone\_pa3)\_protein\_disulfide\_isomerase\_related\_protein\_(erp72)\_mrna,\_comp  
 lete\_  
 l41268\_f\_at\_l41268\_l41268,\_4040\_in\_l41268mrna\_1043-1571,natural\_killer-  
 associated\_transcript(nkat2)\_  
 m31776cds\_35-365,brain\_natriuretic\_protein\_(bnp)\_gene,\_complete\_cds  
 u82311\_39-112,unknown\_protein\_mrna,\_partial\_cds/gb=u82311\_/ntype=rna\_  
 all\_x06661\_1817-2340,mrna\_for\_27-kda\_calbindin\_  
 x13100cds\_3130-3466:in\_reversesequence,\_3496-  
 3592,mrna\_fragment\_for\_myosin\_heavy\_chain  
 x64994cds\_642-912:in\_reversesequence,\_1279-  
 1471,hgmp07i\_gene\_for\_olfactory\_receptor\_

## Metagene 6

hg1139-ht4910\_at\_hg1139-ht4910\_fk506-binding\_protein,\_altsplice\_2  
 m14123cds#4\_3521-3935,\_pol\_fromendogenous\_retrovirus\_herv-  
 k10/gb=m14123\_/ntype=dna\_/annot=cds,\_pol\_f  
 m27396mrna\_1389-1842,asparagine\_synthetase\_mrna,\_complete\_cds  
 m89470\_2855-3271,paired-box\_protein\_(pax2)\_mrna,\_complete\_cds  
 s73885\_1537-2082,\_ap-4=basic\_helix-loop-helix\_dna-  
 binding\_protein\_[human,\_cervical\_carcinoma,\_hela\_c  
 u35005\_764-1278,jnk1\_beta2\_protein\_kinase\_(jnk1b2)\_mrna,\_complete\_cds  
 u51333\_2437-3005,hexokinase\_iii\_(hk3)\_mrna,\_complete\_cds\_  
 u73738\_74-107,calcium/calmodulin-  
 dependent\_protein\_kinase\_ii\_delta\_e\_mrna,\_partial\_cds/gb=u73738\_/nt

## Metagene 44

hg3733-ht4003\_at\_hg3733-ht4003\_epiligrin,\_alpha\_3

m65291\_715-  
 1189,natural\_killer\_cell\_stimulatory\_factor\_(nksf)\_mrna,\_complete\_cds,\_clone\_p3  
 5  
 u15422cds#2\_17-269:in\_reversesequence,\_20347-  
 20563,\_prm2\_gene\_(protamine\_2)\_extracted\_fromprotamine(  
 u18297\_1298-1805,mst1\_(mst1)\_mrna,\_complete\_cds

Metagene 461

hg4340-ht4610\_at\_hg4340-ht4610\_soxa  
 u63332\_3-361,super\_cysteine\_rich\_protein\_mrna,\_partial\_cds.  
 u77413\_2543-2975,o-  
 linked\_glcnae\_transferase\_mrna,\_complete\_cds/gb=u77413\_/ntype=rna\_  
 x97675mrna\_3636-  
 4212,\_plakophilin\_2a\_gene\_extracted\_frommrna\_for\_plakophilin\_2a\_and\_b\_  
 all\_z80781\_583-748,h2b/j\_gene

Metagene 418

hg458-ht458\_f\_at\_hg458-ht458\_beta-1-glycoprotein\_1,\_pregnancy-specific\_  
 m22324\_2954-  
 3416,aminopeptidase\_n/cd13\_mrna\_encoding\_aminopeptidase\_n,\_complete\_cds  
 u04343\_815-1361,cd86\_antigen\_mrna,\_complete\_cds  
 u20760\_4534-4966,extracellular\_calcium-sensing\_receptor\_mrna,\_complete\_cds\_  
 u67849\_25-187,beta-galactoside\_alpha2,6-  
 sialyltransferase\_(sialt1)\_mrna,\_exon\_w/gb=u67849\_/ntype=rna  
 x59372mrna\_610-1090,hox4c\_mrna\_for\_a\_homeobox\_protein  
 x65614cds\_10-262:in\_reversesequence,\_19-391,mrna\_for\_calcium-  
 binding\_protein\_sl00p\_  
 x81892cds\_2760-2994:in\_reversesequence,\_3126-3204,mrna\_for\_he6\_tm7\_receptor\_  
 all\_x95525\_2560-3071,mrna\_for\_tafii100\_protein\_

Metagene 413

all\_u03877\_2037-2512,extracellular\_protein\_(s1-5)\_mrna,\_complete\_cds\_

Metagene 329

m27968mrna\_3289-3658,basic\_fibroblast\_growth\_factor\_(fgf)\_mrna,\_complete\_cds\_  
 all\_m31994\_117-538,cytosolic\_aldehyde\_dehydrogenase\_(aldh1)\_gene\_  
 m73780\_3266-3746,integrin\_beta-8\_subunit\_mrna,\_complete\_cds  
 u20860exon#3\_1889-2279,angiotensin\_ii\_typereceptor\_gene,\_complete\_cds\_  
 u65002\_6724-7240,zinc\_finger\_protein\_plag1\_mrna,\_complete\_cds  
 all\_x04688\_227-798,mrna\_for\_t-cell\_replacing\_factor\_(interleukin-5)

Metagene 317

j03242\_1155-1324,insulin-like\_growth\_factor\_ii\_mrna,\_complete\_cds\_  
 j05068\_984-1494,transcobalamin\_i\_mrna,\_complete\_cds  
 m32578\_1131-1191,mhc\_ii\_hla-dr\_beta-1\_mrna\_(dr2.3),\_5'\_end\_  
 all\_x79981\_3411-3946,ve-cadherin\_mrna

Metagene 271

m10901mrna\_4325-4655,glucocorticoid\_receptor\_alpha\_mrna,\_complete\_cds  
 m88338\_1465-1867,serum\_constituent\_protein\_(mse55)\_mrna,\_complete\_cds  
 u03891\_90-576,phorbolin\_i\_mrna,\_partial\_cds  
 u77643\_1462-1972,k12\_protein\_precursor\_mrna,\_complete\_cds  
 x74795cds\_1923-2181:in\_reversesequence,\_2272-2488,p1-cdc46\_mrna\_  
 all\_x78669\_1114-1643,erc-55\_mrna\_

Metagene 245

y09912mrna\_757-1315,ap-2\_beta\_gene

Metagene 185

af009301\_2752-3262,teb4\_protein\_mrna,\_complete\_cds/gb=af009301/\_ntype=rna\_  
 u73304mrna\_4973-5447,cb1\_cannabinoid\_receptor\_(cnr1)\_gene,\_complete\_cds.  
 x53414mrna\_907-1453,mrna\_for\_peroxisomal\_l-alanine:glyoxylate\_aminotransferase\_  
 x59739mrna\_5061-5473,zfx\_mrna\_for\_puttranscription\_activator,\_isoform\_2  
 x60955cds\_2-147:in\_reversesequence,\_154-168,tyrrp\_gene\_for\_tyrosinase-  
 related\_protein\_(trp-1)\_(parti

Metagene 163

d63882\_1015-1568,hs1im15\_mrna\_for\_hslim15,\_complete\_cds  
 hg2188-ht2258\_at\_hg2188-ht2258\_paired\_box\_hup1\_  
 m37825\_624-1044,fibroblast\_growth\_factor-5\_(fgf-5)\_mrna,\_complete\_cds  
 m60092mrna\_1743-2295,myoadenylate\_deaminase\_(ampd1)\_mrna,\_complete\_cds\_  
 s67798\_1420-1930,\_ph-20\_[human,\_testis,\_mrna,\_1973\_nt]  
 u49065\_1400-1922,interleukin-1\_receptor-  
 related\_protein\_mrna,\_complete\_cds/gb=u49065/\_ntype=rna  
 u82671mrna#2\_1536-1776:in\_reversesequence,\_106561-106657,\_hsp1-  
 a\_gene\_extracted\_fromcosmids\_qc14e2,\_  
 all\_u83303\_1160-2035,\_gcp-2\_gene\_(granulocyte\_chemotactic\_protein-  
 2)\_extracted\_fromline-1\_reverse\_tr  
 all\_x91148\_3331-3824,mrna\_for\_microsomal\_triglyceride\_transfer\_protein\_

Metagene 103

u59877\_295-750,low-mr\_gtp-binding\_protein\_(rab31)\_mrna,\_complete\_cds\_

x51441cds\_28-  
 65:in\_reversesequence,\_228,mrna\_for\_serum\_amyloid\_a\_(saa)\_protein\_partial,\_clone\_pas3-a  
 all\_x52075\_5011-5273,gene\_for\_sialophorin\_(cd43)  
 all\_z11559\_2897-3480,mrna\_for\_iron\_regulatory\_factor\_  
 all\_z29331\_1560-1981,(23k/3)\_mrna\_for\_ubiquitin-conjugating\_enzyme\_ubch2\_

Metagene 80

hg2479-ht2575\_at\_hg2479-ht2575\_helix-loop-helix\_protein\_sef2-1d  
 m55682cds\_1132-1467:in\_reversesequence,\_439-  
 571,carilage\_matrix\_protein\_(cmp)\_gene\_  
 s77583\_4-  
 66,\_hervk10/hummtv\_reverse\_transcriptase\_homolog\_{clone\_rt244}\_[human,\_multiple\_sclerosis,\_

Metagene 55

d13626\_1857-2373,mrna\_for\_kiaa0001\_gene,\_complete\_cds

Metagene 417

hg3299-ht3476\_at\_hg3299-ht3476\_acetyl-coenzyme\_a\_carboxylase\_  
 u79265\_1269-1623,clone\_23614\_mrna\_sequence\_  
 x12901cds\_2080-2431:in\_reversesequence,\_2551-2629,mrna\_for\_villin\_

Metagene 287

d17525mrna\_3966-4446,mrna\_for\_precursor\_of\_p100\_serine\_protease\_of\_ra-reactive\_factor,\_complete\_cds  
 d28483\_944-1466,scr3\_mrna\_for\_rna\_binding\_protein\_scr3,\_complete\_cds\_  
 d28532\_1223-1763,mrna\_for\_renal\_na+-dependent\_phosphate\_cotransporter,\_complete\_cds  
 d31628cds\_781-1132,gene\_for\_4-hydroxyphenylpyruvic\_acid\_dioxygenase\_(hpd),\_complete\_cds\_  
 hg2707-ht2803\_at\_hg2707-ht2803\_serine/threonine\_kinase\_  
 j04990cds\_371-683:in\_reversesequence,\_2929-2989,cathepsin\_g\_gene,\_complete\_cds  
 j05257\_1239-  
 1713,(clones\_mdp4,\_mdp7)\_microsomal\_dipeptidase\_(mdp)\_mrna,\_complete\_cds  
 l02321\_1089-1509,glutathione\_s-transferase\_(gstm5)\_mrna,\_complete\_cds  
 l08485\_1759-2257,gaba-benzodiazepine\_receptor\_alpha-5-subunit\_(gabra5)\_mrna,\_complete\_cds  
 m34065mrna\_1526-1952,cdc25hs\_mrna,\_complete\_cds  
 s68287\_662-  
 1124,\_chlordecone\_reductase\_{clone\_hakra}\_[human,\_liver,\_mrna,\_1167\_nt]  
 u64863\_1556-2030,hpd-1\_(hpd-1)\_mrna,\_complete\_cds

Metagene 225



d21205\_1715-2279,mrna\_for\_estrogen\_responsive\_finger\_protein,\_complete\_cds\_  
hg2271-ht2367\_s\_at\_hg2271-ht2367\_profilaggrin  
hg2981-ht3125\_s\_at\_hg2981-ht3125\_epican,\_altsplice\_1\_  
l17330\_88-586,pre-t/nk\_cell\_associated\_protein\_(6h9a)\_mrna,\_complete\_cds\_  
l76927mrna\_760-1330,galactokinase\_(galk1)\_gene,\_complete\_cds\_  
m31520mrna\_2-  
l31,ribosomal\_protein\_s24\_mrna,ribosomal\_protein\_s24\_mrna,ribosomal\_protein\_s24  
\_mrna\_  
u52111mrna#3\_2176-  
2659,xq28\_genomic\_dna\_in\_the\_region\_of\_the\_ald\_locus\_containing\_the\_genes\_for\_c  
rea  
u57317\_2551-2989,p300/cbp-associated\_factor\_(p/caf)\_mrna,\_complete\_cds\_  
u66468\_586-1126,cell\_growth\_regulator\_cgrr11\_mrna,\_complete\_cds\_

Metagene 169

d50928\_2629-3019,mrna\_for\_kiaa0138\_gene,\_complete\_cds  
hg2417-ht2513\_at\_hg2417-ht2513\_dynein,\_heavy\_chain,\_cytoplasmic  
m15958cds\_12-282:in\_reversesequence,\_6718-6778,gastrin\_gene,\_complete\_cds\_  
u68162mrna\_3059-  
3585,\_mpl\_gene\_(thrombopoietin\_receptor)\_extracted\_fromthrombopoietin\_receptor\_  
(mpl)  
all\_x60484\_683-858,h4/e\_gene\_for\_h4\_histone  
x68505\_2403-2879,mrna\_for\_myocyte-specific\_enhancer\_factor(mef2)

Metagene 132

d37781\_4150-4705,mrna\_for\_protein-tyrosine\_phosphatase\_hptpeta,\_complete\_cds\_  
j00209mrna\_366-878,leukocyte\_interferon\_(ifn-alpha)\_alpha-c\_mrna,complete\_cds\_  
m90696\_1168-1738,cathepsin\_s\_(ctss)\_mrna,\_complete\_cds\_  
u03735exon#3\_970-1517,mage-3\_antigen\_(mage-3)\_gene,\_complete\_cds\_

Metagene 105

u38276\_2969-3509,semaphorin\_iii\_family\_homolog\_mrna,\_complete\_cds  
all\_x17093\_3834-4023,hla-f\_gene\_forleukocyte\_antigen\_f  
all\_x59798\_3705-4192,prad1\_mrna\_for\_cyclin\_

Metagene 104

d78611\_1893-2331,mest\_mrna,\_complete\_cds\_  
l01406\_1010-1562,growth\_hormone-releasing\_hormone\_receptor\_mrna,\_complete\_cds\_  
m20919cds\_478-568:in\_reversesequence,\_899-  
927,dna\_with\_a\_hepatitis\_b\_virus\_surface\_antigen\_(hbsag)\_g

Metagene 24

l34357\_1655-2165,gata-4\_mrna,\_complete\_cds  
 u09860\_3095-3653,enterokinase\_mrna,\_complete\_cds\_  
 u33448cds\_773-1108:in\_reversesequence,\_1666-1883,putative\_g-protein-  
 coupled\_receptor\_(gpr16)\_gene,\_c  
 u40370\_1443-  
 1929,3',5'\_cyclic\_nucleotide\_phosphodiesterase\_(hspde1a3a)\_mrna,\_complete\_cds\_  
 all\_x02750\_1332-1729,liver\_mrna\_for\_protein\_c  
 z47727cds\_6-150:in\_reversesequence,\_28-313,mrna\_for\_rna\_polymerase\_ii\_subunit  
 z80780cds\_2-339,h2b/h\_gene.

Metagene 366

ad000092cds#7\_730-1062:in\_reversesequence,\_99587-99822,\_hypotheticalserine-  
 threonine\_protein\_kinase\_  
 d50405\_1628-2054,mrna\_for\_rpd3\_protein,\_complete\_cds\_  
 d50925\_3408-3918,mrna\_for\_kiaa0135\_gene,\_partial\_cds\_  
 d87442\_2204-2684,mrna\_for\_kiaa0253\_gene,\_partial\_cds\_  
 l04490\_954-1362,(clone\_cc6)\_nadh-  
 ubiquinone\_oxidoreductase\_subunit\_mrna,\_3'\_end\_cds\_  
 l37033\_1039-1480,fk-506\_binding\_protein\_homologue\_(fkbp38)\_mrna,\_complete\_cds\_  
 m92269cds\_6175-6626:in\_reversesequence,\_6958-7053,1-  
 type\_calcium\_channel\_hfcc\_mrna,\_complete\_cds  
 u94585\_1810-2308,requiem\_homolog\_(hsreq)\_mrna,\_complete\_cds.  
 all\_x02596\_4186-  
 4733,mrna\_for\_bcr\_(breakpoint\_cluster\_region)\_gene\_in\_philadelphia\_chromosome  
 all\_x69550\_1266-1801,mrna\_for\_rho\_gdp-dissociation\_inhibitor\_1\_  
 x80200\_1428-1866,mln62\_mrna  
 all\_x80497\_3995-4428,phkla\_mrna  
 z21488cds\_2749-3016:in\_reversesequence,\_3179-3326,contactin\_mrna  
 all\_z48054\_2544-3067,mrna\_for\_peroxisomal\_targeting\_signal(skl\_type)\_receptor\_

Metagene 121

d00749exon\_346-525,t\_cell\_surface\_antigen\_cd7\_gene\_  
 hg1877-ht1917\_s\_at\_hg1877-ht1917\_myelin\_basic\_protein,\_altsplice\_form\_4  
 hg4126-ht4396\_at\_hg4126-ht4396\_zinc\_finger\_protein\_hzf4  
 m97287\_2345-2885,mar/sar\_dna\_binding\_protein\_(satb1)\_mrna,\_complete\_cds  
 x98178cds\_567-607,mrna\_for\_mach-beta-4\_protein/gb=x98178\_/ntype=rna  
 y07755exon#2-3\_16-204,s100a2\_gene,\_exon\_1,and\_3\_  
 z30426\_at\_z30426\_z30426,not\_in\_gb\_record,gene\_for\_early\_lymphocyte\_activation\_a  
 ntigen\_cd69,\_exon\_1

Metagene 49

hg4316-ht4586\_at\_hg4316-ht4586\_transketolase-like\_protein

Metagene 382

hg4458-ht4727\_at\_hg4458-ht4727\_immunoglobulin\_heavy\_chain,\_vdjc\_regions  
 all\_100058\_470-855,(gh)\_germline\_c-myc\_proto-oncogene,\_5'\_flank  
 u16258\_1212-1776,i\_kappa\_br\_mrna,\_complete\_cds\_  
 all\_x82629\_1744-2297,mrna\_for\_mox-2  
 x97324cds\_749-1277,mrna\_for\_adipophilin/gb=x97324\_/ntype=rna\_

Metagene 365

ad001527cds#1\_317-575:in\_reversesequence,\_3640-3802,\_comment\_for\_location\_3447-  
 3655:\_blastx\_gi|10329  
 m31423cds\_322-640:in\_reversesequence,\_1200-1320,cerebellar-degeneration-  
 related\_antigen\_(cdr34)\_gene  
 u44060\_2395-2845,homeodomain\_protein\_(prox\_1)\_mrna,\_complete\_cds\_  
 u57093\_501-969,small\_gtp-binding\_protein\_rab27b\_mrna,\_complete\_cds\_

Metagene 281

d28235exon#10\_1923-2282,ptgs2\_gene\_for\_prostaglandin\_endoperoxide\_synthase-  
 2,\_complete\_cds\_  
 all\_k02545\_752-1044,\_tcrb\_gene\_extracted\_fromt-cell\_receptor\_germline\_beta-  
 chain\_j-beta-1\_gene\_clust  
 all\_x98330\_15142-15731,mrna\_for\_ryanodine\_receptor\_2\_

Metagene 180

m21188mrna\_2754-3204,insulin-degrading\_enzyme\_(ide)\_mrna,\_complete\_cds\_  
 s66896\_1272-  
 1638,\_squamous\_cell\_carcinoma\_antigen=serine\_protease\_inhibitor\_[human,\_mrna,\_1  
 711\_nt]  
 u06452\_923-1475,melanoma\_antigen\_recognized\_by\_t-cells\_(mart-1)\_mrna\_  
 u13616\_14235-14709,ankyrin\_g\_(ank-3)\_mrna,\_complete\_cds\_  
 all\_x70340\_3545-4062,mrna\_for\_transforming\_growth\_factor\_alpha\_

Metagene 155

m26683\_416-510,interferon\_gamma\_treatment\_inducible\_mrna\_  
 m60314\_1582-2044,transforming\_growth\_factor-beta\_(tgf-beta)\_mrna,\_complete\_cds\_  
 u02310\_2946-3372,fork\_head\_domain\_protein\_(fkhr)\_mrna,\_complete\_cds\_  
 u57796\_3322-3784,zinc\_finger\_protein\_(ld5-1)\_mrna,\_complete\_cds\_  
 all\_u60116\_905-966:not\_in\_gb\_record,skeletal\_muscle\_lim-  
 protein\_slim2\_mrna,\_partial\_cds\_

Metagene 79

u00802\_1922-2463,drebrin\_e2\_mrna\_(dbn1),\_complete\_cds\_  
 u77594\_245-599,tazarotene-induced\_gene(tig2)\_mrna,\_complete\_cds\_

u86136\_8094-8472,telomerase-associated\_protein\_tp-1\_mrna,\_complete\_cds\_  
x82494mrna\_3527-3965,mrna\_for\_fibulin-2

Metagene 186

m11726exon#1\_49-163:in\_reversesequence,\_1559-  
2534:not\_in\_gb\_record,pancreatic\_polypeptide\_gene,\_comp  
u15590\_306-840,heat\_shock\_protein\_27\_(hsp27)\_mrna,\_complete\_cds

Metagene 166

af001359\_2-  
27,dna\_mismatch\_repair\_protein\_(hmlh1)\_mrna,\_alternatively\_spliced,\_partial\_cds  
/gb=af0013  
hg627-ht5097\_s\_at\_hg627-ht5097\_rhesus\_(rh)\_blood\_group\_system\_ce-  
antigen,\_altsplice\_2,\_rhvi  
hg627-ht5098\_s\_at\_hg627-ht5098\_rhesus\_(rh)\_blood\_group\_system\_ce-  
antigen1,\_altsplice\_3,\_rhviii  
105144\_2488-2598,(clone\_lamda-hpec-  
3)\_phosphoenolpyruvate\_carboxykinase\_(pck1)\_mrna,\_complete\_cds\_  
all\_105187\_2284-2339,small\_proline-rich\_protein(sprrla)\_gene,\_complete\_cds\_  
118877exon#2\_980-1530,mage-12\_protein\_gene,\_complete\_cds\_  
120469\_499-996,truncated\_dopamine\_d3\_receptor\_mrna,\_complete\_cds.  
m23323mrna\_779-1309,membrane\_protein\_(cd3-epsilon)\_gene  
s72503\_1692-  
1870,\_hkr1=inward\_rectifier\_potassium\_channel\_[human,\_hippocampus,\_mrna,\_1913\_n  
t]  
u12707\_1280-1744,wiskott-aldrich\_syndrome\_protein\_(wasp)\_mrna,\_complete\_cds  
u15641\_760-1283,transcription\_factor\_e2f-4\_mrna,\_complete\_cds  
u20979\_2612-3068,chromatin\_assembly\_factor-i\_p150\_subunit\_mrna,\_complete\_cds\_  
u73167cds#2\_79-  
834,\_h\_luca14.2a\_gene\_extracted\_fromcosmid\_luca14,\_h\_luca14.2a\_gene\_extracted\_f  
romcos  
x87344mrna#26\_769-945,dma,\_dmb,\_hla-  
z1,\_ipp2,\_lmp2,\_tap1,\_lmp7,\_tap2,\_dob,\_dqb2\_and\_ring8,\_9,andgene  
x97064cds\_1988-2210:in\_reversesequence,\_2435-  
2678,mrna\_for\_sec23a\_isoform,\_2748bp  
z30644cds\_1860-1918:in\_reversesequence,\_2130-  
2138,mrna\_for\_chloride\_channel\_(putative)\_2163bp\_

Metagene 34

hg3992-ht4262\_at\_hg3992-ht4262\_cpg-enriched\_dna,\_clone\_e35\_  
j02843cds\_1103-1451:in\_reversesequence,\_14089-  
14119,cytochrome\_p450iie1\_(ethanol-inducible)\_gene,\_co  
m54927mrna\_2349-2907,myelin\_proteolipid\_protein\_mrna,\_complete\_cds\_  
u38480\_1008-1521,retinoid\_x\_receptor-gamma\_mrna,\_complete\_cds  
x05608exon#4\_172-406:not\_in\_gb\_record,gene\_for\_neurofilament\_subunit\_nf-1\_

Metagene 22

af001787\_990-1150,uncoupling\_proteinmrna,\_complete\_cds/gb=af001787\_/ntype=rna  
s81957mrna#1\_40-112,\_bmp-5=bone\_morphogenic\_protein-  
5\_{promoter}\_[human,\_genomic,\_1116\_nt]/gb=s81957  
all\_x55777\_1833-  
2326,\_putorf\_gene\_extracted\_frommahlavu\_hepatocellular\_carcinoma\_hhc(m)\_dna\_

Metagene 323

l49229cds\_2-  
87,retinoblastoma\_susceptibility\_protein\_(rb1)\_gene,\_with\_abp\_deletion\_in\_exon\_  
22\_(l1191  
y09305cds\_267-675:in\_reversesequence,\_711-  
771,mrna\_for\_protein\_kinase,\_dyrk4,\_partial\_  
y10517mrna\_252-606,mrna\_for\_cd108\_protein/gb=y10517\_/ntype=rna\_

Metagene 266

u18467\_1436-1946,pregnancy-specific\_beta\_1-  
glycoprotein(psg7)\_mrna,\_complete\_cds  
u65918\_1248-1820,putative\_rna\_binding\_protein\_(dazh)\_mrna,\_complete\_cds  
z78290\_44-109,mrna\_(clone\_ld7).

Metagene 94

u66581cds\_963-1275:in\_reversesequence,\_1547-1745,putative\_g\_protein-  
coupled\_receptor\_(gpr22)\_gene,\_c  
u73799\_34-265,dynactin\_mrna,\_partial\_cds/gb=u73799\_/ntype=rna  
u88892\_31-241,tenascin-c\_mrna,\_splice\_variant\_tncfn-  
ad2,\_partial\_cds/gb=u88892\_/ntype=rna  
all\_x73501\_11784-13955,gene\_for\_cytokeratin\_20\_  
x97249cds\_1720-2230,mrna\_for\_leucine-rich\_primary\_response\_protein\_1\_  
all\_x97261\_25-  
333,mrna\_for\_metallothionein\_isoform\_1r,mrna\_for\_metallothionein\_isoform\_1r\_  
all\_z32684\_4621-5042,xk\_mrna\_for\_membrane\_transport\_protein

Metagene 285

d37931\_395-911,mrna\_for\_rnase\_4,\_complete\_cds  
hg3731-ht4001\_at\_hg3731-ht4001\_immunoglobulin\_heavy\_chain,\_vdjrc\_regions\_  
hg4668-ht5083\_s\_at\_hg4668-ht5083\_transcription\_factor\_mef2,\_altsplise\_2  
l23333\_725-1305,corticotropin\_releasing\_factor\_receptor\_mrna,\_complete\_cds.  
l38503\_531-993,glutathione\_s-transferase\_theta(gstt2)\_mrna,\_complete\_cds\_  
m13981\_1253-1300,inhibin\_a-subunit\_mrna,\_complete\_cds  
all\_m35093\_2155-  
2456,secreted\_epithelial\_tumor\_mucin\_antigen\_(muc1)\_gene,\_complete\_cds\_  
u15932\_1928-2294,dual-specificity\_protein\_phosphatase\_mrna,\_complete\_cds\_  
u79249\_873-1359,clone\_23839\_mrna\_sequence

x65727cds#1\_199-591,\_gstalpha\_locus\_gene\_(glutathione\_s-  
transferase)\_extracted\_fromgstalpha\_gene\_for  
all\_x77166\_798-1183,gene\_for\_kunitz-type\_protease\_inhibitor,\_hkib9\_  
x95097mrna\_924-1503,mrna\_for\_vip2\_receptor  
all\_z46261\_490-899,dna\_for\_histone\_h3a\_

Metagene 367

hg4236-ht4506\_f\_at\_hg4236-ht4506\_zinc\_finger\_protein\_znf138  
l32606\_1862-2196,homeobox-like\_mrna  
m61826exon\_72-568,alpha-spectrin\_gene  
u09279\_1375-1777,type\_xix\_collagen\_(coll9a1)\_mrna,\_partial\_cds\_  
u38964cds\_1096-1146:in\_reversesequence,\_1291-  
1359,pms2\_related\_(hpmsr2)\_gene,\_complete\_cds\_  
u79301\_999-1509,clone\_23842\_mrna\_sequence  
x00540\_at\_x00540\_x00540,not\_in\_gb\_record,gene\_encoding\_prolactin,\_exonand\_joine  
d\_cds\_  
all\_x15088\_1146-1276,gnat1\_mrna\_for\_transducin\_alpha-chain\_

Metagene 269

hg3985-ht4255\_at\_hg3985-ht4255\_cpg-enriched\_dna,\_clone\_e04\_  
m16967\_6338-6806,coagulation\_factor\_v\_mrna,\_complete\_cds\_  
m59941\_2557-2965,gm-csf\_receptor\_beta\_chain\_mrna,\_complete\_cds\_  
u00672\_3067-3577,interleukin-10\_receptor\_mrna,\_complete\_cds\_  
u79526\_1787-2327,orphan\_g-  
protein\_coupled\_receptor\_dez\_isoform\_a\_mrna,\_complete\_cds\_  
reverse\_z49208\_20545-  
20696,dna\_from\_cosmid\_l161a8,\_huntington\_disease\_region,\_chromosome\_4p16.3

Metagene 30

j04132\_919-1417,t\_cell\_receptor\_zeta-chain\_mrna,\_complete\_cds  
m76559\_3065-3521,neuronal\_dhp-sensitive,\_voltage-  
dependent,\_calcium\_channel\_alpha-2b\_subunit\_mrna,\_c  
m81882mrna\_1835-2261,glutamate\_decarboxylase\_(gad65)\_mrna,\_complete\_cds  
s68874\_113-469,\_ep3\_prostanoid\_receptor\_ep3-  
i\_{3'\_region,\_alternatively\_spliced}\_[human,\_mrna\_partia  
u00921exon#3\_273-313:not\_in\_gb\_record,lst-1\_gene,\_complete\_cds\_  
u01828\_5837-5942,microtubule-associated\_protein(map2)\_mrna,\_complete\_cds  
u20759\_3683-3758,parathyroid\_cell\_calcium-sensing\_receptor\_mrna,\_complete\_cds  
u29943\_1609-2065,elav-like\_neuronal\_protein-2\_hel-n2\_mrna,\_complete\_cds  
u31628\_1015-1507,interleukin-  
15\_receptor\_alpha\_chain\_precursor\_(il15ra)\_mrna,\_complete\_cds\_  
x02883exon#4\_568-736,gene\_for\_t-  
cell\_receptor\_alpha\_chain\_c\_region/gb=x02883\_/ntype=dna\_/annot=exon  
all\_x70811\_2067-2566,mrna\_for\_betaadrenergic\_receptor\_  
all\_x81832\_1592-2163,mrna\_for\_glucose-  
dependant\_insulinotropic\_polypeptide\_receptor\_gene\_  
x86570\_1208-1532,mrna\_for\_acidic\_hair\_keratin\_1  
y07683\_951-1413,mrna\_for\_p2x3\_purinoceptor/gb=y07683\_/ntype=rna

Metagene 115

all\_m16441\_2260-  
2855,\_lymphotoxin\_gene\_extracted\_fromtumor\_necrosis\_factor\_and\_lymphotoxin\_gene  
s,\_co

Metagene 23

all\_x77748\_2815-3296,mrna\_for\_metabotropic\_glutamate\_receptor\_type\_3\_  
x84003cds\_140-305:in\_reversesequence,\_373-  
379,tafiil18\_mrna\_for\_transcription\_factor\_tfiid\_  
y10510mrna\_13-268,mrna\_for\_cd67s\_protein/gb=y10510\_/ntype=rna

Metagene 405

ab000381exon#2-4\_45-395:not\_in\_gb\_record,dna\_for\_gpi-anchored\_molecule-  
like\_protein,\_complete\_cds\_  
all\_d16154\_2725-2751:not\_in\_gb\_record,gene\_for\_cytochrome\_p-450c11,\_exon\_3-  
9/gb=d16154\_/ntype=dna\_/a  
j02982\_23-439,glycophorin\_b\_mrna,\_complete\_cds\_  
l10373\_1311-1713,(clone\_ccg-b7)\_mrna\_sequence  
l21893\_1039-1537,na/taurocholate\_cotransporting\_polypeptide\_mrna,\_complete\_cds\_  
m13928mrna\_542-1020,delta-aminolevulinate\_dehydratase\_mrna,\_complete\_cds.  
all\_m29037\_3259-3548,\_humanbeta-  
hydroxysteroid\_dehydrogenase\_(17bhsdi)\_gene,\_exons\_1-5,\_complete\_cds  
s78825\_523-667,\_idl\_(idl-b)=transcription\_regulator\_helix-loop-  
helix\_protein\_{alternatively\_spliced}  
u12424\_2016-2564,mitochondrial\_glycerol-3-  
phosphate\_dehydrogenase\_mrna,\_complete\_cds\_  
u61276\_4243-4777,transmembrane\_protein\_jagged(hj1)\_mrna,\_complete\_cds\_  
all\_u83598\_780-  
815,death\_domain\_receptorsoluble\_form\_(ddr3)\_mrna,\_partial\_cds,death\_domain\_rec  
eptors  
v01510mrna\_506-  
1022,\_pomc\_gene\_(proopiomelanocortin)\_extracted\_fromgene\_coding\_for\_acth\_and\_be  
ta-lph  
x92493mrna\_2160-2672,mrna\_for\_stm-7\_protein  
y10511mrna\_16-343,mrna\_for\_cd176\_protein/gb=y10511\_/ntype=rna

Metagene 4

ac002477cds\_444-988,pac\_clone\_dj327a19\_from\_xq25-  
q26,\_complete\_sequence/gb=ac002477\_/ntype=dna\_/anno  
hg4243-ht4513\_at\_hg4243-ht4513\_zinc\_finger\_protein\_znf155  
j00129mrna#1\_1282-1552:not\_in\_gb\_record,fibrinogen\_beta-  
chain\_mrna,\_partial\_cds\_  
all\_m58026\_831-1240,nb-1\_mrna,\_complete\_cds  
u30255\_977-1493,phosphogluconate\_dehydrogenase\_(hpgdh)\_gene,\_complete\_cds

u37022mrna\_860-1322,cyclin-dependent\_kinase(cdk4)\_gene,\_complete\_cds\_  
u67191\_3391-3967,multiple\_exostosis-like\_protein\_(extl1)\_mrna,\_complete\_cds\_  
u67369\_2300-2720,growth\_factor\_independence-1\_(gfi-1)\_mrna,\_complete\_cds\_  
u85245\_3310-3718,phosphatidylinositol-4-phosphate\_5-  
kinase\_type\_ii\_beta\_mrna,\_complete\_cds.  
u97018\_3439-3853,echinoderm\_microtubule-  
associated\_protein\_homolog\_huemap\_mrna,\_complete\_cds  
xl3461cds\_88-422:in\_reversesequence,\_1502-1737,intronless\_calmodulin-  
like\_gene\_(clp\_gene)\_for\_calmod  
all\_x72632\_1746-2326,mrna\_encoding\_rev-erbaalpha\_(internal\_fragment).  
z48314cds\_2683-3086:in\_reversesequence,\_3110-3249,mrna\_for\_apomucin\_

Metagene 410

d17547\_2106-2262,mrna\_for\_dopachrome\_tautomerase\_(tyrosinase-related\_protein-  
2),\_complete\_cds  
k02054mrna\_238-676,gastrin-releasing\_peptide\_mrna,\_complete\_cds  
l33404\_464-890,stratum\_corneum\_chymotryptic\_enzyme\_mrna,\_complete\_cds  
m64108\_2031-2571,udulinmrna,\_3'\_end\_  
s83198\_412-916,\_bplp=basic\_proline-  
rich\_protein\_[human,\_lacrima\_gland,\_mrna,\_947\_nt]  
u60206\_1537-2003,stress\_responsive\_serine/threonine\_protein\_kinase\_krs-  
1\_mrna,\_complete\_cds  
u73960\_566-1022,adp-ribosylation\_factor-like\_proteinmrna,\_complete\_cds

Metagene 398

hg2507-ht2603\_at\_hg2507-ht2603\_potassium\_channel,\_voltage-gated\_kcnc1  
j03258mrna\_4003-4561,vitamin\_d\_receptor\_mrna,\_complete\_cds\_  
k02268mrna\_3155-3677,enkephalin\_b\_(enkb)\_gene,\_5'\_flank\_and  
l05606\_1219-1741,myosin\_binding\_protein\_h\_mrna,\_complete\_cds\_  
l12392\_9795-10257,huntington\_disease\_(hd)\_mrna,\_complete\_cds\_  
l15533mrna\_236-764,pancreatitis-associated\_protein\_(pap)\_gene,\_complete\_cds\_  
l76380mrna\_2459-2969,(clone\_hsnme29)\_cgrp\_typerceptor\_mrna,\_complete\_cds\_  
all\_m16424\_135-664,beta-hexosaminidase\_alpha\_chain\_(hexa)\_gene\_  
s78296\_2596-3076,\_neurofilament-66\_[human,\_fetal\_brain,\_mrna,\_3197\_nt]  
u57092\_317-779,small\_gtp-binding\_protein\_rab30\_  
u76369\_13-325,cationic\_amino\_acid\_transporter-  
2b\_(atrc2)\_mrna,\_partial\_cds/gb=u76369\_/ntype=rna  
x52425mrna\_3032-3536,il-4-r\_mrna\_for\_the\_interleukinreceptor

Metagene 309

d88146\_1156-1408,mrna\_for\_udp-galactose\_transporter\_2,\_complete\_cds  
hg2175-ht2245\_s\_at\_hg2175-ht2245\_myosin,\_heavy\_polypeptide\_10,\_non-muscle  
hg3991-ht4261\_at\_hg3991-ht4261\_cpg-enriched\_dna,\_clone\_e18\_  
all\_m19989\_804-1279,platelet-  
derived\_growth\_factor\_(pdgfa)\_a\_chain\_gene,platelet-derived\_growth\_fact  
u30313\_372-  
756,diadenosine\_tetraphosphatase\_mrna,\_complete\_cds/gb=u30313\_/ntype=rna  
u66077\_1401-1822,daz\_mrna,\_3'\_utr



u79272\_699-1179,clone\_23720\_mrna\_sequence  
 x98337cds\_643-971:in\_reversesequence,\_1061-1256,mrna\_for\_complement\_factor\_h-  
 related\_protein\_4

Metagene 214

d26135\_3247-3619,mrna\_for\_diacylglycerol\_kinase\_gamma,\_complete\_cds  
 hg3105-ht3281\_s\_at\_hg3105-ht3281\_atpase,\_cu2+\_transporting\_  
 s78774\_411-717,\_na+/ca2+\_exchanger\_[human,\_neuroblastoma\_x\_glioma\_hybrid\_ng108-  
 15\_cells,\_mrna\_partia  
 x98225cds\_31-331,mrna\_for\_gastrin-binding\_protein/gb=x98225\_/ntype=rna\_

Metagene 38

d21267mrna\_1481-1979,mrna\_for\_highly\_expressed\_protein\_  
 d83781\_4231-4729,mrna\_for\_kiaa0197\_gene,\_partial\_cds\_  
 hg3930-ht4200\_at\_hg3930-ht4200\_stearoyl-coenzyme\_a\_desaturase\_  
 l42176\_844-1384,(clone\_35.3)\_dral\_mrna,\_complete\_cds  
 l49054\_587-1067,t(3;5)(q25.1;p34)\_fusion\_gene\_npm-mlf1\_mrna,\_complete\_cds.  
 m95167mrna\_3333-3897,dopamine\_transporter\_(slc6a3)\_mrna,\_complete\_cds\_  
 u32376\_2548-3028,channel\_associated\_protein\_of\_synapse\_(chapsyn-  
 110)\_mrna,\_complete\_cds  
 x78712cds\_1319-1637:in\_reversesequence,\_1691-  
 1823,mrna\_for\_glycerol\_kinase\_testis\_specific\_2  
 x82209\_7019-7511,mn1\_mrna  
 y10505mrna\_94-658,mrna\_for\_cd104\_protein/gb=y10505\_/ntype=rna

Metagene 456

u30246\_3599-4019,bumetanide-sensitive\_na-k-  
 cl\_cotransporter\_(nkcc1)\_mrna,\_complete\_cds\_

Metagene 153

hg4245-ht4515\_at\_hg4245-ht4515\_forkhead\_family\_afx1  
 m84349mrna\_1366-1852,transmembrane\_protein\_(cd59)\_gene\_

Metagene 422

d14678\_1244-1748,mrna\_for\_kinesin-related\_protein,\_partial\_cds\_  
 d31833\_1212-1768,mrna\_for\_vasopressin\_v1b\_receptor,\_complete\_cds\_  
 d86043\_1741-1829,mrna\_for\_shps-1,\_complete\_cds\_  
 l03427\_4325-4844,zinc\_finger\_protein\_basonuclin\_mrna,\_complete\_cds\_  
 l15344\_1360-1768,high\_molecular\_weight\_b\_cell\_growth\_factor\_mrna\_sequence  
 m85165\_1311-1809,srf\_accessory\_protein\_1a\_(sap-1)\_mrna,\_complete\_cds  
 m95936\_1148-1466,protein-serine/threonine\_(akt2)\_mrna,\_complete\_cds

s78271\_4580-5111, \_sb1.8/dxs423e=mitosis-specific\_chromosome\_segregation\_protein\_smcl\_homolog\_[human,  
u03905\_1438-1858, monocyte\_chemoattractant\_proteinreceptor\_(mcp-  
lrb)\_alternatively\_spliced\_mrna, \_comp  
u09002\_5527-6082, n-methyl-d-  
aspartate\_receptor\_modulatory\_subunit\_2a\_(hnr2a)\_mrna, \_complete\_cds  
u13395\_994-1450, oxidoreductase\_(hhcma56)\_mrna, \_complete\_cds  
u28281\_1162-1618, secretin\_receptor\_mrna, \_complete\_cds  
u50531\_4295-4847, brca2\_region, \_mrna\_sequence\_cg030\_  
u66618\_1518-2016, swi/snf\_complex\_60\_kda\_subunit\_(baf60b)\_mrna, \_complete\_cds  
u85767\_13-505, myeloid\_progenitor\_inhibitory\_factor-1\_mpif-1\_mrna, \_complete\_cds\_  
x14767mrna\_1685-1832, mrna\_for\_gaba-a\_receptor, \_betasubunit

## Metagene 272

m86917\_2402-2972, oxysterol-binding\_protein\_(osbp)\_mrna, \_complete\_cds\_  
u19142\_69-510, gage-1\_protein\_mrna, \_complete\_cds  
u30872\_9600-10116, mitosis\_mrna, \_complete\_cds\_  
all\_u66061\_134531-176445, germline\_t-  
cell\_receptor\_beta\_chain\_tcrbv17slalt, \_tcrbv2s1, \_tcrbv10s1p, \_tcr  
u79297\_1095-1575, clone\_23589\_mrna\_sequence\_  
u90268\_1427-1703, krit1\_mrna, \_complete\_cds  
all\_x07024\_4938-5257, x\_chromosome\_mrna\_for\_ccg1\_protein\_invin\_cell\_proliferation  
x16504cds\_781-1266:in\_reversesequence, \_1283-1354, eno3\_mrna\_for\_beta-  
enolase\_(ec\_4.2.1.11).

## Metagene 258

ab000816\_783-1357, mrna\_for\_bmalld, \_partial\_cds/gb=ab000816\_/ntype=rna  
d17716\_1820-2390, mrna\_for\_n-  
acetylglucosaminyltransferase\_v, \_complete\_cds/gb=d17716\_/ntype=rna\_  
d25539\_3997-4375, mrna\_for\_kiaa0040\_gene, \_complete\_cds  
hg742-ht742\_at\_hg742-ht742\_latent\_membrane\_protein\_lmp1  
107597\_2496-3036, ribosomal\_protein\_s6\_kinase(rps6ka2)\_mrna, \_complete\_cds\_  
m10014cds#1\_1048-1264:in\_reversesequence, \_9512-  
9722, fibrinogen\_gamma\_chain\_and\_gamma-prime\_chain\_gen  
m28825\_1513-2047, thymocyte\_antigen\_cdla\_mrna, \_complete\_cds\_  
u03274\_1497-1941, biotinidase\_mrna, \_complete\_cds  
u51241cds\_717-1029:in\_reversesequence, \_1257-  
1497, eosinophil\_eotaxin\_receptor\_(cmkbr3)\_gene, \_complete  
all\_x63755\_579-994, mrna\_for\_high-sulphur\_keratin\_  
x80343cds\_435-807:in\_reversesequence, \_1006-  
1036, p35\_mrna\_for\_regulatory\_subunit\_of\_cdk5\_kinase  
all\_x83929\_2707-3257, mrna\_for\_typedesmocollin\_

## Metagene 280

u60665\_1603-2149, testis\_specific\_basic\_protein\_(tsbp), \_complete\_cds

## Metagene 248

m16474mrna\_1788-2223,fetal\_butyrylcholinesterase\_mrna,\_complete\_cds  
 u25433\_2428-  
 2842:not\_in\_gb\_record,protein\_associated\_with\_tumorigenic\_conversion\_(catr1.3)\_  
 mrna,\_com  
 u59423\_1481-1943,smad1\_mrna,\_complete\_cds  
 x76538\_433-931,mpv17\_mrna

Metagene 416

all\_m16404\_1576-2153,m2\_muscarinic\_acetylcholine\_receptor\_gene\_  
 m73746\_2409-  
 2894,lutropin/choriogonadotropin\_receptor\_(lhgr)\_mrna,\_complete\_cds

Metagene 3

j00117mrna\_9-428,chorionic\_gonadotropin\_(hcg)\_beta\_subunit\_mrna,\_complete\_cds  
 m12759cds\_65-335:in\_reversesequence,\_1020-1260,ig\_j\_chain\_gene  
 all\_m85220\_15-  
 201,heavy\_chain\_disease\_iga\_chain\_gene,\_ch3\_region\_with\_a\_369\_bp\_deletion,\_3'\_e  
 nd  
 s71043mrna\_442-  
 970,\_ig\_alpha\_2=immunoglobulin\_a\_heavy\_chain\_allotype{constant\_region,\_germ\_lin  
 e}\_[hu  
 u24152\_1879-2215,p21-activated\_protein\_kinase\_(pak1)\_gene,\_complete\_cds  
 all\_x60992\_2450-3021,cd6\_mrna\_for\_t\_cell\_glycoprotein\_cd6

Metagene 472

h46990\_40-  
 355,\_yo16d02.s1cdna\_clone\_178083\_3'\_similar\_to\_gb:j02625\_cytochrome\_p450\_1ie1\_(  
 human);  
 m86873mrna\_155-367,type\_a\_plasminogen\_related\_gene\_  
 s42303\_3537-4029,\_n-  
 cadherin\_[human,\_umbilical\_vein\_endothelial\_cells,\_mrna,\_4132\_nt]\_  
 all\_z80776\_596-795,h2a/g\_gene

Metagene 457

d10202\_1209-1557,mrna\_for\_platelet-activating\_factor\_receptor,\_complete\_cds  
 d13643\_3585-4131,mrna\_for\_kiaa0018\_gene,\_complete\_cds  
 d49387\_401-917,mrna\_for\_nadp\_dependent\_leukotriene\_b4\_12-  
 hydroxydehydrogenase,\_partial\_cds/gb=d49387  
 hg4606-ht5011\_at\_hg4606-ht5011\_centraactin,\_alpha\_  
 j03890mrna#1\_482-1022:not\_in\_gb\_record,\_sp-  
 c1\_gene\_(pulmonary\_surfactant\_protein\_sp-c)\_extracted\_fro  
 k03195\_2303-2813,(hepg2)\_glucose\_transporter\_gene\_mrna,\_complete\_cds\_  
 l13210\_1668-2214,mac-2\_binding\_protein\_mrna,\_complete\_cds

120348exon\_15-219: not\_in\_gb\_record, oncomodulin\_gene  
 142563mrna\_3011-3443, (clone\_lsw34)\_non-gastric\_h,k-atpase\_(atplal1)\_gene  
 m27504\_2078-  
 2626, topoisomerase\_type\_ii\_(topo\_ii)\_mrna, \_partial\_cds/gb=m27504\_/ntype=rna\_  
 m28215\_130-676, gtp-binding\_protein\_(rab5)\_mrna, \_complete\_cds  
 u20648\_316-766, zinc\_finger\_protein\_(znf154)\_mrna, \_partial\_cds  
 y00318cds#1\_1317-1653: in\_reversesequence, \_1814-  
 1916, mrna\_for\_complement\_control\_protein\_factor\_i  
 all\_z15108\_1535-2130, mrna\_for\_protein\_kinase\_c\_zeta

Metagene 443

ab000468\_2302-2860, mrna\_for\_zinc\_finger\_protein, \_clone\_res4-26, \_complete\_cds\_  
 ab002533\_1726-2128, mrna\_for\_qip1, \_complete\_cds\_  
 reverse\_ac002077\_3475-3730, cosmid\_clone\_luca17\_from\_3p21.3\_  
 ad000092cds#2\_714-1008: in\_fullsequence, \_87557-87797, \_hypotheticalserine-  
 threonine\_protein\_kinase\_r31  
 d16480\_2089-2641, mrna\_for\_mitochondrial\_enoyl-coa\_hydratase/3-hydroxyacyl-  
 coa\_dehydrogenase\_alpha-su  
 d38552\_1532-2012, mrna\_for\_kiaa0073\_gene, \_partial\_cds\_  
 d63475\_1309-1819, mrna\_for\_kiaa0109\_gene, \_complete\_cds\_  
 d63477\_4745-5243, mrna\_for\_kiaa0143\_gene, \_partial\_cds\_  
 d79206exon#5\_1513-2053, gene\_for\_ryudocan\_core\_protein, \_exon1-5, \_complete\_cds\_  
 d85245\_1248-1806, mrna\_for\_tr3beta, \_complete\_cds\_  
 all\_d87017\_16956-  
 20256, \_c7\_segment\_gene\_extracted\_from(lambda)\_dna\_for\_immunoglobulin\_light\_chain\_  
 d87116\_1514-2048, mrna\_for\_map\_kinase\_kinase\_3b, \_complete\_cds\_  
 hg2290-ht2386\_at\_hg2290-ht2386\_calcitonin  
 hg2755-ht2862\_at\_hg2755-ht2862\_t-plastin  
 hg2887-ht3031\_at\_hg2887-ht3031\_sry-related\_hmg-boxprotein  
 hg331-ht331\_at\_hg331-ht331\_tenascin  
 hg3897-ht4167\_at\_hg3897-ht4167\_sodium\_channel, \_type\_iii, \_alpha\_subunit, \_brain  
 hg3925-ht4195\_s\_at\_hg3925-ht4195\_surfactant\_protein\_sp-a2\_delta\_  
 j02906mrna\_1254-1782, cytochrome\_p450iif1\_protein\_(cyp2f)\_mrna, \_complete\_cds\_  
 l25444\_2124-2694, (tafii70-alpha)\_mrna, \_complete\_cds\_  
 m22960mrna\_1352-1760, protective\_protein\_mrna, \_complete\_cds\_  
 m24439exon\_492-912, liver/bone/kidney-type\_alkaline\_phosphatase\_(alpl)\_gene\_  
 m60284cds\_835-1144: in\_reversesequence, \_251-479, neurokinin\_a\_receptor\_(nk-  
 2r)\_gene\_  
 m68941mrna\_3078-3618, protein-tyrosine\_phosphatase\_mrna, \_complete\_cds\_  
 m91669\_4061-4636, bullous\_pemphigoid\_autoantigen\_bp180\_gene, \_3'\_end\_  
 m92303\_3057-3633, voltage-dependent\_calcium\_channel\_beta-  
 1\_subunit\_mrna, \_complete\_cds\_  
 m95623exon#14-15\_2-  
 383: not\_in\_gb\_record, pbgd\_gene\_(hydroxymethylbilane\_synthase)\_extracted\_fromhy  
 dr  
 s38742\_1370-1835, \_hox11=hox11\_homeodomain\_{homeobox}\_[human, \_mrna, \_1988\_nt]\_  
 s65583mrna\_588-1068, \_sp-10=intra-  
 acrosomal\_protein\_{alternatively\_spliced}\_[human, \_liver, \_genomic, \_2  
 s87759\_1823-  
 2321, \_protein\_phosphatase\_2c\_alpha\_[human, \_teratocarcinoma, \_mrna, \_2346\_nt]  
 u01337exon#16\_412-553, ser/thr\_protein\_kinase\_(a-raf-1)\_gene, \_complete\_cds\_  
 u04898\_1421-1877, orphan\_hormone\_nuclear\_receptor\_roralpha2\_mrna, \_complete\_cds\_  
 u11292\_2353-2863, ki\_nuclear\_autoantigen\_mrna, \_complete\_cds\_  
 u15655\_2102-2576, ets\_domain\_protein\_erf\_mrna, \_complete\_cds\_

u25034\_588-1127,neuronatin\_beta\_mrna,\_complete\_cds\_  
 u25956mrna\_1470-2046,p-selectin\_glycoprotein\_ligand\_(selplg)\_gene  
 u30894\_2068-2626,n-sulphoglucosamine\_sulphohydrolase\_mrna,\_complete\_cds  
 u32439\_1324-1822,regulator\_of\_g-  
 protein\_signaling\_similarity\_(rgs7)\_mrna,\_partial\_cds  
 u32674cds\_593-1060:in\_reversesequence,\_1181-  
 1191,orphan\_receptor\_gpr9\_(gpr9)\_gene,\_partial\_cds  
 u39573\_2173-2689,salivary\_peroxidase\_mrna,\_complete\_cds  
 u40391mrna\_464-980,serotonin\_n-acetyltransferase\_gene,\_complete\_cds\_  
 u40434\_1561-2071,mesothelin\_or\_cak1\_antigen\_precursor\_mrna,\_complete\_cds\_  
 u42031\_1655-2201,54\_kda\_progesterone\_receptor-  
 associated\_immunophilin\_fkbp54\_mrna,\_partial\_cds\_  
 u43374\_775-1069,normal\_keratinocyte\_mrna\_  
 u45973\_1634-2192,phosphatidylinositol\_(4,5)bisphosphate\_5-  
 phosphatase\_homolog\_mrna,\_partial\_cds  
 u46751\_1562-  
 2012,phosphotyrosine\_independent\_ligand\_p62\_for\_the\_lck\_sh2\_domain\_mrna,\_comple  
 te\_cds  
 u49857\_314-749,transcriptional\_activator\_mrna,\_complete\_cds  
 u50330\_3071-3515,procollagen\_c-proteinase\_(pcp-2)\_mrna,\_complete\_cds\_  
 u68111mrna\_858-1374,protein\_phosphatase\_inhibitor(ppp1r2)\_gene  
 u70671\_695-1115,ataxin-2\_related\_protein\_mrna,\_partial\_cds\_  
 u72206\_3122-  
 3590,guanine\_nucleotide\_regulatory\_factor\_(lfp40)\_mrna,\_complete\_cds\_  
 u92457\_2832-3375,metabotropic\_glutamate\_receptormrna,\_complete\_cds  
 x05855cds\_12-  
 65:not\_in\_gb\_record,histone\_h3.3\_gene\_exon\_2,histone\_h3.3\_gene\_exon\_2\_  
 all\_x07290\_1212-1723,hf.12\_gene\_mrna\_  
 all\_x07767\_1948-2516,mrna\_for\_camp-  
 dependent\_protein\_kinase\_catalytic\_subunit\_type\_alpha\_(ec\_2.7.1.3  
 all\_x07948\_3-428,mrna\_for\_transition\_protein(tp1)\_  
 x59932mrna\_1557-2063,mrna\_for\_c-src-kinase\_  
 all\_x66945\_3582-3931,n-sam\_mrna\_for\_fibroblast\_growth\_factor\_receptor  
 x78687exon#6\_172-670,g9\_gene\_encoding\_sialidase  
 x79865cds\_267-411:in\_reversesequence,\_922,mrp17\_mrna  
 x81372cds\_701-791:in\_reversesequence,\_1027-1195,mrna\_for\_biphenyl\_hydrolase-  
 related\_protein  
 all\_x89066\_3817-4019,mrna\_for\_trpc1\_protein  
 all\_x91504\_970-1523,mrna\_for\_arpl\_protein  
 all\_x94232\_2035-2528,mrna\_for\_novel\_t-cell\_activation\_protein  
 all\_x98482\_45-  
 72,tnnt2\_gene\_exon/gb=x98482\_/ntype=dna\_/annot=mrna,tnnt2\_gene\_exon/gb=x98482\_  
 ntype=d  
 all\_z12962\_31-398,mrna\_for\_homologue\_to\_yeast\_ribosomal\_protein\_l41  
 z22548cds\_310-547:in\_reversesequence,\_684-894,thiol-  
 specific\_antioxidant\_protein\_mrna\_  
 z73497cds\_28-  
 229,dna\_sequence\_from\_cosmid\_u240c2,\_between\_markers\_dxs366\_and\_dxs87\_on\_chromo  
 some\_xco

Metagene 430

d87458\_3244-3784,mrna\_for\_kiaa0282\_gene,\_partial\_cds\_  
 m99564\_2505-2991,(clone\_dn10mel)\_p\_protein\_mrna,\_complete\_cds\_

## Metagene 426

d30037\_609-1179,mrna\_for\_phosphatidylinositol\_transfer\_protein\_(pi-tpbeta),\_complete\_cds\_  
 all\_j03027\_3437-3996,mhc\_i\_hla-6.09\_gene,\_complete\_cds\_  
 all\_m14306\_171-361,beta-a3/a1-crystallin\_gene\_(hu-beta-a3/a1)  
 all\_m30703\_55-142:not\_in\_gb\_record,amphiregulin\_(ar)\_gene\_  
 u14407\_601-1147,interleukin(il15)\_mrna,\_complete\_cds\_  
 u33054\_1584-2010,g\_protein-coupled\_receptor\_kinase\_grk4\_mrna,\_alpha\_splice\_variant,\_complete\_cds\_  
 x94629\_618-1128,mrna\_for\_metaphase\_chromosomal\_protein  
 y10518mrna\_138-648,mrna\_for\_cd202\_protein/gb=y10518/\_ntype=rna\_  
 z83804\_29-261,mrna\_for\_axonemal\_dynein\_heavy\_chain\_(partial,\_id\_hdhc7).

## Metagene 406

u06454\_1832-2288,amp-activated\_protein\_kinase\_(hampk)\_mrna,\_complete\_cds\_  
 all\_y00705\_5-356,ptsi\_mrna\_for\_pancreatic\_secretory\_inhibitor\_(expressed\_in\_neoplastic\_tissue)

## Metagene 393

j03474cds\_3-255,serum\_amyloid\_a\_gene,\_complete\_cds\_  
 all\_m63262\_161-540:in\_m63262cds\_231-340,5-lipoxygenase\_activating\_protein\_(flap)\_gene\_  
 all\_x51441\_55-90,mrna\_for\_serum\_amyloid\_a\_(saa)\_protein\_partial,\_clone\_pas3-alpha,mrna\_for\_serum\_amy  
 x75042cds\_1607-1817:in\_reversesequence,\_2024-2252,rel\_proto-oncogene\_mrna\_

## Metagene 381

af005361\_1159-1663,importin\_alphamrna,\_complete\_cds/gb=af005361/\_ntype=rna\_  
 hg3731-ht4001\_r\_at\_hg3731-ht4001\_immunoglobulin\_heavy\_chain,\_vdjrc\_regions\_  
 l38616mrna\_1184-1634,brain\_and\_reproductive\_organ-expressed\_protein\_(bre)\_gene,\_complete\_cds  
 u46746\_1183-1708,dystrobrevin-epsilon\_mrna,\_complete\_cds\_  
 all\_u61500\_6060-6577,gt334\_protein\_(gt334)\_gene\_mrna,\_complete\_cds\_

## Metagene 361

m16364\_749-1311,creatine\_kinase-b\_mrna,\_complete\_cds\_  
 m64554mrna\_1602-1962,\_f13a1\_gene\_(coagulation\_factor\_xiib)\_extracted\_fromfactor\_xiii\_b\_subunit\_gene  
 u07794\_cds2\_at\_u07794\_u07794,not\_in\_gb\_record,tyrosine\_kinase\_(txk)\_gene

## Metagene 357

hg3432-ht3620\_s\_at\_hg3432-ht3620\_fibroblast\_growth\_factor\_receptor\_k-sam,\_altssplice\_3,\_k-sam\_iii\_  
 s79048\_61-421,\_lprp=phl\_elf1\_[human,\_lacrimal\_gland,\_mrna\_partial,\_507\_nt]  
 u39657\_2341-2863,map\_kinase\_kinase(mkk6)\_mrna,\_complete\_cds\_  
 u97188\_3602-4010,putative\_rna\_binding\_protein\_koc\_(koc)\_mrna,\_complete\_cds\_  
 x66417cds\_230-524:in\_reversesequence,\_658-766,cask\_mrna\_for\_kappa-casein

## Metagene 354

aj000480cds\_116-650,mrna\_for\_c8fw\_phosphoprotein/gb=aj000480\_/ntype=rna\_  
 d21241exon#2\_2-72,\_ovary-\_and\_prostate-specific\_exonfromcytochrome\_p-  
 450\_aromatase\_gene,\_multiple\_ex  
 d30742\_1211-1697,mrna\_for\_calmodulin-dependent\_protein\_kinase\_iv,\_complete\_cds\_  
 d80011\_4259-4793,mrna\_for\_kiaa0189\_gene,\_complete\_cds\_  
 hg1980-ht2023\_at\_hg1980-ht2023\_tubulin,\_beta\_2\_  
 hg2264-ht2360\_at\_hg2264-  
 ht2360\_atpase,\_ca2+\_transporting,\_plasma\_membrane\_1,\_altssplice\_6\_  
 hg273-ht273\_at\_hg273-ht273\_lymphocyte\_antigen\_hla-g3\_  
 hg3517-ht3711\_at\_hg3517-ht3711\_alpha-1-antitrypsin,\_5'\_end\_  
 hg620-ht620\_at\_hg620-ht620\_tyrosine\_phosphatase,\_epsilon\_  
 l05424\_cds2\_at\_l05424\_l05424,not\_in\_gb\_record,\_cd44\_gene\_(cell\_surface\_glycoprotein\_cd44)\_extracted\_  
 l10844\_1646-2213,cellular\_growth-regulating\_protein\_mrna,\_complete\_cds\_  
 l14848\_802-1181,mhc\_i-related\_protein\_mrna,\_complete\_cds\_  
 l28957\_685-1231,ctp:phosphocholine\_cytidyltransferase\_mrna,\_complete\_cds\_  
 all\_m23178\_2889-3818,homologue-  
 1\_of\_gene\_encoding\_alpha\_subunit\_of\_murine\_cytokine\_(mip1/sci),\_compl  
 m27436mrna\_1638-  
 1979,tissue\_factor\_gene,\_complete\_cds,\_with\_a\_alu\_repetitive\_sequence\_in\_the\_3'  
 \_untr  
 m27819\_3060-3426,anion\_exchange\_protein(ae1,\_band\_3)\_mrna,\_complete\_cds\_  
 m33318mrna\_1538-1583,cytochrome\_p450ia3\_(cyp2a3)\_mrna,\_complete\_cds\_  
 m62324\_1584-2052,modulator\_recognition\_factor\_i\_(mrf-1)\_mrna,\_3'\_end\_  
 u30888\_1892-2420,trna-guanine\_transglycosylase\_mrna,\_complete\_cds\_  
 u40571\_1695-2073,alpha1-syntrophin\_(snt\_a1)\_mrna,\_complete\_cds\_  
 u82310\_19-229,unknown\_protein\_mrna,\_partial\_cds/gb=u82310\_/ntype=rna\_  
 u82818\_1005-1058,ucp3s\_mrna,\_complete\_cds/gb=u82818\_/ntype=rna\_  
 u84551\_cds2\_at\_u84551\_u84551,not\_in\_gb\_record,dystrobrevin\_(dtn)\_gene\_  
 x03934cds\_255-423:in\_reversesequence,\_3890-4112,t-  
 cell\_antigen\_receptor\_gene\_t3-delta\_  
 all\_x07619\_658-1162,mrna\_for\_cytochrome\_p450\_db1\_variant\_b\_  
 x12458mrna\_1566-2046,\_p3\_protein\_(aa\_1-1382)\_gene\_extracted\_fromp3\_gene\_  
 all\_x13967\_3247-3806,mrna\_for\_leukaemia\_inhibitory\_factor\_(lif/hilda)  
 x16901cds\_411-711:in\_reversesequence,\_866-  
 1094,mrna\_for\_rap30\_subunit\_of\_transcription\_initiation\_fa  
 x52599cds\_295-649,mrna\_for\_beta\_nerve\_growth\_factor  
 x94563mrna#1\_109-  
 123,\_exon\_1b;\_used\_only\_in\_typetranscripts\_fromdbi/acbp\_gene\_exon&/gb=x94563\_/n  
 type  
 y10506mrna\_251-593,mrna\_for\_cd110\_protein/gb=y10506\_/ntype=rna\_  
 y10615cds\_115-535,cyrn2\_gene/gb=y10615\_/ntype=dna\_/annot=cds\_

all\_z46632\_2953-3206,hspde4c1\_gene\_for\_3',5'-  
cyclic\_amp\_phosphodiesterase,hspde4c1\_gene\_for\_3',5'

Metagene 346

u45974\_1007-1517,phosphatidylinositol\_(4,5)\_bisphosphate\_5-  
phosphatase\_homolog\_mrna,\_partial\_cds\_  
u79304\_1102-1630,clone\_23909\_mrna,\_partial\_cds.  
x05839mrna\_2298-  
2467,\_transforming\_growth\_factor\_betaprecursor\_gene\_extracted\_fromtransforming\_  
growt

Metagene 340

l34838\_40-586,early\_placenta\_insulin-  
like\_peptide\_epil\_(insl4)\_mrna,\_complete\_cds\_  
all\_u05255\_159-  
188,glycophorin\_hep2\_mrna,\_partial\_cds,glycophorin\_hep2\_mrna,\_partial\_cds  
u31501\_2359-  
2773,fragile\_x\_mental\_retardation\_syndrome\_related\_protein\_(fxr2)\_mrna,\_complet  
e\_cds\_  
u37689\_344-752,rna\_polymerase\_ii\_subunit\_(hsrpb8)\_mrna,\_complete\_cds\_  
x15943mrna\_884-1220:in\_reversesequence,\_7046-7076,\_huamn\_calcitonin/alpha-  
cgrp\_gene

Metagene 336

u08021\_447-909,nicotinamide\_n-methyltransferase\_(nnmt)\_mrna,\_complete\_cds  
all\_x83107\_1867-2348,bmx\_mrna\_for\_cytoplasmic\_tyrosine\_kinase

Metagene 333

u96191\_19-439,trophoblast\_hypoxia-regulated\_factor-5\_(hrf-  
5)\_mrna,\_3'\_end/gb=u96191\_/ntype=rna\_  
all\_x13955\_675-827,mrna\_for\_myosin\_alkali\_light\_chain  
x64877cds\_417-762:in\_reversesequence,\_889-  
894,mrna\_for\_serum\_protein,mrna\_for\_serum\_protein

Metagene 322

hg2229-ht2306\_at\_hg2229-ht2306\_paired\_box\_hup1\_  
m54914exon\_1099-1666,follicle-stimulating\_hormone\_beta-subunit\_gene

Metagene 267



hg544-ht544\_at\_hg544-ht544\_endothelial\_cell\_growth\_factor\_  
 l05072exon#10\_375-907,interferon\_regulatory\_factorgene,\_complete\_cds\_  
 l07261mrna\_283-  
 505,alpha\_adducin\_mrna,\_partial\_cds\_including\_alternate\_exons\_a\_and\_b\_(trimmed\_  
 to\_889  
 l37360\_146-698,(clone\_hehk1-1)\_ehk1\_receptor\_tyrosine\_kinase\_ligand\_(efl-  
 2)\_mrna,\_complete\_cds  
 l77567mrna\_947-1231,mitochondrial\_citrate\_transport\_protein\_(ctp)\_mrna,\_3'\_end  
 m25667\_1086-1200,neuronal\_growth\_protein\_43\_(gap-43)\_mrna,\_complete\_cds  
 m32886\_351-843,sorcin\_cp-22\_mrna,\_complete\_cds\_  
 u07151\_395-869,gtp\_binding\_protein\_(arl3)\_mrna,\_complete\_cds\_  
 u29175\_5199-5223,transcriptional\_activator\_(brgl)\_mrna,\_complete\_cds.  
 u30827\_1253-1817,splicing\_factor\_srp40-3\_(srp40)\_mrna,\_complete\_cds  
 u30999\_25-379,(memc)\_mrna,\_3'\_utr/gb=u30999\_/ntype=rna\_  
 u51432\_1557-2079,nuclear\_protein\_skip\_mrna,\_complete\_cds.  
 u53830\_1469-1835,interferon\_regulatory\_factor\_7a\_mrna,\_complete\_cds\_  
 u60873\_115-439,clone\_137308\_mrna,\_partial\_cds  
 u79261\_883-1422,clone\_23959\_mrna,\_partial\_cds  
 all\_xl4813\_1077-1618,liver\_mrna\_for\_3-oxoacyl-coa\_thiolase\_  
 x64177cds\_8-147:in\_reversesequence,\_2-277,mrna\_for\_metallothionein  
 x94333\_1617-2157,mrna\_for\_tgn46\_protein  
 x97074cds\_182-398:in\_reversesequence,\_704-782,mrns\_for\_clathrin-  
 associated\_protein  
 z46376mrna\_4703-5249,hk2\_mrna\_for\_hexokinase\_ii\_

## Metagene 264

d21239\_3475-3997,mrna\_for\_c3g\_protein,\_complete\_cds  
 d49958\_1830-2346,fetus\_brain\_mrna\_for\_membrane\_glycoprotein\_m6,\_complete\_cds\_  
 d88613\_1068-1518,mrna\_for\_hgcma,\_complete\_cds  
 d88667\_1298-1652,mrna\_for\_cerebroside\_sulfotransferase,\_complete\_cds\_  
 hg1098-ht1098\_at\_hg1098-ht1098\_cystatin\_d  
 hg2161-ht2231\_at\_hg2161-ht2231\_translocation-  
 associated\_notch\_(drosophila)\_homolog  
 hg2191-ht2261\_at\_hg2191-ht2261\_crystallin\_beta\_b3\_  
 hg3477-ht3670\_at\_hg3477-ht3670\_cd4\_antigen\_  
 hg3928-ht4198\_at\_hg3928-ht4198\_surfactant\_protein\_sp-a1\_delta\_  
 hg4336-ht4606\_at\_hg4336-ht4606\_bactericidal\_bpi'gene\_  
 hg4535-ht4940\_s\_at\_hg4535-ht4940\_dematin\_  
 j02888\_453-915,quinone\_oxidoreductase\_(nqo2)\_mrna,\_complete\_cds  
 k03008cds\_90-118:not\_in\_gb\_record,\_gamma-g2-psi\_gene\_extracted\_fromgamma-c-  
 crystallin\_(gamma-3)\_gene  
 l11372\_497-  
 893,protocadherin\_43\_mrna,\_3'\_end\_of\_cds\_for\_alternative\_splicing\_pc43-12\_  
 l17327\_16-196,pre-t/nk\_cell\_associated\_protein\_(3b3)\_mrna,\_3'\_end  
 l40904mrna\_1228-  
 1656,hsapiens\_peroxisome\_proliferator\_activated\_receptor\_gamma,\_complete\_cds\_  
 m12625mrna\_893-1259:in\_reversesequence,\_1599-1683,lecithin-  
 cholesterol\_acyltransferase\_mrna,\_complet  
 m14123cds#1\_263-665,\_pol\_fromendogenous\_retrovirus\_herv-  
 k10/gb=m14123\_/ntype=dna\_/annot=cds,\_pol\_fro  
 all\_m16707\_590-  
 631,histone\_h4\_gene,\_complete\_cds,\_clone\_fo108,histone\_h4\_gene,\_complete\_cds,\_c  
 lone\_f  
 m21302\_402-514,small\_proline\_rich\_protein\_(sprii)\_mrna,\_clone\_174n\_

m21904cds\_1189-1549:in\_reversesequence,\_372-  
 378,4f2\_glycosylated\_heavy\_chain\_(4f2hc)\_antigen\_gene\_  
 m61733\_2454-2934,erythroid\_membrane\_protein\_4.1\_mrna,\_complete\_cds  
 m90366\_1683-2175,zona\_pellucida\_glycoprotein(zp2)\_mrna,\_complete\_cds  
 m91585\_3719-4175,br140\_mrna,\_complete\_cds  
 s80267\_1304-1872,\_p72syk\_{g\_insertion\_nucleotide\_92}\_[human,\_jurkat\_e6-  
 1\_j.cam1\_cells,\_mrna\_partial\_  
 u01120\_2484-2982,glucose-6-phosphatase\_mrna,\_complete\_cds  
 u04270\_3505-3973,putative\_potassium\_channel\_subunit\_(h-erg)\_mrna,\_complete\_cds\_  
 u07856cds#5\_1300-  
 1846,endogenous\_retrovirus\_in\_complement\_c4a\_gene,\_a3\_allele,\_herv-  
 k(c4)\_(gag),\_(po  
 u11090\_733-1243,hydroxyindole-o-methyltransferase\_promoter\_a-  
 derived\_(hiomt)\_mrna,\_complete\_cds  
 u13666cds\_671-989:in\_reversesequence,\_1329-1413,g\_protein-  
 coupled\_receptor\_(gpr1)\_gene,\_complete\_cds  
 u18244\_1166-1640,excitatory\_amino\_acid\_transporter\_mrna,\_complete\_cds  
 u18543\_1853-2339,zinc-finger\_protein\_mrna,\_complete\_cds  
 all\_u19107\_3423-3658,znf127\_(znf127)\_gene,\_complete\_cds\_  
 u19977\_735-1227,preprocarboxypeptidase\_a2\_(procpa2)\_mrna,\_complete\_cds\_  
 u20582\_1180-1690,actin-like\_peptide\_mrna,\_partial\_cds  
 u20657\_2439-2890:not\_in\_gb\_record,ubiquitin\_protease\_(unph)\_proto-  
 oncogene\_mrna,\_complete\_cds\_  
 u31342mrna\_1173-1629,nucleobindin\_gene\_  
 u33317mrna\_25-421,defensin(hd-6)\_gene,\_complete\_cds  
 u33761\_1017-1557,cyclin\_a/cdk2-associated\_p45\_(skp2)\_mrna,\_complete\_cds  
 u36501\_1704-2148,sp100-b\_(sp100-b)\_mrna,\_complete\_cds  
 u43148\_6015-6483,patched\_homolog\_(ptc)\_mrna,\_complete\_cds  
 u48263\_627-1173,pre-pro-orphanin\_fq\_(ofq)\_mrna,\_complete\_cds\_  
 u49973cds#1\_764-  
 1340,\_orf1;\_mer37;\_putative\_transposase\_similar\_to\_pogo\_element\_fromtiger1\_tra  
 nspos  
 u59878\_469-895,low-mr\_gtp-binding\_protein\_(rab32)\_mrna,\_partial\_cds  
 u76010\_1520-1964,putative\_zinc\_transporter\_znt-3\_(znt-3)\_mrna,\_complete\_cds  
 u77845\_1515-1905,htrip\_(htrip)\_mrna,\_complete\_cds  
 u78793\_6-29,folate\_receptor\_alpha\_(hfr)\_mrna,\_partial\_cds/gb=u78793\_/ntype=rna\_  
 u86759\_1374-1856,netrin-2\_like\_protein\_(ntn2l)\_mrna,\_complete\_cds  
 all\_u90543\_2501-  
 2545,butyrophilin\_(btfl)\_mrna,\_complete\_cds,butyrophilin\_(btfl)\_mrna,\_complete\_  
 cds  
 u95019\_2358-2862,voltage-dependent\_calcium\_channel\_beta-  
 2c\_subunit\_mrna,\_complete\_cds  
 all\_x04297\_3519-4090,mrna\_for\_na,k-atpase\_alpha-subunit  
 all\_x05246\_1045-1556,testis-specific\_pgk-  
 2\_gene\_for\_phosphoglycerate\_kinase\_(atp:3-phospho-d-glycera  
 all\_x53800\_377-961,mrna\_for\_macrophage\_inflammatory\_protein-2beta\_(mip2beta)\_  
 x76942cds\_24-420:in\_reversesequence,\_487-527,mrna\_for\_72.1\_protein  
 x92518mrna\_4077-4127,mrna\_for\_hmgi-c\_protein\_  
 x96783mrna\_1442-2015,syt\_v\_gene\_(genomic\_and\_cdna\_sequence)\_  
 all\_x97058\_1042-1565,mrna\_for\_p2y6\_receptor  
 y08200\_1496-2006,mrna\_for\_rab\_geranylgeranyl\_transferase,\_alpha-subunit  
 all\_z71460\_2546-3033,mrna\_for\_vacuolar-type\_h(+)-atpase\_115\_kda\_subunit

Metagene 255

d10922\_1288-1808,mrna\_for\_fm1p-related\_receptor\_(hm63)\_  
 m11567mrna\_188-  
 620,angiogenin\_gene,\_complete\_cds,\_and\_three\_alu\_repetitive\_sequences

Metagene 253

ab002356\_5330-5807,mrna\_for\_kiaa0358\_gene,\_complete\_cds/gb=ab002356\_/ntype=rna\_  
 l11701\_2320-2609,phospholipase\_d\_mrna,\_complete\_cds  
 l42374mrna\_1836-2389,pp2a\_b56-beta\_mrna,\_complete\_cds\_  
 m19508exon#1\_2-98,\_mpo\_frommyeloperoxidase\_gene,\_exons\_1-  
 4/gb=m19508\_/ntype=dna\_/annot=exon\_  
 all\_m32879\_690-1129,steroid\_11-beta-hydroxylase\_(cyp11b1)\_gene,steroid\_11-beta-  
 hydroxylase\_(cyp11b1)  
 m81182\_2831-3314,peroxisomal\_70\_kd\_membrane\_protein\_mrna,\_complete\_cds  
 u25975\_1675-1795,serine\_kinase\_(hpak65)\_mrna,\_partial\_cds  
 u47686\_2174-  
 2747,signal\_transducer\_and\_activator\_of\_transcription\_stat5b\_mrna,\_complete\_cds  
 all\_u67092\_1093-1868:not\_in\_gb\_record,ataxia-  
 telangiectasia\_locus\_protein\_(atm)\_gene,\_exons\_1a,\_1b,\_  
 all\_x16609\_6641-7241,mrna\_for\_ankyrin\_(variant\_2.1)  
 x51953exon#1-2\_37-  
 64:not\_in\_gb\_record,ucp\_gene\_for\_uncoupling\_protein\_exonsand/gb=x51953\_/ntype=d  
 na\_  
 all\_x52228\_1631-2103,mrna\_for\_secreted\_epithelial\_tumour\_mucin\_antigen\_  
 x58528mrna\_2689-3193,pmp70\_mrna\_for\_a\_peroxisomal\_membrane\_protein\_  
 x95808mrna\_5503-  
 6037,mrna\_for\_protein\_encoded\_by\_a\_candidate\_gene,\_dxs6673e,\_for\_mental\_retarda  
 tion  
 z11899cds\_446-706:in\_reversesequence,\_989-  
 1074,otf3\_mrna\_encoding\_octamer\_binding\_protein\_3b  
 z22951mrna\_717-  
 1231,of\_p65\_gene\_encoding\_p65\_subunit\_of\_transcription\_factor\_nf-kappab\_  
 reverse\_z68280\_34936-  
 35175,dna\_sequence\_from\_cosmid\_l25a3,\_huntington's\_disease\_region,\_chromosome\_4

Metagene 172

m22430\_300-732,rasf-a\_pla2\_mrna,\_complete\_cds  
 u80669\_863-1403,androgen\_regulated\_homeobox\_protein\_(nkx3.1)\_mrna,\_complete\_cds  
 z70222cds\_3-213:in\_reversesequence,\_25-37,mrna\_for\_orf\_(clone\_icrfp507g2490)

Metagene 123

d90064\_1806-2184,cgm6\_mrna\_for\_cd66b\_(nca-95)  
 m87507\_751-1177:in\_reversesequence,\_1012-1130,\_homo\_sapien\_interleukin-  
 1\_beta\_convertase\_(il1bce)\_mr  
 m91556\_4785-5343,voltage-gated\_sodium\_channel\_mrna,\_complete\_cds.  
 u82275\_1335-1647,immunoglobulin-like\_transcriptmrna,\_complete\_cds\_  
 x15675mrna\_1522-1840,ptr7\_mrna\_for\_repetitive\_sequence/gb=x15675\_/ntype=rna

Metagene 119

d00003\_1681-1981,liver\_cytochrome\_p-450\_mrna,\_complete\_cds,liver\_cytochrome\_p-450\_mrna,\_complete\_cds  
 m74047\_1878-2316,steroid\_5-alpha-reductase(srd5a2)\_mrna,\_complete\_cds\_  
 s53911\_2110-  
 2584,\_cd34=glycoprotein\_expressed\_in\_lymphohematopoietic\_progenitor\_cells\_{alte  
 rnatively  
 u42360mrna\_867-1346,n33\_gene  
 x54867mrna\_783-1293,mrna\_for\_nkg2-a\_gene\_  
 x65663cds\_83-137,sox-6\_mrna/gb=x65663\_/ntype=rna\_  
 y11174cds\_48-  
 516:in\_reversesequence,\_600,mrna\_for\_rp3\_gene/gb=y11174\_/ntype=rna\_

Metagene 118

d12620\_1535-1965,mrna\_for\_cytochrome\_p-450ltbv\_  
 d38522\_3436-3958,mrna\_for\_kiaa0080\_gene,\_partial\_cds\_  
 d63861exon#10\_90-656,dna\_for\_cyclophilin\_40,\_complete\_cds  
 hg831-ht831\_at\_hg831-ht831\_potassium\_channel\_  
 j02883mrna\_55-493,colipase\_mrna,\_complete\_cds  
 l40393mrna\_1754-2222,(clone\_s171)\_mrna,\_complete\_cds  
 m94172\_6837-7328,n-type\_calcium\_channel\_alpha-1\_subunit\_mrna,\_complete\_cds\_  
 u05589\_877-1453,ribosomal\_protein\_s1\_homolog\_mrna,\_partial\_cds\_  
 u08854\_1612-  
 2040,udp\_glucuronosyltransferase\_precursor\_(ugt2b15)\_mrna,\_complete\_cds  
 u16954\_1099-1579,(af1q)\_mrna,\_complete\_cds\_  
 u17327\_6523-7081,neuronal\_nitric\_oxide\_synthase\_(nos1)\_mrna,\_complete\_cds  
 u35637\_8831-9367,nebulin\_mrna,\_partial\_cds/gb=u35637\_/ntype=rna  
 u47926\_1546-1996,unknown\_protein\_b\_mrna,\_complete\_cds  
 u90546\_1301-  
 1344,butyrophilin\_(bt4f)\_mrna,\_complete\_cds,butyrophilin\_(bt4f)\_mrna,\_complete\_  
 cds  
 x02158mrna\_949-1219,gene\_for\_erythropoietin\_  
 all\_x06562\_3951-4396,mrna\_for\_growth\_hormone\_receptor  
 x14474cds\_669-710,mrna\_for\_microtubule-associated\_tau\_protein  
 all\_x86400\_560-1155,mrna\_for\_gamma\_subunit\_of\_sodium\_potassium\_atpase  
 all\_x98176\_772-1022,mrna\_for\_mach-beta-1\_protein/gb=x98176\_/ntype=rna  
 z69030cds\_838-1186,mrna\_for\_gammaisoform\_of\_61kda\_regulatory\_subunit\_of\_pp2a

Metagene 112

j04621mrna\_2879-3347,heparan\_sulfate\_proteoglycan\_(hspg)\_core\_protein,\_3'\_end  
 all\_m27749\_245-348,immunoglobulin-  
 related\_14.1\_protein\_mrna,\_complete\_cds,immunoglobulin-related\_14.  
 all\_x51730\_4462-5003,mrna\_and\_promoter\_dna\_for\_progesterone\_receptor\_

Metagene 89

hg2139-ht2208\_f\_at\_hg2139-ht2208\_beta-1-glycoprotein\_1,\_pregnancy-specific\_

m22403exon#2\_1749-2224,blood\_platelet\_membrane\_glycoprotein\_ib-  
 alpha\_(gpib)\_gene,\_complete\_cds,\_clon  
 u31201\_cds1\_at\_u31201\_u31201,not\_in\_gb\_record,laminin\_gamma2\_chain\_gene\_(lamc2)  
 ,laminin\_gamma2\_chain  
 u73167cds#4\_1050-1254:in\_reversesequence,\_13521-  
 13767:not\_in\_gb\_record,\_h\_luca14.2a\_gene\_extracted\_f  
 x58288mrna\_4517-4955,hr-ptpu\_gene\_for\_protein\_tyrosine\_phosphatase\_  
 all\_x66276\_3221-3734,mrna\_for\_skeletal\_muscle\_c-protein

Metagene 78

af005887\_1969-  
 2413,atf\_family\_member\_atf6\_(atf6)\_mrna,\_complete\_cds/gb=af005887\_/ntype=rna  
 d00860\_1546-  
 2020,mrna\_for\_phosphoribosyl\_pyrophosphate\_synthetase\_(ec\_2.7.6.1)\_subunit\_i\_  
 d13370exon#5\_193-637,apx\_gene\_encoding\_apex\_nuclease,\_complete\_cds\_  
 d50550\_3217-3475,llgl\_mrna,\_complete\_cds\_  
 d85131\_1126-1679,mrna\_for\_myc-associated\_zinc-  
 finger\_protein\_ofislet,\_complete\_cds  
 d87989\_597-1095,mrna\_for\_udp-  
 galactose\_transporter\_related\_isozyme\_1,\_complete\_cds\_  
 hg982-ht982\_s\_at\_hg982-ht982\_pre-t/nk-cell-associated\_protein\_1f6  
 j03263\_667-1218,lysosome-  
 associated\_membrane\_glycoprotein\_(lamp\_a)\_mrna,\_complete\_cds  
 104282\_1873-2329,caccc\_box-binding\_protein\_mrna,\_complete\_cds  
 115189\_1520-2081,mitochondrial\_hsp75\_mrna,\_complete\_cds.  
 125876\_359-785,protein\_tyrosine\_phosphatase\_(cip2)mrna,\_complete\_cds  
 143579\_6-  
 403,(clone\_110298)\_mrna/gb=143579\_/ntype=rna,(clone\_110298)\_mrna/gb=143579\_/nty  
 pe=rna  
 m24766\_1513-2055,(clone\_phaiv2-12)\_alpha-  
 2\_collagen\_type\_iv\_(col4a2)\_mrna,\_3'\_end  
 m31169cds\_2-71,propionyl-coa\_carboxylase\_beta-subunit\_(beta-  
 pcc)\_gene,\_partial\_cds\_(mutant\_delta-atc  
 m34423\_1856-2312,beta-galactosidase\_(glb1)\_mrna,\_complete\_cds  
 m36429\_827-1412,transducin\_beta-2\_subunit\_mrna,\_complete\_cds\_  
 m60891mrna\_6-411,uroporphyrinogen\_decarboxylase\_(uro-  
 d)\_gene,\_partial\_cds/gb=m60891\_/ntype=dna\_/anno  
 m94250exon#4-5\_43-  
 301:not\_in\_gb\_record,retinoic\_acid\_inducible\_factor\_(mk)\_gene\_exons\_1-  
 5,\_complete\_  
 u10323\_963-1467,nuclear\_factor\_nf45\_mrna,\_complete\_cds\_  
 u14417\_567-  
 1017,ral\_guanine\_nucleotide\_dissociation\_stimulator\_mrna,\_partial\_cds\_  
 u28963\_567-1143,gps2\_(gps2)\_mrna,\_complete\_cds\_  
 u29171\_1340-1742,casein\_kinase\_i\_delta\_mrna,\_complete\_cds  
 u35835\_2404-2859,dna-pk\_mrna,\_partial\_cds  
 u47105\_616-1174,h105e3\_mrna,\_complete\_cds  
 u50553\_2647-3079,helicase\_like\_protein\_mrna,\_complete\_cds  
 u61734cds\_461-628:in\_reversesequence,\_710-  
 767,protein\_trafficking\_protein\_(s3111125)\_mrna,\_complete  
 u72935mrna#1\_7752-  
 7898,\_atrx\_gene\_(putative\_dna\_dependent\_atpase\_and\_helicase)\_extracted\_fromputa  
 tiv  
 u73477\_440-885,acidic\_nuclear\_phosphoprotein\_pp32\_mrna,\_complete\_cds\_

u78722\_1523-1965,zinc\_finger\_protein\_165\_(zpf165)\_mrna,\_complete\_cds  
 u81802\_2557-3043,ptdins\_4-kinase\_(pi4kb)\_mrna,\_complete\_cds  
 x54199mrna\_2616-3006:in\_reversesequence,\_3118,mrna\_for\_gars-airs-gart  
 x55448exon#13\_150-670,\_g6pd\_gene\_(glucose-6-  
 phosphate\_dehydrogenase)\_extracted\_fromg6pd\_gene\_for\_glu  
 x55544cds\_350-626:in\_reversesequence,\_984-1110,cdna\_for\_treb\_protein  
 x55885mrna\_587-1049,mrna\_for\_a\_presumptive\_kdel\_receptor\_  
 x58521cds\_1250-1544:in\_reversesequence,\_1701-1785,mrna\_for\_p62\_nucleoporin  
 x66397cds\_6605-6977:in\_reversesequence,\_7352-7442,tpr\_mrna  
 all\_x66503\_1125-1690,adenylosuccinate\_synthetase\_mrna  
 all\_x78925\_1966-2447,hzf2\_mrna\_for\_zinc\_finger\_protein\_  
 x90872cds\_288-600:in\_reversesequence,\_799,mrna\_for\_gp25l2\_protein\_  
 z49107cds\_619-947:in\_reversesequence,\_1046-1259,mrna\_for\_galectin\_  
 z54367cds\_13580-14031:in\_reversesequence,\_14140,gene\_for\_plectin  
 z97054cds#2\_428-  
 968,dna\_sequence\_from\_pac\_339a18\_on\_chromosome\_xp11.2contains\_kiaa0178\_gene,\_si  
 milar

Metagene 58

x02544cds\_256-544:in\_reversesequence,\_688-772,mrna\_for\_alpha1-  
 acid\_glycoprotein\_(orosomucoid)\_  
 all\_x78932\_421-976,hzf9\_mrna\_for\_zinc\_finger\_protein\_

# PATENT COOPERATION TREATY

# PCT

## DECLARATION OF NON-ESTABLISHMENT OF INTERNATIONAL SEARCH REPORT

(PCT Article 17(2)(a) and Rule 39)


Applicant's or agent's file reference 5251.01	<b>IMPORTANT DECLARATION</b>	Date of mailing (day/month/year) 15. 07. 2003
International application No. PCT/US02/038216	International filing date (day/month/year) 12-11-2002	(Earliest) Priority Date (day/month/year) ---
International Patent Classification (IPC) or both national classification and IPC G06N 3/12		
Applicant DUKE UNIVERSITY		

This International Searching Authority hereby declares, according to Article 17(2)(a), that **no international search report will be established** on the international application for the reasons indicated below.

1. ☒ The subject matter of the international application relates to:
  - a. ☐ scientific theories.
  - b. ☒ mathematical theories.
  - c. ☐ plant varieties.
  - d. ☐ animal varieties.
  - e. ☐ essentially biological processes for the production of plants and animals, other than microbiological processes and the products of such processes.
  - f. ☐ schemes, rules or methods of doing business.
  - g. ☐ schemes, rules or methods of performing purely mental acts.
  - h. ☐ schemes, rules or methods of playing games.
  - i. ☐ methods for treatment of the human body by surgery or therapy.
  - j. ☐ methods for treatment of the animal body by surgery or therapy.
  - k. ☐ diagnostic methods practised on the human or animal body.
  - l. ☐ mere presentations of information.
  - m. ☐ computer programs for which this International Searching Authority is not equipped to search prior art.
2. ☐ The failure of the following parts of the international application to comply with prescribed requirements prevents a meaningful search from being carried out:
 

☐ the description
 ☐ the claims
 ☐ the drawings
3. ☐ The failure of the nucleotide and/or amino acid sequence listing to comply with the prescribed requirements prevents a meaningful search from being carried out:
 

☐ it does not comply with the prescribed standard  
☐ it is not in the prescribed machine readable form
4. Further comments:  
see extra sheet

Name and mailing address of the International Searching Authority  European Patent Office, P.B. 5818 Patentlaan 2 NL-2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Authorized officer Anders Edlund /LR  Telephone no. 08-450 3674
--	--

The claims relate to subject matter for which no search is required according to Rule 39 PCT. Given that the claims are formulated in terms of such subject matter or merely specify commonplace features relating to its technological implementation, the search examiner could not establish any technical problem which might potentially have required an inventive step to overcome. Hence it was not possible to carry out a meaningful search into the state of the art (Art. 17(2)(a)(i) and (ii) PCT; see EPO Guidelines Part B Chapter VIII, 1-6).

The applicant's attention is drawn to the fact that claims relating to inventions in respect of which no international search report has been established need not be subject of an international preliminary examination (Rule 66.1 (e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following the receipt of the search report or during any Chapter II procedure. If the application proceeds into the regional phase before the EPO, the applicant is reminded that a search may be carried out during examination of the EPO (see EPO Guideline C-VI, 8.5), should the problems which led to the Article 17(2) declaration be overcome.